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Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-JAN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sus scrofa Prkag3
Pig AMPK amna sub
Pig AMPK amna sub
Pig wild-type PRKA
Pig PRKAG3 polymor
Pig PRKAG3 polymor
Pig PRKAG3 polymor
Human AMPK gamma s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human AMPK gamma s
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                                                                                                                 (without alignments)
827.023 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     **SIDSZ/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:**
SIDSZ/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:**
SIDSZ/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:**
SIDSZ/gcgdata/geneseq/geneseqp-embl/AA1983.DAT:**
SIDSZ/gcgdata/geneseq/geneseqp-embl/AA1984.DAT:**
SIDSZ/gcgdata/geneseq/geneseqp-embl/AA1986.DAT:**
SIDSZ/gcgdata/geneseq/geneseqp-embl/AA1986.DAT:**
SIDSZ/gcgdata/geneseq/geneseqp-embl/AA1986.DAT:**
SIDSZ/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:**
SIDSZ/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:**
SIDSZ/gcgdata/geneseq/geneseqp-embl/AA1991.DAT:**
SIDSZ/gcgdata/geneseq/geneseqp-embl/AA1991.DAT:**
SIDSZ/gcgdata/geneseq/geneseqp-embl/AA1991.DAT:**
SIDSZ/gcgdata/geneseq/geneseqp-embl/AA1993.DAT:**
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /SIDS2/gcgdata/qeneseg/genesegp-embl/AA1997.DAT:*/SIDS2/gcgdata/qeneseg/genesegp-embl/AA1998.DAT:*
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                                                                                                                                                                 US-09-826-581-6
2538
1 MEPGLEHALRRTPSWSSLGG......LSDILQALVLSPAGIDALGA
                                                                                               6, 2003, 10:55:08; Search time 78.7881 Seconds
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                    908470 seqs, 133250620 residues
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Maximum Match 100%
Listing first 45 summaries
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AAE00224
AAE22985
AAE22984
AAE22984
AAE22986
AAE22986
                                                               OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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length: 2000000000
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Perfect score:
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Maximum DB 9
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ALIGNMENTS

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11-SEP-2000; 2000WO-EP09896
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This sequence is encoded by the full length cDNA encoding the human AMP-activated protein kinase gamma 3 subunit (PRKAG3). Detecting the presence of the PRKAG3 DNA, or a variant, is useful in determining a risk estimate of a metabolic disease, such as diabetes or obesity, in a subject. The variation may occur in exons 3, 4 or 10. In exon 3 variation may be a substitution of a G for a C at nucleotide 320, resulting in the amino acid substitution PD1A; in exon 4 variation may be a substitution of a T for a C at nucleotide 550; and in exon 10 variation may be a substitution of a T for a C at nucleotide 1037, resulting in the amino acid substitution R340W. There may also be nucleotide variation in intron 6. The numbering of these variations is based on the full length cDNA, rather than on position 1 of the open reading frame.
                                                                                                                                                                                                                                                                                                                                                                                  0;
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                                                                                                                                                                                                                                                                                                                                                                                                            1 MEPGLEHALRRTPSWSSLGGSEHQEMSFLEQENSSSWPSPAVTSSSERIRGKRRAKALRW 60
                                                                                                                                                                                                                                                                                                                                                                                                                            1 MEPGLEHALRRTPSWSSLGGSEHQEMSFLEQENSSSWPSPAVTSSSERIRGKRRAKALRW 60
                                  New variants of human AMP-activated protein kinase gamma3 subunit associated with a metabolic disease e.g. diabetes or obesity and method for determining a risk estimate of diseases in subject by detecting the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 2538; DB 22; Length 489; 100.0%; Pred. No. 7.3e-254; ive 0; Mismatches 0; Indels 0;
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                                                                                                      Disclosure; Fig 5; 25pp; English.
                                                                                                                                                                                                                                                                                                                                                                               489; Conservative
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       N-PSDB; AAH43685
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Human; gamma subunit; adenosine monophosphate-activated kinase; AMPK; strKAG3; diabetes; obesity; myopathy; cardiovascular disease; anorectic; genetic testing; carbohydrate metabolism disorder; skeletal muscle; cystathione beta synthase; CBS; cardiant; gene therapy.
                                              Human AMPK gamma subunit muscle-specific isoform, complete PRKAG3.
                                                                                                                                                                                                                                                                                                                                                                                               253..307
/label= CBS
/note= "Cystathione beta synthase domain"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           domain"
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/note= "Cystathione beta synthase domain"
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/note= "Cystathione beta synthase
                                                                                                                                                                                                                                                                                                                                                                           /note= "RN- mutation site"
                                                                                                                                                                                                                                                         Location/Qualifiers
172..225
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/label= CBS
(first entry)
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                                                                                                                                                                                                               Homo sapiens.
  13-JUN-2001
                                                                                                                                                                                                                                                              Key
Domain
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18-MAY-2000; 2000EP-0401388. 99EP-0402236 10-SEP-1999;

(INRG) INRA INST NAT RECH AGRONOMIQUE. (ANDE/) ANDERSSON L. LOOFT C. (KALM/) KALM E. LOOF/)

Rogel-Gaillard C; Kalm E, Milan D, Robic A, J, Le Roy P, Chardon P; Looft C, Gellin ; Iannuccelli N, Andersson L,

WPI; 2001-244810/25. N-PSDB; AAD03320. New variants of the gamma subunit of vertebrate adenosine monophosphate-activated kinase for diagnosis or treatment of disorders associated with energy metabolism such as diabetes, obesity, and myopathy

Claim 5; Fig 3; 71pp; English.

The present sequence is human adenosine monophosphate (AMPY) acquired kinese (AMPK) gamma subunit muscle-specific isoform, complete PRRAG3. Mutation in Prkag3 results in an altered regulation of carbohydrate metabolism, particularly in skeletal muscle. PRRAG3 is useful as therapeutic for treating carbohydrate metabolism disorders associated with muscle metabolism such as myopathy and disorders associated with muscle metabolism activity, and for restoring a normal AMPK function. PRRAG3 sequence and its functionally altered mutants are useful for the diagnostic evaluation, genetic testing and prognosis of a metabolic disorder, preferably a carbohydrate metabolism disorder. Primers that can detect useful for defecting a dysfunction of carbohydrate metabolism resulting from the expression of a functionally altered allele of PRKAG3.

Transgenic animal and host cell transformed with PRKAG3 or a heterotrimeric AMPK consisting of PRKAG3 or its mutant, are useful for screening compounds able to modulate ARCH activity. Nucleic acid encoding PRKAG3 is useful for detecting mutations in a Prkag3 gene, or in a sequence encoding the first cystathione beta synthase (CBS) domain a genetic polymorphic marker linked to a sequence encoding PRKAG3,

us-09-826-581-6.rag

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220 VANGVRAAPLWDSKKQSFVGMLTITDFILVLHRYYRSPLVQIYEIEQHKIETWREIYLQG 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     280 CFKPLVSISPNDSLFEAVYTLIKNRIHRLPVLDPVSGNVLHILTHKRLLKFLHIFGSLLP 339
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                                                                                                                                              ECELEGILEERPALCLSPQAPFPKLGWDDELRKPGAQIYMRFMQEHTCYDAMATSSKLVI 205
                                                                                                                                                      FDTMLEIKKAFFALVANGVRAAPLWDSKKQSFVGMLTITDFILVLHRYYRSPLVQIYEIE 265
                                                                                                                                                                                                                   QHKIETWREIYLQGCFKPLVSISPNDSLFEAVYTLIKNRIHRLPVLDPVSGNVLHILTHK 325
                                                                                                                                                                                                                             RLLKFLHIFGSLLPRPSFLYRTIQDLGIGTFRDLAVVLETAPILTALDIFVDRRVSALPV 385
                                                                                                                                                                                                                                                                VNECGQVVGLYSRFDVIHLAAQQTYNHI,DMSVGEAL,RQRTLCLEGVLSCQPHESLGEVID 445
                                                                                                                                                                                                                                                                                                     9
                                                                      MSFLEQENSSSWPSPAVTSSSERIRGKRRAKALRWTRQKSVEEGEPPGQGEGPRSRPAAE 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pig. gamma subunit; adenosine monophosphate-activated kinase; AMPK; PRK63; diabetes, obbsity; myopathy; cardiovascular disease; anorectic; genetic testing; carbohydrate metabolism disorder; skeletal muscle; cystathione beta synthase; CBS; cardiant; gene therapy.
                                                                                                                                                                                          MSFLEQENSSSWPSPAVTSSSERIRGKRRAKALRWTRQKSVEEGEPPGQGEGPRSRPTAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rogel-Gaillard C;
                                                       Gaps
                                                     ·;
                                     Length 464;
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                                     DB 22;
                                   Score 2398; DB 22;
Pred. No. 2.2e-239;
0; Mismatches 1;
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and is useful in gene therapy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Sus scrofa Prkag3 splice variant.
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                                   94.5%;
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2000EP-0401388
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                                                    463; Conservative
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LOOFT C.
                                            Similarity
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(ANDE/) ANDERSSON
                   464 AA;
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18-MAY-2000;
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of PRKAG3
                  Sequence
                                   Query Match
Best Local 9
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(KALM/)
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The present sequence is pig adenosine monophosphate (AMP)-activated kinase (AMPK) gamma subunit muscle-specific isoform, PRKAG3 splice variant. PrkAG3 gene is located in the RN locus of chromosome 15.

Wutation in PrkAG3 gene is located in the RN locus of chromosome 15.

Mutation in PrkAG3 results in an altered regulation of carbohydrate metabolism, particularly in skeletal muscle. PRKAG3 is useful as therapeutic for treating carbohydrate metabolism disorders such as diabetes, obesity, and disorders associated with muscle metabolism such as myopathy and cardiovascular diseases, to modulate AMPK activity, and for restoring a normal AMPK function. PRKAG3 sequence and its functionally altered mutants are useful for the diagnostic evaluation, genetic testing and prognosis of a metabolic disorder. Preferably a carbohydrate metabolism disorder. Primers that can detect a genetic polymorphic marker linked to a sequence encoding PRKAG3, are useful for detecting a dysfunction of carbohydrate metabolism resulting from the expression of a functionally altered with PRKAG3 or a function and some content of the present of the pr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   160 CLSPQAPFPKLGWDDELRKPGAQIYMRFMQEHTCYDAMATSSKLVIFDTMLEIKKAFFAL 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            heterotrimeric AMPK consisting of PRRAG3 or its mutant, are useful for screening compounds able to modulate AMPK activity. Nucleic acid encoding PRRAG3 is useful for detecting mutations in a Prkag3 gene, or in a sequence encoding the first cystathione beta synthase (CBS) domain of PRRAG3 and is useful in gene therapy.
                                                                                                                                                                                                                                                    New variants of the gamma subunit of vertebrate adenosine monophosphate-activated kinase for diagnosis or treatment of disorders associated with energy metabolism such as diabetes, obesity, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6 LEQALRRVPGSRGGWELEQLRPEGRGPTTADTPSWSSLGGPKHQEMSFLEQGESRSWPSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----TPSWSSLGGSEHQEMSFLEQENSSSWPSP
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Pred. No. 7.5e-207;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                46;
     å
          Chardon
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82.0%;
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Gellin J,
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Matches 418; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5; Page 70-71;
                                                                                               WPI; 2001-244810/25.
N-PSDB; AAD03321.
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Lannuccelli N,
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204
                                                                                                                                265 EQHKIETWREIYLQGCFKPLVSISPNDSLFEAVYTLIKNRIHRLPVLDPVSGNVLHILTH 324
                                                                                                                                                                                                   384
                                                                                                                                                                                                                                                                   385 VVNECGQVVGLYSRFDVIHLAAQQTYNHLDMSVGEALRQRTLCLEGVLSCQPHESLGEVI 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pig; gamma subunit; adenosine monophosphate-activated kinase; AMPK; PRKAG3; diabetes; obesity; myopathy; cardiovascular disease; anorectic; genetic testing; carbihydrate metabolism disorder; skeletal muscle; cystathione beta synthase; CBS; cardiant; gene therapy; RN locus; chromosome 15.
 145 WECELEGILIEERPALCLSPQAPFPXLGWDDELRKPGAQIYMRFWQEHTCYDAMATSSKLV
                   205 IFDTMLEIKKAFFALVANGVRAAPLWDSKKQSFVGMLTITDFILVLHRYYRSPLVQIYEI
                                                                                  Pig AMPK gamma subunit muscle-specific isoform, complete PRKAG3.
                                                                                                                                                                                                                                                                                                                                    445 DRIAREQVHRLVLVDETQHLLGVVSLSDILQALVLSPAGIDALGA 489
                                                                                                                                                                                                                                                                                                                                                     172..225
/label= CBS
/note= "Cystathione beta synthase domain"
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/note= "Cystathione beta synthase domain"
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/note= "Cystathione beta synthase domain"
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/note= "Cystathione beta synthase domain"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAE00222 standard; Protein; 464
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
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LOOFT C.
KALM E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10-SEP-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sus scrofa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (ANDE/) A
(LOOF/) L
(KALM/) K
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26 MSFLEQENSSSWPSPAVTSSSERIRGKRRAKALRWTRQKSVEEGEPPGQGEGPRSRPAAE 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Screening animals to determine those likely to produce larger litters and improved meat quality traits involves assaying for the presence of polymorphisms in the AMP activated protein kinase regulatory gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a method for screening animals to determine those more likely to produce large litters and improved meat quality traits. The method involves assaying for the presence of a genotype in the sample of genetic material obtained from animal. The genotype is characterised by polymorphism(s) in the AMP activated protein kinase regulatory gamma subunit (PRRAG3) gene. The method is used for screening animals e.g., pigs to determine those most likely to exhibit improved meat quality traits and to produce larger litters. The present sequence is pig PRRAG3 polymorphic variant (PRRAG3-30).
                                                                                                                                                                                                                                   AMP activated protein kinase regulatory gamma subunit; PRKAG3 gene; screening; meat quality; single nucleotide polymorphism; SNP; pig;
                                                                                                                                                                                                                                                                                                                                                                   /note= "Wild type Asn is substituted with Thr due to single nucleotide polymorphism (SNP)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 464;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               44;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              79.3%; Score 2013; DB 23;
86.0%; Pred. No. 1.9e-199;
19; Mismatches
                                                                                                                                                                                                   Pig PRKAG3 polymorphic variant (PRKAG3-30).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 91-93; 109pp; English.
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                                                                                                AAE22985 standard; Protein; 464
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08-JAN-2001; 2001US-260239P. 
18-JUN-2001; 2001US-299111P.
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                                                                                                                                                                09-AUG-2002 (first entry)
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Best Local Similarity
Matches 400; Conserv
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                                                                                                                                                                                                                                                                                                                                                    Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                444
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KRLLKFLHIFGSLLPRPSFLYRTIQDLGIGTFRDLAVVLETAPILTALDIFVDRRVSALP 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VVNETGQVVGLYSRFDVIHLAAQQTYNHLDMNVGEALRQRTLCLEGVLSCQPHETLGEVI 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EQHKIETWREIYLQGCFKPLVSISPNDSLFEAVYTLIKNRIHRLPVLDPVSGNVLHILTH 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence is pig adenosine monophosphate (AMPF) activated kinase (AMPK) gamma subunit muscle-specific isoform, complete PRKAG3. Prekag3 gene is located in the RN locus of Ghromosome 15. Mutation in Prkag3 results in an altered regulation of carbohydrate metabolism, particularly in skeletal muscle. PRKAG3 is useful as therapeutic for treating carbohydrate metabolism disorders such as
                                                                                                                                                                                                                                                                                                                                                                            heterotrimeric AMPK consisting of PRKAG3 or its mutant, are useful for screening compounds able to modulate AMPK activity. Nucleic acid encoding PRKAG3 is useful for detecting mutations in a Prkag3 gene, or in a sequence encoding the first cystathione beta synthase (CBS) domain of PRKAG3 and is useful in gene therapy.
                                                                                                                                                                                                                                                                                                                                         for detecting a dysfunction of carbohydrate metabolism resulting
                                                                          New variants of the gamma subunit of vertebrate adenosine monophosphate-activated kinase for diagnosis or treatment of disorders associated with energy metabolism such as diabetes, obesity, and
                                                                                                                                                                                                                                                                                                evaluation, genetic testing and prognosis of a metabolic disorder, preferably a carbohydrate metabolism disorder. Primers that can detect a genetic polymorphic marker linked to a sequence encoding PRRAG3, are
 Rogel-Gaillard C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MSFLEQENSSSWPSPAVTSSSERIRGKRRAKALRWTRQKSVEEGEPPGQGEGPRSRPAAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STGLEATFPKTTPLAQADP-AGVGTPPTGWDC1.PSDCTASAAGSSTDDVELATEFPATEA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VVNECGQVVGLYSRFDVIHLAAQQTYNHLDMSVGEALRQRTLCLEGVLSCQPHESLGEVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                              diabetes, obesity, and disorders associated with muscle metabolism such as myopathy and cardiovascular diseases, to modulate AMPK activity, and for restoring a normal AMPK function. PRRAGS sequence and its functionally altered mutants are useful for the diagnostic
                                                                                                                                                                                                                                                                                                                                                     from the expression of a functionally altered allele of PRKAG3.
Transgenic animal and host cell transformed with PRKAG3 or a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 464;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DRIAREQVHRLVLVDETQHLLGVVSLSDILQALVLSPAGIDALGA 489
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Milan D, Robic A,
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86.0%; Pred. No. 3e-1
live 19; Mismatches
             Le Roy P,
 Kalm E,
                                                                                                                                           Claim 5; Fig 3; 71pp; English.
             Gellin J,
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 Looft C,
                                     2001-244810/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
ses 400; Conserv
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                                                   N-PSDB; AAD03319.
            Iannuccelli N,
 Andersson L,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Screening animals to determine those likely to produce larger litters and improved meat quality traits involves assaying for the presence of polymorphisms in the AMP activated protein kinase regulatory gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MSFLEQENSSSWPSPAVTSSSERIRGKRRAKALRWTRQKSVEEGEPPGQGEGPRSRPAAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a method for screening animals to determine those more likely to produce large litters and improved meat quality traits. The method involves assaying for the presence of a genotype in the sample of genetic material obtained from animal. The genotype is characterised by polymorphism(s) in the AMP activated protein scharacterised by polymorphism(s) in the AMP activated protein kinase regulatory gamma subunit (PRKAG3) gene. The method is used for screening animals e.g., pigs to determine those most likely to exhibit improved meat quality traits and to produce larger likely to The present sequence is pig wild-type PRKAG3 protein.
                                                                                                                                                                                                                                                                                                                                                                                          /note= "Wild type Asn is replaced with Thr during single nucleotide polymorphism (SNP)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Val is replaced with Ile during polymorphism (SNP)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Wild type Arg is replaced with Gln during nucleotide polymorphism (SNP)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5;
                                                                                                                                                                                                       AMP activated protein kinase regulatory gamma subunit, PRKAG3 screening; meat quality; single nucleotide polymorphism; SNP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 464;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "Wild type Gly is replaced with :
single nucleotide polymorphism (SNP)"
199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Malek M, Plastow G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 2011; DB 23;
Pred. No. 3e-199;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
AAE22984 standard; Protein; 464 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "Wild type
single nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19;
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                                                                                                                                                       Pig wild-type PRKAG3 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 79.2%;
86.0%;
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18-JUN-2001; 2001US-299111P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10-SEP-2001; 2001WO-US28283
                                                                                                   (first entry)
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N-PSDB; AAD36456.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08-SEP-2000;
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                                                                                                   09-AUG-2002
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                                                                                                                                                                                                                                                                                        sus scrofa.
                                                   AAE22984;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VVNECGQVVGLYSRFDVIHLAAQQTYNHLDMSVGEALRQRTLCLEGVLSCQPHESLGEVI 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EQHKIETWREIYLQGCFKPLVSISPNDSLFEAVYTLIKNRIHRLPVLDPVSGNVLHILTH 324
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26 MSFLEQENSSWPSPAVTSSSERIRGKRRAKALRWTRQKSVEEGEPPCQGEGPRSRPAAE
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                                                                                 The invention relates to a method for screening animals to determine those more likely to produce large litters and improved meat quality traits. The method involves assaying for the presence of a genotype in the sample of genetic material obtained from animal. The genotype is characterised by polymorphism(s) in the AMP activated protein kinase regulatory gamma subunit (PRRAG3) gene. The method is used for screening animals e.g., pigs to determine those most likely to exhibit improved meat quality traits and to produce larger litters. The present sequence is pig PRRAG3 polymorphic variant (PRRAG3-199).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 464;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              79.2%; Score 2010; DB 23;
85.8%; Pred. No. 3.8e-199;
ive 20; Mismatches 44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pig PRKAG3 polymorphic variant (PRKAG3-200).
Disclosure; Page 100-102; 109pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 85.8 nes 399; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            464 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        KRLLKFLHIFGSLLPRPSFLYRTIQDLGIGTFRDLAVVLETAPILTALDIFVDRRVSALP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          385 VVNECGQVVGLYSRFDVIHLAAQQTYNHLDMSVGEALRQRTLCLEGVLSCQPHESLGEVI
                                 STGLEATFPKTTPLAQADP-AGYGTPPTGWDCLPSDCTASAAGSSTDDVELATEFPATEA
                                                                                                                                                                                                                       WECELEGLLEERPALCLSPQAPFPKLGWDDELRKPGAQIYMRFMQEHTCYDAMAISSKLV
                                                                                                                                                                                                                                                                                                                                                                                                        IFDTMLEIKKAFFALVANGVRAAPLWDSKKQSFVGMLTITDFILVLHRYYRSPLVQIYEI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           due
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single nucleotide polymorphism (SNP)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Malek M, Plastow G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pig PRKAG3 polymorphic variant (PRKAG3-199).
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2001US-260239P.
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N-PSDB; AAD36459.
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08-JAN-2001;
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pig;

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STGLEATFPKTTPLAQADP-AGVGTPPTGWDCLPSDCTASAAGSSTDDVELATEFPATEA 144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                145 WECELEGLLEERPALCLSPQAPFPKLGWDDELRKPGAQIYMRFMQEHTCYDAMATSSKLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26 MSFLEQENSSSWPSPAVTSSSERIRGKRRAKALRWTRQKSVEEGEPPGQGEGPRSRPAAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a method for screening animals to determine those more likely to produce large litters and improved meat quality traits. The method involves assaying for the presence of a genotype in the sample of genetic material obtained from animal. The genotype is characterised by polymorphism(s) in the AMP activated protein kinase regulatory gamma subunit (PRKAG3) gene. The method is used for screening animals e.g., pigs to determine those most likely to exhibit improved meat quality traits and to produce larger litters. The present sequence is pig PRKAG3 polymorphic variant (PRKAG3-52).
                                                                                                                                                                                                                                                                                                                   /note= "Wild type Gly is substituted with Ser due to single nucleotide polymorphism (SNP)"
                                                                                                                                                          AMP activated protein kinase regulatory gamma subunit; PRKAG3 screening; meat quality; single nucleotide polymorphism; SNP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         79.0%; Score 2005; DB 23; Length 464; 85.8%; Pred. No. 1.3e-198; Live 19; Mismatches 45; Indels 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Plastow G;
                                                                                                                     Pig PRKAG3 polymorphic variant (PRKAG3-52).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Malek M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (IOWA ) UNIV IOWA STATE RES FOUND INC
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    Ä.
AAE22986 standard; Protein; 464
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                                                                                                                                                                                                                                                                                Key
Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rothschild MF,
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                                                                              09-AUG-2002
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                                                                                                                                                                                                                                        Sus scrofa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Sim
Matches 399;
                                         AAE22986;
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                                                                                                                                                                                                   variant.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             385 VVNECGQVVGLYSRFDVIHLAAQQTYNHLDMSVGEALRQRTLCLEGVLSCQPHESLGEVI 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STGLEATFPKTTPLAQADP-AGVGTPPTGWDCLPSDCTASAAGSSTDDVELATEFPATEA 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               180 IFDTMLEIKKAFFALVANGVQAAPLWDSKKQSFVGMLTITDFILVLHRYYRSPLVQIYEI 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KRLLKFLHIFGSLLPRPSFLYRTIQDLGIGTFRDLAVVLETAPILTALDIFVDRRVSALP 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09
                                                                                                                                                                                                                                                                                              Screening animals to determine those likely to produce larger litters and improved meat quality traits involves assaying for the presence of polymorphisms in the AMP activated protein kinase regulatory gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26 MSFLEQENSSSWPSPAVTSSSERIRGKRRAKALRWTRQKSVEEGEPPGQGEGPRSRPAAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            145 WECELEGLLEERPALCLSPQAPFPKLGWDDELRKPGAQIYMRFMQEHTCYDAMATSSKLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EQHKIETWREIYLQGCFKPLVSISPNDSLFEAVYTLIKNRIHRLPVLDPVSGNVLHILTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          205 IPDTMLEIKKAFFALVANGVRAAPLWDSKKQSFVGMLTITDFILVLHRYYRSPLVQIYEI
                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a method for screening animals to determine those more likely to produce large litters and improved meat quality traits. The method involves assaying for the presence of a genotype in the sample of genetic material obtained from animal. The genotype is characterised by polymorphism(s) in the AMP activated protein Kinase requiatory gamma subunit (PRKAG3) gene. The method is used for screening animals e.g., pigs to determine those most likely to exhibit improved meat quality traits and to produce larger litters. The present sequence is pig PRKAG3 polymorphic variant (PRKAG3-200).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         79.1%; Score 2007; DB 23; Length 464; 85.8%; Pred. No. 7.8e-199;
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                                                                                                                                                                                                 Plastow G;
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                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 105-107; 109pp; English.
                                                                                                                                                                                                 Malek M,
                                                                                                                                                        (IOWA ) UNIV IOWA STATE RES FOUND INC.
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                                                                                            2001US-260239P.
2001US-299111P.
                                                                            2000US-231045P
                                                                                                                                                                                                 DC,
                                   10-SEP-2001; 2001WO-US28283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1) Similarity 85.8 399; Conservative
                                                                                                                                                                                                                                  WPI; 2002-393850/42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    464 AA;
                                                                                                                                                                                                                                                         N-PSDB; AAD36460
                                                                                                                                                                                             Rothschild MF,
                                                                                                08-JAN-2001;
18-JUN-2001;
                                                                            08-SEP-2000;
14-MAR-2002
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Local Matches

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205 IFDTMLEIKKAFFALVANGVRAAPLWDSKKQSFVGMLTITDFILVLHRYYRSPLVQIYEI 264

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61 DFILVLHRYYRSPLVQIYEIEQHKIETWREIYLQGCFKPLVSISPND5LFEAVYTLIKNR 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       425 TLCLEGVLSCQPHESLGEVIDRIAREQVHRLVLVDETQHLLGVVSLSDILQALVLSPAGI 484
evaluation, genetic testing and prognosis of a metabolic disorder, preferably a carbohydrate metabolism disorder. Primers that can detect a genetic polymorphic marker linked to a sequence encoding PRRAG3, are useful for detecting a dysfunction of carbohydrate metabolism resulting from the expression of a functionally altered allele of PRKAG3. Transgenic animal and host cell transformed with PRKAG3 or a heterotrimeric AMPK consisting of PRKAG3 or its mutant, are useful for screening compounds able to modulate AMPK activity. Nucleic acid encoding PRKAG3 is useful for detecting mutations in a PrKag3 gene, or in a sequence encoding the first cystathione beta synthase (CBS) domain of PRKAG3 and is useful in gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; gamma subunit; adenosine monophosphate-activated kinase; AMPK; prekKA3; diabetes, obesity; myopathy; cardiovascular disease; anorectic; genetic testing; carbohydrate metabolism disorder; skeletal muscle; cystathione beta synthase; CBS; cardiant; gene therapy; mutant; mutein;
                                                                                                                                                                                                                                                                                             185 MRFMQEHTCYDAMATSSKLVIFDTMLEIKKAFFALVANGVRAAPLWDSKKQSFVGMLTIT
                                                                                                                                                                                                                                                                                                               DFILVLHRYYRSPLVQIYEIEQHKIETWREIYLQGCFKPLVSISPNDSLFEAVYTLIKNR
                                                                                                                                                                                                                                                                                                                                                                                                                       IHRLPVLDPVSGNVLHILTHKRLLKFLHIFGSLLPRPSFLYRTIQDLGIGTFRDLAVVLE
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                                                                                                                                                                                                                             61.1%; Score 1551; DB 22;
100.0%; Pred. No. 7.7e-152;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAE00329 standard; Protein; 305 AA.
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18-MAY-2000; 2000EP-0401388.
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                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                            Best Local Similarity
Matches 305; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DALGA 305
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Misc-difference 40
                                                                                                                                                                                                305 AA;
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                                                                                  299
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                                                                                                                KRLLKFLHIFGSLLPRPSFLYRTIQDLGIGTFRDLAVVLETAPILTALDIFVDRRVSALP 384
                                                                                                                                                                              VVNECGQVVGLYSRFDVIHLAAQQTYNHLDMSVGEALRQRTLCLEGVLSCQPHESLGEVI 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRKAG3; diabetes; obesity; myopathy; cardiovascular disease; anorectic; genetic testing; carbohydrate metabolism disorder; skeletal muscle; cystathione beta synthase; CBS; cardiant; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New variants of the gamma subunit of vertebrate adenosine monophosphate-activated kinase for diagnosis or treatment of disorders associated with energy metabolism such as diabetes, obesity, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ooft C, Kalm E, Milan D, Robic A, Rogel-Gaillard C; Gellin J, Le Roy P, Chardon P;
   The present sequence is human adenosine monophosphate (AMP)-activated kinase (AMPK) gamma subunit muscle-specific isoform, PRKAG3. Mutation in Prkag3 results in an altered regulation of carbobhydrate metabolism, particularly in skeletal muscle. PRKAG3 is useful as therapeutic for treating carbohydrate metabolism disorders as diabetes, obesity, and disorders associated with muscle metabolism such as myopathy and cardiovascular diseases, to modulate AMPK activity, and for restoring a normal AMPK function. PRKAG3 sequence and its functionally altered mutants are useful for the diagnostic
                                                                                                                                 EQHKIETWREIYLQGCFKPLVSISPNDSLFEAVYTLIKNRIHRLPVLDPVSGNVLHILTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; gamma subunit; adenosine monophosphate-activated kinase; AMPK;
                                                                                                                                                                                                                                            DRIAREQVHRLVLVDETQHLLGVVSLSDILQALVLSPAGIDALGA 489
                                                                                                                                                                                                                                                             Human AMPK gamma subunit muscle-specific isoform, PRKAG3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 4; Page 55-57; 71pp; English.
                                                                                                                                                                                                                                                                                                                                                           AA.
                                                                                                                                                                                                                                                                                                                                                       AAE00221 standard; Protein; 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11-SEP-2000; 2000WO-EP09896.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99EP-0402236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-MAY-2000; 2000EP-0401388
                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200120003-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Iannuccelli N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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Length 305;

(INRG)

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Note: The present sequence is not shown in the specification, but is derived from the human Prkag3 sequence SEQ.ID.NO.4 shown in page 57-58 of sequence listing (AAE00221).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 185 MRFWQEHTCYDAMATSSKLVIFDTMLEIKKAFFALVANGVRAAPLWDSKKQSFVGMLTIT 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  245 DFILVLHRYYRSPLVQIYEIEQHKIETWREIYLQGCFKPLVSISPNDSLFEAVYTLIKNR 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DFILVLHRYYRSPLVQIYEIEQHKIETWREIYLQGCFKPLVSISPNDSLFEAVYTLIKNR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IHRLPVLDPVSGNVLHILTHKRLLKFLHIFGSLLPRPSFLYRTIQDLGIGTFRDLAVVLE 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TAPILTALDIFVDRRVSALPVVNECGQVVGLYSRFDVIHLAAQQTYNHLDMSVGEALRQR 424
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MRFMQEHTCYDAMATSSKLVIFDTMLEIKKAFFALVANGIRAAPLWDSKKQSFVGMLTIT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        evaluation, genetic testing and prognosis of a metabolic disorder, preferably a carbohydrate metabolism disorder. Primers that can detect a genetic polymorphic marker linked to a sequence encoding PRKAG3, are useful for detecting a dysfunction of carbohydrate metabolism resulting from the expression of a functionally altered allele of PRKAG3.
                                                                                                                                                                       New variants of the gamma subunit of vertebrate adenosine monophosphate-activated kinase for diagnosis or treatment of disorders associated with energy metabolism such as diabetes, obesity, and
                                                                                                                                                                                                                                                                                              The present sequence is a V40I mutant of human muscle-specific isoform of gamma subunit of adenosine monophosphate (AMP)-activated kinase (AMPK) Prkag3. This mutant sequence results in decreased glycogen content in human skeletal muscle.
                                                                                     Rogel-Gaillard C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                 Mutation in Prkag3 results in an altered regulation of carbohydrate metabolism, particularly in skeletal muscle. PRKAG3 is useful as therapeutic for treating carbohydrate metabolism disorders such as
                                                                                                                                                                                                                                                                                                                                                                                                                    diabetes, obesity, and disorders associated with muscle metabolism such as myopthy and cardiovascular diseases, to modulate AMPK activity, and for restoring a normal AMPK function. PRKAG3 sequence and its functionally altered mutants are useful for the diagnostic
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                                                                                     Robic A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61.1%; Score 1550; DB 22; 99.7%; Pred. No. 9.8e-152; ive 1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                     n D, Robic
Chardon P;
NAT RECH AGRONOMIQUE.
L.
                                                                                     Milan
                                                                                                       Le Roy P,
                                                                                                                                                                                                                                                               Disclosure; Page -; 71pp; English.
                                                                                     Kalm E,
                                                                                                       Gellin J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            304; Conservative
                                                                                     Looft C,
                                                                                                                                      WPI; 2001-244810/25.
INRA INST A
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Best Local Similarity
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                                LOOFT C.
                                                                                                    Iannuccelli N,
                                                   (KALM/) KALM E.
                                                                                     Andersson L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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                                                                                                                                                                                                                                myopathy
                (ANDE/)
                                  LOOF/)
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Transgenic animal and host cell transformed with PRKAG3 or a heterotrimeric AMPK consisting of PRKAG3 or its mutant, are useful for screening compounds able to modulate AMPK activity. Nucleic acid encoding PRKAG3 is useful for detecting mutations in a Prkag3 gene, or in a sequence encoding the first cystathione beta synthase (CBS) domain of PRKAG3 and is useful in gene therapy.

Note: The present sequence is not shown in the specification, but
                                                                                                                                                                                                                                                                                                                                                                               Human: gamma subunit; adenosine monophosphate-activated kinase; AMPK; PRKAG3; diabetes; Obesity; myopathy; cardiovascular disease; anorectic; genetic testing; carbohydrate metabolism disorder; skeletal muscle; cystathione beta synthase; CBS; cardiant; gene therapy; mutant; mutein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mutation in Prizag results in an altered regulation of carbohydrate metabolism, particularly in skeletal muscle. PRKAG3 is useful as therapeutic for treating carbohydrate metabolism disorders such as diabetes, obesity, and disorders associated with muscle metabolism such as myopathy and cardiovascular diseases, to modulate AMPK activity, and for restoring a normal AMPK function. PRKAG3 sequence and its functionally altered mutants are useful for the diagnostic evaluation, genetic testing and prognosis of a metabolic disorder, preferably a carbohydrate metabolism disorder. Primers that can detect a genetic polymorphic marker linked to a sequence encoding PRKAG3, are useful for detecting a dysfunction of carbohydrate metabolism resulting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New variants of the gamma subunit of vertebrate adenosine monophosphate-activated kinase for diagnosis or treatment of disorders associated with energy metabolism such as diabetes, obesity, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rogel-Gaillard C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence is a R41Q mutant of human muscle-specific isoform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of gamma subunit of adenosine monophosphate (AMP)-activated kinase (AMPK) Prkag3. This mutant sequence results in increased glycogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              from the expression of a functionally altered allele of PRKAG3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "Wild-type Arg substituted with Gln"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Robic A,
don P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Milan D, Rob
v P, Chardon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (INRG ) INRA INST NAT RECH AGRONOMIQUE. (ANDE/) ANDERSSON L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                              AAE00328 standard; Protein; 305 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kalm E, M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        content in human skeletal muscle.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11-SEP-2000; 2000WO-EP09896.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10-SEP-1999; 99EP-0402236
18-MAY-2000; 2000EP-0401388
                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gellin J,
                                                                                                                                                                                                                                                                                                     Human Prkag3 R41Q mutant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Looft C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-244810/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOOFT C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (KALM/) KALM E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tannuccelli N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200120003-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                              13-JUN-2001
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                                                                                                                                                        AAE00328;
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RESULT 12
AAE00328
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us-09-826-581-6.rag

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18-MAY-2000; 2000EP-0401388.
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                                                       0;
derived from the human Prkag3 sequence SEQ.ID.NO.4 shown in page 57-58 sequence listing (AAE00221).
                                                                     185 MRFWQEHTCYDAMATSSKLVIFDTMLEIKKAFFALVANGVRAAPLWDSKKQSFVGMLTIT 244
                                                                                                              484
                                                                                                                                                                                                         245 DFILVLHRYYRSPLVQIYEIEQHKIETWREIYLQGCFKPLVSISPNDSLFEAVYTLIKNR 304
                                                                                                                                    IHRLPVLDPVSGNVLHILTHKRLLKFLHIFGSLLPRPSFLYRTIQDLGIGTFRDLAVVLE 364
                                                                                                                                                                   TAPILTALDIFVDRRVSALPVVNECGQVVGLYSRFDVIHLAAQQTYNHLDMSVGEALRQR 424
                                                                               PRKAG3; diabetes; obesity; myopathy; cardiovascular disease; anorectic; genetic testing; carbohydrate metabolism disorder; skeletal muscle; cystathione beta synthase; CBS; cardiant; gene therapy; RN locus;
                                                                                                                                                                           TLCLEGVLSCQPHESLGEVIDRIAREQVHRLVVLVDETQHLLGVVSLSDILQALVLSPAGI
                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                     Pig; gamma subunit; adenosine monophosphate-activated kinase; AMPK;
                                                       0;
                                        Length 305;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label- CBS
/note= "Cystathione beta synthase domain"
241..284.
/label- CBS
                                                                                                                                                                                                                                                                                                                                                                                                                                         "Cystathione beta synthase domain"
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                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label= CBS
/note= "Cystathione beta synthase domain"
                                                                                                                                                                                                                                                                                                                                     Pig AMPK gamma subunit muscle-specific isoform, PRKAG3.
                                         /;
2e-151;
0;
                                       DB 22;
                                       Score 1547; DB
Pred. No. 2e-15
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                       AA.
                                                                                                                                                                                                                                                                                      AAE00220 standard; Protein; 305
                                       61.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  'label≈ CBS
                                                                                                                                                                                                                                                                                                                      (first entry)
                                              Best_Local Similarity 99.7
Matches 304; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          . 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                 .148
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                                                                                                                                                                                                                                 DALGA 489
                                                                                                                                                                                                                                               DALGA 305
                        305 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200120003-A2
                                                                                                                                                                                                                                                                                                                                                                                    chromosome 15
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                                                                                                                                                                                                                                                                                                                                                                                                   Sus scrofa
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                                                                                                                                    305
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                        Sequence
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                                       Query Match
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Domain
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(AMP) activated kinase (AMPK) gamma rubunit muscle-specific isoform, perkad3 pred is located in the RN locus of chromosome 15.

Mutation in Prkad3 results in an altered regulation of carbohydrate metabolism, particularly in skeletal muscle. PRKAG3 is useful as therapeutic for treating carbohydrate metabolism disorders such as diabetes, obesity, and disorders associated with muscle metabolism such as myopathy and cardiovascular diseases, to modulate AMPK activity, and for restoring a normal AMPK function. PRKAG3 sequence and its functionally altered mutants are useful for the diagnostic evaluation, genetic testing and prognosis of a metabolic disorder. Preferably a carbohydrate metabolism disorder. Primers that can detect a genetic polymorphic marker linked to a sequence encoding PRKAG3, are cuseful for detecting a dysfunction of carbohydrate metabolism resulting from the expression of a functionally altered allele of PRKAG3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DFILVLHRYYRSPLVQIYEIEQHKIETWREIYLQGCFKPLVSISPNDSLFEAVYTLIKNR 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             305 IHRLPVLDPVSGNVLHILTHKRLLKFLHIFGSLLPRPSFLYRTIQDLGIGTFRDLAVVLE 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    heterotrimeric AMPK consisting of PRRAG3 or its mattant, are useful for screening compounds able to modulate AMPK activity. Nucleic acid encoding PRRAG3 is useful for detecting mutations in a Prkag3 gene, or in a sequence encoding the first cystathione beta synthase (CBS) domain of PRRAG3 and is useful in gene therapy.
                                                                                                                                                                                                                                                                                                                                                         monophosphate-activated kinase for diagnosis or treatment of disorders associated with energy metabolism such as diabetes, obesity, and
                                                                                                                                                  Rogel-Gaillard C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   185 MRFWQEHTCYDAMATSSKLVIFDTMLEIKKAFFALVANGVRAAPLWDSKKQSFVGMLTIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TAPILTALDIFVDRRVSALPVVNECGQVVGLYSRFDVIHLAAQQTYNHLDMSVGEALRQR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present amino acid sequence is pig adenosine monophosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 305;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Transgenic animal and host cell transformed with PRKAG3 or a
                                                                                                                                                                                                                                                                                                                                New variants of the gamma subunit of vertebrate adenosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                  Robic A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 1507; DB 22;
Pred. No. 2.8e-147;
1; Mismatches 5;
                                                                                                                                                  ooft C, Kalm E, Milan D, Robic
Gellin J, Le Roy P, Chardon P;
(INRG ) INRA INST NAT RECH AGRONOMIQUE.
(ANDE/) ANDERSSON L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 4; Fig 2; 71pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59.4%;
97.0%;
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                                                                                                                                                  Looft C,
                                                                                                                                                                                                                                      WPI; 2001-244810/25.
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Best Local Similarity
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                                                                                                                                                                                                                                                                           N-PSDB; AAD03295
                                                                                                                                                                              Tannuccelli N,
                                                                                          (KALM/) KALM E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DALGA
                                                                                                                                                  Andersson L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            296;
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Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                    485 DALGA 489
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                                                                                                                                    305 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sus scrofa.
                                                                                                                                       Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                        301
                                                                                                                                                                                                                                                                                               305
                                                                                                                                                           Query Match
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                                                                                                                                                                        Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence is a V401 mutant of muscle-specific isoform of gamma subunit of adenosine monophosphate (AMP)-activated kinase (AMP)-pragal from Sus scrofa. This mutant sequence results in decreased glycopen content in pig skeletal muscle.

Wutation in Prkag3 results in an altered regulation of carbohydrate metabolism, particularly in skeletal muscle. PKRAG3 is useful as therapeutic for treating carbohydrate metabolism disorders such as diabetes, obesity, and disorders associated with muscle metabolism such as myopathy and cardiovascular diseases, to modulate AMPK activity, and for restoring a normal AMPK function. PKRAG3 sequence and its functionally altered mutants are useful for the diagnostic evaluation, genetic testing and prognosis of a metabolic disorder, preferably a carbohydrate metabolism disorder. Primers that can detect
                                                                                                                       PRKAG3; diabetes; obesity; myopathy; cardiovascular disease; anorectic; genetic testing; carbohydrate metabolism disorder; skeletal muscle; cystathione beta synthase; CBS; cardiant; gene therapy; mutant; mutein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New variants of the gamma subunit of vertebrate adenosine monophosphate-activated kinase for diagnosis or treatment of disorders associated with energy metabolism such as diabetes, obesity, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rogel-Gaillard C;
                                                                                                              gamma subunit; adenosine monophosphate-activated kinase; AMPK;
                                                                                                                                                                                                                                                              /note= "Wild-type Val substituted with Ile"
                                                                                                                                                                                                                                       'note= "Cystathione beta synthase domain"
                                                                                       Sus scrofa AMPK gamma chain isoform Prkag3 mutant (R41Q).
                                                                                                                                                                                                                                                                                 /label= CBS
/note= "Cystathione beta synthase domain"
                                                                                                                                                                                                                                                                                                                   /label= CBS
/note= "Cystathione beta synthase domain"
                                                                                                                                                                                                                                                                                                                                                               /note= "Cystathione beta synthase domain'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Robic A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Im E, Milan D, Robic
Le Roy P, Chardon P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAT RECH AGRONOMIQUE.
L.
                                                                                                                                                                                                      Location/Qualifiers
                     AAE00226 standard; Protein; 305 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kalm E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 9; Page -; 71pp; English.
                                                                                                                                                                                                                                                                                                                               /note= "Cysta
241..294
/label= CBS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-MAY-2000; 2000EP-0401388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Looft C, Kal
Gellin J,
                                                                 (first entry)
                                                                                                                                                                                                                                                                                                        170..223
                                                                                                                                                                                                                                                                        148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (INRG ) INRA INST
(ANDE/) ANDERSSON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOOFT C.
                                                                                                                                                                                                                                                  Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (KALM/) KALM E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Andersson L, L
Iannuccelli N,
                                                                                                                                                                                                                                                                                                                                                                                       WO200120003-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                        10-SEP-1999;
                                                                 13-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                            22-MAR-2001
                                                                                                                                                                               Sus scrofa.
                                           AAE00226;
                                                                                                                                                           variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          myopathy
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RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241 TLCLEGVLSCQPHETLGEVIDRIVREQVHRLVLVDETQHLLGUVSLSDILQALVLSPAGI 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IHRLPVLDPVSGNVLHILTHKRLLKFLHIFGSLLPRPSFLYRTIQDLGIGTFRDLAVVLE 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               365 TAPILTALDIFVDRRVSALPVVNECGQVVGLYSRFDVIHLAAQQTYNHLDMSVGEALRQR 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09
                        useful for detecting a dysfunction of carbohydrate metabolism resulting from the expression of a functionally altered allele of PRKAG3.

Transgenic animal and host cell transformed with PRKAG3 or a present of consisting of PRKAG3 or its mutant, are useful for screening compounds able to modulate AMPK activity. Nucleic acid encoding PRKAG3 is useful for detecting mutations in a Prkag3 gene, or in a sequence encoding the first cystathione beta synthase (CBS) domain of PRKAG3 and is useful in gene therapy.

Note: The present sequence is not shown in the specification, but is derived from the porcine Prkag3 sequence shown in Fig 2 (AABO0220).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pig; gamma subunit; adenosine monopnospinate-activated names. PRKAG3; diabetes; obesity; myopathy; cardiovascular disease; anorectic; genetic testing; carbohydrate metabolism disorder; skeletal muscle; cystathione beta synthase; CBS; cardiant; gene therapy; mutant; mutein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          185 MRFMQEHTCYDAMATSSKLVIFDTMLEIKKAFFALVANGVRAAPLWDSKKQSFVGMLTIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MHFMQEHTCYDAMATSSKLVIFDTMLEIKKAFFALVANGIRAAPLMDSKKQSFVGMLTIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           245 DFILVLHRYYRSPLVQIYEIEQHKIETWREIYLQGCFKPLVSISPNDSLFEAVYTLIKNR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 425 TLCLEGVLSCQPHESLGEVIDRIAREQVHRLVLVDETQHLLGVVSLSDILQALVLSPAGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
genetic polymorphic marker linked to a sequence encoding PRKAG3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 305;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "Wild-type Arg substituted with Gln"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label= CBS
/note= "Cystathione beta synthase domain"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        59.3%; Score 1506; DB 22; 96.7%; Pred. No. 3.6e-147;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 3.66
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
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/label= CBS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          295; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              heterotrimeric AMPK consisting of PRKAG3 or its mutant, are useful for screening compounds able to modulate AMPK activity. Nucleic acid encoding PRKAG3 is useful for detecting mutations in a Prkag3 gene, or in a sequence encoding the first cystathione beta synthase (CBS) domain of prkAG3 and is useful in gene therapy.

Note: The present sequence is not shown in the specification, but is derived from the porcine Prkag3 sequence shown in Fig 2 (AAE00220).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  useful for detecting a dysfunction of carbohydrate metabolism resulting from the expression of a functionally altered allele of PRKAG3. Transgenic animal and host cell transformed with PRKAG3 or a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New variants of the gamma subunit of vertebrate adenosine monophosphate-activated kinase for diagnosis or treatment of disorders associated with energy metabolism such as diabetes, obesity, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         evaluation, genetic testing and prognosis of a metabolic disorder, preferably a carbohydrate metabolism disorder. Primers that can detect a genetic polymorphic marker linked to a sequence encoding PRRAG3, are
                                                                                                                                                                                                                                                                                                                                                                     Rogel-Gaillard C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence is a R410 mutant of muscle-specific isoform of gamma subunit of adenosine monophosphate (AMP)-activated kinase (AMFX) Prkag3 from Sus scrofa. This mutant sequence results in increased glycogen content in pig skeletal muscle.

Mutation in Prkag3 results in an altered regulation of carbohydrate metabolism, particularly in skeletal muscle. PrkAG3 is useful as therapeutic for treating carbohydrate metabolism disorders such as such as myopathy and disorders associated with muscle metabolism such as such as myopathy and cardiovascular diseases, to modulate AMPK activity, and for restoring a normal AMPK function. PrkAG3 sequence and its functionally altered mutants are useful for the diagnostic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 1503; DB 22; Length 305;
Pred. No. 7.3e-147;
5; Mismatches 5; Indels 0
241..294
/label= CBS
/note= "Cystathione beta synthase domain"
                                                                                                                                                                                                                                                                                                                                                                 Robic A,
                                                                                                                                                                                                                                                                                                                                                                 Andersson L, Looft C, Kalm E, Milan D, Robic
Iannuccelli N, Gellin J, Le Roy P, Chardon P;
                                                                                                                                                                                                                                                                   (INRG ) INRA INST NAT RECH AGRONOMIQUE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 9; Page -; 71pp; English.
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                                                                                                                                                               11-SEP-2000; 2000WO-EP09896.
                                                                                                                                                                                                   10-SEP-1999; 99EP-0402236.
18-MAY-2000; 2000EP-0401388
                                                                                                                                                                                                                                                                                    ANDERSSON L.
LOOFT C.
                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-244810/25
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                             (KALM/) KALM E.
                                                                                WO200120003-A2.
                                                                                                                       22-MAR-2001
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                                                                                                                                                                                                                                                                                    (ANDE/)
(LOOF/)
    Domain
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365 TAPILTALDIFVDRRVSALPVVNECGQVVGLYSRFDVIHLAAQQTYNHLDMSVGEALRQR 424
            TLCLEGVLSCQPHESLGEVIDRIAREQVHRLVLVDETQHLLGVVSLSDILQALVLSPAGI
                                                                                                                                                                     6, 2003, 11:01:00
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Job time: 80.7881 secs
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301 DALGA 305
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IHRLPVLDPVSGNVLHILTHKRLLKFLHIFGSLLPRPSFLYRTIQDLGIGTFRDLAVVLE 364
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6, 2003, 10:58:29 ; Search time 31.6865 Seconds (without alignments) 1483.588 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                               OM protein - protein search, using sw model
                                                                                                                                                June
                                                                                                                                                Run on:
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US-09-826-581-6 2538 1 MEPGLEHALRRIPSNSSLGG......LSDILQALVLSPAGIDALGA 489 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283224 Total number of hits satisfying chosen parameters:

283224 seqs, 96134422 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 10% Maximum Match 100% Listing first 45 summaries

Database :

PIR_73:*
1: pir1:*
2: pir2:*
3: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

RESULT

two-component hybr hypothetical prote	IMP dehydrogenase	IMP dehydrogenase	hypothetical prote	hypothetical prote	conserved hypothet	probable acetoin u	MJ1225-related pro	yhcv homolog MTH18	IMP dehydrogenase	hypothetical prote	conserved hypothet	conserved hypothet	probable transcrip	_IMP dehydrogenase
AD2103 A64478	E71456	AF3344	F72780	C75148	T36952	A72781	н69232	B69119	E75015	C97543	AD2762	C71188	T03446	C72264
21	Н	7	~	~	N	~	,1	~	7	~	7	~1	~	7
1344	486	157	287	282	223	278	284	122	485	382	382	285	895	482
5.1 1344 5.0 168	5.0 486	4.9 157				4.7 278		4.7 122	4.7 485	4.6 382	4.6 382	4.6 285	4.6 895	4.5 482
129.5 5.1 1344 126.5 5.0 168	5.0	4.9	4.9	4.8	4.7	4.7	4.7	4.7	4.7	4.6	4.6	4.6	4.6	4.5

ALIGNMENTS

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A;Wolecule type: DNA
A;Residus: 1-32 CLADA!
A;Cross-references: EMBL:Z72637; NID:g1322666; PIDN:CAA96823.1; PID:g1322667; GSPDB::
A;Experimental source: strain S288C
submitted to the EMBL Data Library, June 1993
A;Description: Correct end of the ORF for the CDC20 gene of Saccharomyces cerevisiae
A;Reference number: S48507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A:Wolecule type: DNA
A:Residues: 1-274 <MC2>
A:Cross-references: EMBL:269944; NID:91217974; PIDN:CAA93805.1; PID:91217975; GSPDB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  probable 5'-AMP-activated, gamma subunit family - fission yeast (Schizosaccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           186 RFMQEHTCYDAMATSSKLVIFDTMLEIKKAFFALVANGVRAAPLWDSKKQSFVGMLTITD 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILVLHRYYRSPLVQIYEIEQHKIETWREIYLQGCFKPL------VSISPNDSLF 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           84 FINVIQYYFSNP------DKFELVDKLQLDG-LKDIERALGVDQLDTASIHPSRPLF 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EAVYTLIKNRIHRLPVLDPVSGN----VLHILTHKRLLKFLHIFGSLLPRPS-FLYRTIQ 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                350 DLGIGTFRDLAVVLETAPILTALDIFVDRRVSALPVVNECGQVVGLYSRFDVIHLAAQQT 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             410 YNHLDMSVGEALRQRTLCLEGVLSCQPHESLGEVIDRIAREQVHRLVLVDETQHLLGVVS 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24 KFLNSKISYDVLPVSYRLIVLDTSLLVKKSLNVLLQNSIVSAPLMDSKISRFAGLLITTID 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C:Species: Schizosaccharomyces pombe
C:Date: 20-Jul-1996 #sequence_revision 13-Mar-1997 #text_change 20-Jun-2000
C:Accession: T38059; S67444
                                                                                                                                   A;Molecule type: DNA
A;Residues: 1-21 <DOI>
A;Cross-references: EMBL:D16506; NID:g391938; PIDN:BAA03958.1; PID:g2160324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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A;Reference number: 221766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Description: involved in derepression of glucose-repressed genes C; Superfamily: CAT3 protein C; Keywords: nucleus; transcription regulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2; Length 274;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 322;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Score 457; DB 1; Length 322; Pred. No. 7.9e-28; 66; Mismatches 108; Indels
                                                                                                                                                                                                                     R; Lauquin, G. submitted to the Protein Sequence Database, May 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14.8%; Score 375.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Gene: SGD:SNF4; CAT34; MIPS:YGL115w
A;Cross-references: SGD:S0003083; MIPS:YGL115w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Map position: 1
A;Introns: 12/3; 54/1; 173/3; 226/1
C;Superfamily: CAT3 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18.0%;
34.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 18.09
Best Local Similarity 34.29
Matches 106; Conservative
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LSDILKYILL 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      470 LSDILQALVL 479
                                                                                                                                                                                                                                                                         A;Reference number: S64122
A;Accession: S64125
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                                                                                                            A; Accession: S48508
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C:Function:
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N.Alternate names: CAT3 protein; protein G2945; protein YGL115w
C.Species: Saccharomyces cerevisiae
C.Date: 30-Jun-1989 #sequence_revision
C.Accession: A38906; JT0316; S48508; S64125
R.Celenza, JL.; Eng, F.J.; Carlson, M.
Mol. Cell. Biol. 9, 5045-5054, 1989
A:Pitle: Molecular analysis of the SNF4 gene of Saccharomyces cerevisiae: evidence for A:Reference number: A33480; MUID:90097921; PMID:2481228
A:Reference number: A33480; MUID:90097921; PMID:2481228
A:Residues: 1-322 cCEL
A:Residues: 1-322 cCEL
A:Residues: 1-322 cCEL
A:Schueller, H.J.; Entian, K.D.
Gene 67, 247-257, 1988
A:Title: Molecular characterization of yeast regulatory gene CAT3 necessary for glucose
A:Reference number: JT0316; MUID:89006284; PMID:3049255
                               hypothetical protein T20F7.6 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: T5-oct-1999 #text_change 18-Feb-2000
C;Accession: T25899
R;Miller, N.; Gattung, S.
submitted to the EMBL Data Library, April 1997
A;Bescription: The sequence of C. elegans cosmid T20F7.
A;Bescription: The sequence of C. elegans cosmid T20F7.
A;Bescription: Tr5899
A;Status: preliminary, translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-478 < MIL.>
A;Coss-references: EMBL:U97550; PIDN:AAB52856.1; GSPDB:GN00028; CESP:T20F7.6
A;Experimental source: strain Bristol N2; clone T20F7
C;Genetics:
A;Gene: CESP:T20F7.6
A;Map position: X
A;Introns: 33/3; 112/2; 144/1; 205/3; 263/2; 300/3; 380/3; 402/2; 451/1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               182 QIYMRFMQEHTCYDAMATSSKLVIFDTMLEIKKAFFALVANGVRAAPLWDSK-KQSFVGM 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 LTITOFILVLHRYYRS------PLVQI--YEIEQHKIETWRE-IYLQGCFKPLVS 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                287 ISPNDSLFEAVYTLIKNRIHRLPVLDPVSGNVLHILTHKRLLKFLHIFGSLLPRPSFLYR 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    347 TIQDLGIGTFRDLAVVLETAPILTALDIFVDRRVSALPVV - NECGQVVGLYSRFDVIHLA 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPKELGIGTWSGIRVVFPDTQLVDCLD11LLNKGVSGLPVVERETFKVVDMYSRFDAVGIA 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                278 LE---NRLDITVKEALAFKS---QGGPMKNDERVVSVRDNESFWKAVNVLVDHNVHRLCA 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           406 AQQTYNHLDMSVGEALRQRTLCLEG-----VLSCQPHESLGEVIDRIAREQVHRLVL 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 38 EAFARLLWINQCYEAMPSSSKMVVFDGGLLMHKAFNGLLAQSTRHVLLSDPDFGGKLDGI 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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R:Doi, A.; Doi, K.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 19.2%; Score 488; DB 2; Best Local Similarity 36.7%; Pred. No. 5.4e-30; Matches 119; Conservative 69; Mismatches 106.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         458 VDETQHLLGVVSLSDILQALVLSP 481
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A;Molecule type: DNA
A;Residues: 1-322 <SCH>
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Qy g ōχ qq ŏλ QC \tilde{o} qq

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A; Introns: 5/3; 45/2; 72/1; 105/3; 153/3; 179/2; 200/3; 225/3; 255/3; 349/3; 397/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein R53.7 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15.0ct-1999 #text_change 15.0ct-1999
C;Accession: T24248
R;Wilkinson, J.
Submitted to the EMBL Data Library, October 1995
A;Reference number: 219863
A;Accession: T24248
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Roicale type: DNA
A;Residues: 1.460 (WIL)
A;Cross_references: EMBL:Z66515; PIDN:CAA91351.1; GSPDB:GN00020; CESP:R53.7
A;Experimental source: clone R53
C;Genetics:
A;Gene: CESP:R53.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 AQIYMRFMQEHTCYDAMATSSKLVIFDTMLEIKKAFFALVANGVRAAPLWDSKKQSFVGM 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Clacession: T25824
Rijonson, D.
submitted to the EMBL Data Library, August 1996
A; Description: The sequence of C. elegans cosmid T0186.
A; Reference number: 220100
A; Reference number: 220100
A; Reference number: 220100
A; Restructs preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-43 -3.0H
A; Residues: 1-43 -3.0H
A; Residues: 1-43 -3.0H
A; Residues: EMBL: 167950; PIDN: AAB07568.1; GSPDB: GN00028; CESP: T0186.3
A; Experimental source: strain Bristol N2; clone T0186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241 LT----ITDFILVL--HRYYRSPLVQIYEIEQHKIETWREIYLQGCFKPLVSISPNDSLF 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         135 FNMGHCLTAILLVAAGNREVASKTL-----VEFLKEIGSGN----IICSGVQNSVW 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EAVYTLIKNRIHRLPVLD---PVSGNVLHILTHKRLLK-------FLHIFGSLL 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   339 PRPSFLYRTIQDLGIGTFRD--LAVVLETAPILTALDIFVDRRVSALPVVNECGQVVGLY 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    291 ARKDIILEIMSHQGGNFHDM-----LKEPVKILQSLQSRLVYGRSSYTVFETVAKMMTSD 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             397 SRFDVI-HLAAQQTYNHLDMSVGEALRQRTLCLEGVLS----CQPHESLGEVIDRIAREQ 451
                                                                           T25854
hypothetical protein T01B6.3 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15.0ct-1999 #sequence_revision 15.0ct-1999 #text_change 18-Feb-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26.3%; Pred. No. 2.1e-09;
tive 59; Mismatches 121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 217.5; DB 2;
Pred. No. 5e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8.7%; Score 222; DB 2;
16.3%; Pred. No. 2.1e-09;
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A;Introns: 30/1; 133/1; 407/3
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Matches 85; Conserv
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Best Local Similarity
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A;Gene: CESP:T01B6.3
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AAUthors: Hunter, J.L.; Jenklus, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.A.; Li, J.H.; Li, Y. Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
AAUthors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, Kef, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
AATILLE: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
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                                                                                                                                                                                                                                             175 ELRKPGAQIYMRFMQEHTCYDAMATSSKLVIFDTMLEIKKAFFALVANGVRAAPLWDSKK 234
                                                                                                                                                                                                         235 QSFVGMLTITDFILVLHRYYRSPLV--QIYEIEQHKIETWREIYLQ-GCFKP-LVSISPN 290
                                                                                                                                                                                                                                                                                                                   291 DSLFEAVYTLIKNRIHRLPVLDPVSGN-----VLHIITHKRLLKFLHIFGSLLPRPSFLY 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                            223 GVRAAPLWDSKKQSFVGMLTITDFILVLHRY--YRSPLVQIYEIEQHKIETWRE--IYLQ 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        240 GILKCICRYFRHSSSSL----PILQQPICSIPLGTWVPRIGESSSKPLATLRPHASLGSA 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RT-IQDLGIGTFRDLAVVLETAPILTALDIFVDRRVSALPVVNECGQVVGLYSRFDVIHL 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 279 GCF-----KPLVSISPNDSLFEAVYTLIKNKIHRLPVL----DPVSGNVLHILTHK 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           326 RLLK-----FLHIFGSLLPRPSFLYRTIQDLGIGTF------RDLAVVLETAPILTA 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     372 LDIFVDRRVSALPVVNECGQVVGLYSRFDVIHLAAQQTYN--HL-DMSVGEALR--QRTL 426
                                                                                                                                        6 ETQKGALKEIQAPIRSRTSYDVLPTSFRLIVFDVTLFVKTSLSLLTLNNIVSAPLWDSEA 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A.Gross-references: GB:AE005172; NID:q2342682; PIDN:AAB70406.1; GSPDB:GN00141
C;Genetics:
                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                  15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9.6%; Score 244.5; DR 2; Length 391; 29.5%; Pred. No. 3.8e-11;
                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                      Pred. No. 1.3e-21;
1; Mismatches 106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       :68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241 IQDGDYSNLDLSVGEALLKRPANFDGVHTCR 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    405 AAQQTYNHLDMSVGEALRQRTLCLEGVLSCQ 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29.5%; Pred. m...
+ive 53; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLEGVLS-----CQPHESLGEVIDRIA 448
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31.7%; Pic.
                      Similarity 31.7
16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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nes 79; Conserv
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A; Residues: 1-391 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Accession: B86222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Map position: 1
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Best Local Si
Matches 79;
                                                                                                                                                                                                                                                                                                                                                                                                                             346
                   Best Local
Matches 8
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g à a Ö QQ ∇ Op ŏ

QY 385 VVNECGQVVGLYSRFDVIHLAAQQTYNHLD-MSVGBALRORTL 426 I	RRESULT 9 T46197 T46197 T46197 T46197 Pypothetical protein T8P19.40 - Arabidopsis thaliana C; Species: Arabidopsis thaliana (mouse-ear cress) C; Date: 04.Feb-2000 #sequence_revision 04.Feb-2000 #text_change 04-Feb-2000 C; Accession: T46197 R; Choisne, N.; Robert, C.; Brottier, P.; Wincker, P.; Cattolico, L.; Artiquenave, F.; submitted to the Protein Sequence Database, December 1999 A; Reference number: 223008 A; Reference number: 223008 A; Status: preliminary A; Molecule type: DNA A; Residues: 1424 CCHO> A; Cross-references: EMBL:ALJ3315 A; Experimental source: cultivar Columbia; BAC clone T8P19 C; Genetics: A; Map position: 3 A; Introns: 69/1: 126/3; 178/3; 270/3; 325/2 A; Note: T8P19.40	Query Match 7.8%; Score 198; DB 2; Length 424; Best Local Similarity 22.5%; Pred. No. 1.4e-07; Matches 89; Conservative 82; Mismatches 140. Qy 162 SPQAPFPKLGWDDELRKPGAQIYMREWQEHTCYDAMATSSKLVIFDTM-LEIK- 213	Qy 348 IQDLGIGTERDLAVVLETAPILTALDIFVDRRVSALPVVNECGQ-VVGLYSRFDV-IH 403 1 ::	RESULT 10 T18227 hypothetical protein - yeast (Candida albicans) C, Species: Candida albicans C, Species: 15-Oct.1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999 C; Accession: T18227
Matches 105; Conservative 87; Mismatches 169; Indels 121; Gaps 20; QY 62 RQKSVEGEPPGQGEGPRS	QY 197 MATSSKLVIFDTMLEIKKAFFALVANGVRAAPLMDSKKQSFVGMLTITDFILVLHRYY 254 DD 152 CPNNSKVIIIDASTPTTAAFRIMRDHNITTLIVWDTSDARHVKRNILTLTDFILVLHRYY 259 QY 255 RSPLVQIXEIEQHKIETWREIYLQGGFKPLWSISPNDSLFBAVYLIKNRIHRLPVLDPW 314 DD 210 ETPPADGQULRASDILSGNQLVSVSISSKILDLCEELHQNRLHRVVLDDA 260 QY 315 SGNVLHILTHKRLLKFLHFGSLLPRPSFLYRTIQDLGIGTFRDLAVYLETAPILTALDI 374 DD 261 K-EVVNISVRRYLALHFGGSLLPRPSFLYRTIQDLGIGTFRDLAVYLETAPILTALDI 374 CQY 315 FVDRRVSALPVVNECQQVVGLYSRFDVIHLAAQQTVNHLDMSVGBALRQRTYRAMED 319 QY 375 FVDRRVSALPVVNECQQVVGLYSRFDVIHLAAQQTVNHLDMSVGBALRQRTYRAMED 373 QY 428 LEGVLSCQPHESLGEVIDRIAREQVHRLVLVDETQHLLGVVSLSDILQALVL 479 11 1 1 1 1 1 1 1 1 1	SP 481 SP 481 SP 425 S	Query Match 8.4%; Score 214; DB 2; Length 379; Best Local Similarity 23.5%; Pred. No. 7.1e-09; 10.0.7.1e-09; Matches 85; Conservative 73; Mismatches 122; Indels 82; Gaps 17; 17; QY 188 MORHCYDAMATSKLVIPDTMLEIKARFALVANGVRAALWDS 232 1; Db 17 LKEKKVKDMAVGKRLVEVPYTASLAQIMNTLVANKIVAVPVAAPPGQWIGAGGSMIVES 76 0 QY 233 KKQSFVGMLTITDFILUVLHRYYRSPLVQIYEIEQHKIETWREIYLQG 279 1; Db 77 DKQTGAVRKHYIGMVTMLDILAHIAGDDHI.SCGDNITQDLDQRMSDSVSSIIGHSFEG 134	Qy 280 CFKPLVSISPNDSLFEAVYTLIKNRIHRLPVLDPVSGNVLHILTH 324 ::: : : :

13;

Gaps

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Ritheologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alo Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim Rizzo, M.; Roney, T.; Rowley, D.; Sakano, H.
A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tall A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tall A; Fer. M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A; Reference and analysis of chromosome 1 of the plant Arabidopsis.
A; Accession: D96832
                                                                                                                                                                                                                                                                                                                                                                                                               281 FKPLVSISPNDSLFEAVYTLIKNRIHR--LPVLDPVSGN-------VLHILTHK 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         129 -----TLNPNTSVLECMEVFSKG-IHRALVPVESSIESNNTIAGVELIESASAYKMLTQM 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          326 RLLKFL--HIFGSLLPRPSFLYRTIQDLGIGTFRDLAVVLETAPILTALDIFVDRRVSAL 383
                                                                                                                                                                                                                                                                                 -VLHRYYRSPLVQIYEIEQHKIE---TWREIYLQGC 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    91 AAKPGOWLGAGGSMIVELDKOSGSARKQYIGWVTMLDVVAHIAGDDGESGLDKKMAAPVS 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      260 QIYEIEQHKIETWREIYLQGCFKPLVSISPNDSLFEAVYTLIKNRIHRLPVLDPVSGNVL 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               320 HILTHKRLLKFLHIFGSL--LPRPSFLYRTIQDL-GI--GTFRDLAVVLETAPILT---- 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           384 PVVN-------ECGQVVGLYSRFDVIHLAAQQTYNHLDMSVGEALRQRTLCL 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----DSKKQSFVGMLTITDFIL------VLHRYYRSPLV 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Cross-references: GB: AE005173; NID: 95902384; PIDN: AAD55486.1; GSPDB: GN00141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "If variable is trabiologis that and (mouse ear cress)
C: Date: 02-Mar-2001 *sequence_revision 02-Mar-2001 *text_change 31-Mar-2001
                                                                                                                                                      ----DSKKOS
                                                                                                                                                                                               17 TAKDLIVRNRRLVEVPYTATLSHAMNTLVANSISALPVAAPPCHWIGAGGSMIMESDKOT
                                                                                                                                                                                                                                                                                                                         183 DLLRFLKDHHFDDL---KTVLSRSISDLG-AVNDSVYAITERTTVSNAINVMKGALLNAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      182 QIYMRFWQEHTCYDAMATSSKLV-----IFD-----TMLEIKKAFFALVANGVRAAPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   37 QSYSRLMQ-FKVKDLMIDKRRLVEVPDNATLGDALNIMTILGIKP-----VANRVRAVPV
                                                                                 81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |:|| ::| |:::| |:::| || || REVVSCGVESTMEEAIEKVVTRGVHRVWVMDQQGLLQGVVSLTDIIRSL 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          429 EGVLSCQPHESLGEVIDRIAREQVHRLVLVDETQHLLGVVSLSDILQAL 477
                    Length 352;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -
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                                                                                     Indels
                                                                                                                                                  192 TCYDAMATSSKLVIFDTMLEIKKAFFALVANGVRAAPL----W--
                    DB 2;
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                 7.5%; Score 189.5; DB 2
23.2%; Pred. No. 5.1e-07;
                                                                                 Mismatches
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                                                                                                                                                                                                                                                                                 -----FVGMLTITDFIL----
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                                                                                 Conservative
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                                                   Similarity
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A;Molecule type: DNA
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                                                                              81;
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                       Query Match
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C.Species: Arabidopsis thaliana (mouse-ear cress)
C.Jate: O.S.-Mar.2001 #sequence_revision 02-Mar-2001 #text_change 31-Dec-2001
C.Jate: O.S.-Mar.2001 #sequence_revision 02-Mar-2001 #text_change 31-Dec-2001
C.Jate: O.S.-Mar.2007
C.Jate: O.S.-Mar.2007
C.Jate: O.S.-Mar.2007
C.Jate: O.S.-Mar.2007
A.Jate: O.S.-Mar.2007
R;Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, November 1998
A;Reference number: 218831
A;Accession: 11827
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Recule type: DNA
A;Residues: 1-629 < RAR>
A;Residues: 1-629 < RAR>
C;Genetics: C;Genetics: A;Residues: A;Coss-references: EMBL:AL033501; NID:e1341022; PID:e1341023; PIDN:CAA21985.1
                                                                                                                                                                                                                                                                                                                                                                                                                                              17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    71 PPGQGEGPRSRPAAESTGLEATFPKTTPLAQADPAGVGTPPTGWDCLPSDCTASAAGSST 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGGSISATAPGSTQHYLHHHPSRKTSIVEILSSPPPLPTDPNDPIHQLSLSRHASTSSNK 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    173 -DDELRKPGAQIYMRFMQEHTC-----YDAMATSSKLVIFDTMLEIKKAFFALVAN 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SSSQSIAPGSTA----ITNHAFSLVDWSEIPLTELTESNKLISIHSSHSVQSAFETLLKY 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ------KIETWREIYLQGCFK-----PLVSISPNDSLFEAVYTLIKNRIHRLPVLDPV 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             235 EFVTQTISKAKRGEVPVEFIIKLHPKNPFIKFNETDTLFSVMETL-GNGVHRIAITNEE 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  315 SGNVLHILTHKRLLKFLHIFGSLLPRPSF-LYRTIQDLGIGTFRDLAVVLETAPILTALD 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               294 GNKITGILSQRRLIKYMWENARRFPSLDFYLTSTLQDLKIGSSNPI-TIYEDOMLIEALH 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IFVDRRVSALPVVNECGQVVGLYSRFDVIHLAAQQTYNHLDMSV----GEALRQRTLCLE 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GVRAAPLWDSKK--QSFVGMLTI------TDFILVLHRYYRSPL------VQIYEIEQH 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              353 KMFNERVSSLAVIDRSRTLIGNISIVDVKNVTSSKNSHLLFKSVLNFISYNLSQKGI-EE 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Residues: 1-352 <STO>
A;Cross-references: GB:AE005172; NID:95103830; PIDN:AAD39660.1; GSPDB:GN00141
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 PPQPRQMPKSPRLSTST---SSGPSAVPNLLGSPR--PSPPQLQHQPSSASTSSTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      131 DDVELATEFPAT-----EAWECELEGLLEERPALCLSPQAPFPKLGW-----
                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                              78;
                                                                                                                                                                                                                                                                                                                                                                             Length 629;
                                                                                                                                                                                                                                                                                                                                                                      : Score 196; DB 2; Length 629; Pred. No. 3.6e-07; 80; Mismatches 208; Indels
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                                                                                                                                                                                                                                                                                                                                                                         7.78;
21.68;
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Best Local Similarity 21.68
Matches 101; Conservative
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Cyperacs: 26-Aug-1994 #sequence_revision 09-Sep-1994 #text_change 19-Apr-2002
Cyperacs: 26-Aug-1994 #sequence_revision 09-Sep-1994 #text_change 19-Apr-2002
R.Accession: $46088; $46090
R.Riegar, M.
A.Reference number: $45734
A.Accession: $46088
A.Reference number: $45734
A.Accession: $46088
A.Reference number: $1-527 < RIE>
A.Residuaes: 1-527 < RIE>
A.Residuaes: 1-527 < RIE>
A.Residuaes: 1-527 < RIE>
A.Reperimental source: strain $288C
A.Reperimental source: strain $288C
A.Reperimental source: strain $288C
A.Reference number: $45782
submitted to the EMBL Data Library, July 1999
A;Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome s A;Reference number: A75001
A;Accession: G75056
A;Status: preliminary
A;Catus: preliminary
A;Residues: 1-392 < KAM>A;Residues: 1-392 < KAM>A;Catus: DNA
A;Catus: DNA
A;Catus: DNA
A;Catus: Catus: DNA
A;Catus: Catus: 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            227 APLWDSKKQSFVGMLTITDFILVL---HRYYRSPLVQIYEIEQHKIETW-----REIY 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 RVVAEEFGKRKVEEF---MTKDVITLGPDDTVAKALATMRDHGISRIPVVDEEGKLEGLV 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SRFDVI-----HLAAQQTYNHLDMSVGE-----ALRQRTLCLEGVLSCQPHESLGEVID 445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   71 PPGQGEGPRSRPAAESTGL--EATFPKTTPLAQADPAG-----VGTPPTGWDCLPSDCT 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   277 LQGCFKPLVSISPNDSLFEAVYTLIKNRIHRLPVLDPVSGNVLHILTHKRLLKFLHIFGS 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           337 LLPRPSFLYRTIQDLGIGTFRDLAVVLETAPILTALDIFVDRRVSALPVVNECGQVVGLY 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9 PPSQSNSSNNLPTSRHASIVEMLSTPPLLPHVQVNDTDDKEQPEESTPPT----AT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          49;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 392;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein YBR214w - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein YBR1501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5.2%; Score 158; DB 2; Length 527 Similarity 21.5%; Pred. No. 0.00025; 10618 4; Conservative 63; Mismatches 182; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      54; Mismatches 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                 6.4%; Score 161.5; DB 2
33.4%; Pred. No. 8.8e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RIAREQVHRLVLVDETQHLLGVVSLSDIL 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      233 TMKDNNIDGLVVVDENNKVVGILTVKDLL 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Cross-references: EMBL: 236083; MIPS: YBR214w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Species: Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                         A, Experimental source: strain Orsay C, Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Experimental source: strain S288C
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A;Map position: 2R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SGD:SDS24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63;
                                                                                                                                                                                                                                                                                                                                                               A;Gene: PAB0961
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Best Local Si
Matches 63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      397
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical protein T17F3.17 [imported] - Arabidopsis thaliana Grouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Accession: B96720
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.M.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Denkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A;Tile: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
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          NI-TGPELVESASAYAMLSQMDLISFFFDQSSQLHGILSHTVTDLSAIHNTVLALTSQAR 253
                                                                                -------VVGLYSRFDV--IHLAAQQTYN 411
                                                                                                                        HLDMSVGEALRQ--RTLCLEG-----VLSCQPHESLGEVIDRIAREQVHRLVLVDET 461
                                                                                                                                                                                                                                                                | :: | :: ||| :: ||| 313 -LPLNALEFVEKIPRTLLFTAATSTPGRELVTCHVTSTLAQVIHWVTTKRVHRVWVDQN 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        262 YEI----EQHKIETWREIYLQGCFKPLVSISPNUSLFEAVYTLIKNRIHRLPVLDPVSGN 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          194 YEVILQEEPFKSTTVRTILKSFRWAPFLPVSTESSMLSVMLLLSKYRLRNVPVIKTGEPD 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VLHILTHKRLLK-----FLHIFGSLLPRPSFLYRTIQDLGIGTFRDLAVV-LETA 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 254 IKNYVTQSAVVHGLEGCKGRDWFDHI--SALP-----ISDLGLPFMSPNEVISIESE 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P-ILTALDIFVDRRVSALPVVNECG-QVVGLYSRFDVIHLAAQQ------TYNHLDM 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     304 ELILEAFKRMRDNNIGGLPVVEGLNKKIVGNISMRDIRYLLLQPEVFSNFRQLTVKSFAT 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SVGEALRQRILCLEGVLSCQPHESLGEVIDRIAREQVHRL-VLVDETQHLLGVVSLSDIL 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       364 KIATAGEEYGLAIPAI-TCRPDSTLGSVINSLASRSVHRVYVAAGDENELYGVITLRDV1 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Residues: 1-447 <STO>
A;Cross-references: GB:AE005173; NID:g6358813; PIDN:AAF07393.1; GSPDB:GN00141
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C:Species: Pyrococcus abyssi
C:Species: 20-Aqq-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999
C:Accession: G75056
R;anonymous, Genoscope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      38;
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ilarity 25.5%; Pred. No. 8.1e-05;
Conservative 39; Mismatches 107
                                                                                ---ALDIFVDRRVSALPVVNECGQ---
                                                                                                                                                                                                                                                                                                                                                               462 QHLLGVVSLSDILQALVLS 480
                                                                                                                                                                                                                                                                                                                                                                                                              GGLQGLVSLTDII-AVVRS 389
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Matches 63; Conserv
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A;Status: preliminary
A;Molecule type: DNA
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                                                                                                                                                                                                                    412
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123 ASAAGSSTDDVELATEFPATEAWECELEGILEERPAICLSPQAPFPKLGW 172	173 DDELRKPGAQIYMRFWQEHTCYDAMATSSKLVIFDTMLEIKKAFFALVANGVRAAPLWDS 232 1	233 KKQSFVGMLTITDFILVLHRYYRSPLVQIYEIEQHKIETWREIYLQGCFKP 283	LVSISPNDSLFEAVYTLIKNRIHRLPVLDEVSGNVLHILTHKRLLKFLHIFGSLLP 339 : - :: : : : :	340 RPSFLYRTIQDLGIGTFRDLAVVLETAPILTALDIFVDRRVSALPVVNEC 389 ::	390 GQVVGLYSRFDVIHLAAQQTYNHLDMSVGEALRQRTLCLEGVLSCQPHESLG 441	EVIDRIAREQVERLVIV 458 ::::alii:li:l RTLAKIVATKSHRIMIV 396
3 ASAA : 1 AAAP	3 DDEL	3 KKQS : 1	t LVSI : 1 FYKL	O RPSF	COVE	2 EVIC : 0 RTLA
12:	173	233	284	341	39(380
QY QD	QY	QY Db	Qy	Qy Db	Qy Db	QY da

Search completed: June 6, 2003, 11:03:34 Job time: 34.6865 secs

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June 6, 2003, 10:57:04; Search time 17.9842 Seconds (without alignments) 1127.761 Million cell updates/sec
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2538
1 MEPGLEHALRRFPSWSSLGG......LSDILQALVLSPAGIDALGA 489
GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                      OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                         Title:
Perfect score:
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Run on:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Minimum DB seq length: 0 Maximum DB seq length: 200000000

SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Q55434 synechocyst Q09826 schizosacch Q9wtq2 rattus norv Q9eg60 rattus norv Q58139 methanococc P13199 herpesvirus Q9z114 helicobacte P56088 helicobacte P56088 helicobacte P56088 helicobacte P56088 helicobacte P56088 nelsobacte P56088 nelsobacte P56088 nelsobacte P56088 nelsobacte Q96ruz homo sapien	088480 rattus norv Q62059 mus musculu
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100 999.5 98.5 97.5 97.5 97.5	97 96.5
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ALIGNMENTS

RESULT 1

112892

Total number of hits satisfying chosen parameters:

112892 seqs, 41476328 residues

Searched:

AAKI	
A :	
AC E	•
15	10-001-2001 (Rel. 40, Created) 16-00T-2001 (Rel. 40, Last sequence update)
IG	16-OCT-2001 (Rel. 40, Last annotation update)
DE	ted protein ki
DE N	(AMPK gamma3). ppknc3 ob nmpkc3
s C	Francis Or Anterior Homo canions (Timman)
88	
8	Primates;
XO	
RN	[1]
RP	SEQUENCE FROM N.A.
KX 6	MEDLINE=20164049; PubMed=10698692;
RA E	Cheung F.C., Sait 1.F., Davies S.F., Hardle D.G., Carling D.; "Characterization of AMD-activated protein Pinaso comma-submoit
T L	
RI	HOCKER, I. 346:659-664(2000)
KN.	
КР	SEQUENCE FROM N.A.
Ω	TISSUE=Skeletal muscle;
RX	MEDLINE=20280150; PubMed=10818001;
RA	arger V., Robic
RA	Rogel-Gaillard C., Paul S., Iannuccelli N., Rask L., Ronne H.,
RA	Lundstroem K., Reinsch N., Gellin J., Kalm E., Le Roy P., Chardon P.,
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RT	"A mutation in PKKAG3 associated with excess glycogen content in pig
Z i	SKELECH INUSCIE:
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ع د ا	SOUTHERSTS BY DEPOSITION OF ACCOUNTING OF TAILI ACLD
3 8	REGULATES CHOI-ESTEROL SYNTHESIS VIA PHOSPHORYLATION AND
88	INACTIVATION OF HYDROXYMETHYLGGLUTARYL-COA REDUCTASE AND HORMONE-
ပ္ပ	SENSITIVE LIPASE. THIS IS A REGULATORY SUBUNIT. IT MAY PLAY A ROLE
೮	IN THE REGULATION OF ENERGY METABOLISM IN SKELETAL MUSCLE.
ខ	-!- SUBUNIT: HETEROTRIMER OF AN ALPHA CATALYTIC SUBUNIT, A BETA AND A
႘	GAMMA NON-CATALYTIC REGULATORY SUBUNITS.
႘	-!- TISSUE SPECIFICITY: SKELETAL MUSCLE, WITH WEAK EXPRESSION IN HEART
၁ (AND PANCREAS.
ဗ္ဗ	-!- SIMILARITY: BELONGS TO THE 5'-AMP-ACTIVATED PROTEIN KINASE, GAMMA
3 5	
3 5	-!- SIMILARIIY: CONTAINS 4 CBS DUMAINS.
3 6	
3 8	Associated the Swiss Institute of Ricinformatics and the FWRI cutstation
_ව	sean Bioinformatics Institute. There are no restrictions on it
8	as its content is in no
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ဗ္ဗ ဗ	or send an email to license@isb-sib.ch).
3 2	EMBL: A.1249977 CARKS117 1. ALT INTO
N. N.	EMBL; AF214519; AAF73987.1;

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                                                                                                                                                                                                                                                                       146 ECELEGILEERPALCLSPQAPFPKLGWDDELRKPGAQIYMRFMQEHTCYDAMATSSKLVI
                                                                                                                                                                                                                                                                                                              FDTMLEIKKAFFALVANGVRAAPLWDSKKQSFVGMLTITDFILVLHRYYRSPLVQIYEIE
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                                                                                                                                                                                                                                                                                                                                                              326 RLLKFLHIFGSLLPRPSFLYRTIQDLGIGTFRDLAVVLETAPILTALDIFVDRRVSALPV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-OCT-2001 (Rel. 40, Last annotation update)
5'-AMP-activated protein kinase, gamma-3 subunit (AMPK gamma-3 chain)
                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Milan D., Jeon J.-T., Looft C., Amarger V., Robic A., Thelander M., Rogel-Gaillard C., Paul S., Iannuccelli N., Rask L., Ronne H.,
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                                                                                                                                                                           ö
                                                                                                                                                         Length 464;
                                                                                             T -> A (IN REF. 1).
MQ -> IE (IN REF. 1).
Q -> K (IN REF. 1).
ALGA -> PSGPEKI (IN REF. 1).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RIAREQVHRLVLVDETQHLLGVVSLSD1LQALVLSPAGIDALGA 464
                                                                                                                                                                          Indels
                                                                                                                                      53985C2C77003A63 CRC64;
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Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae,
                                                                                                                                                     94.5%; Score 2398; DB 1;
99.8%; Pred. No. 3.7e-174;
iive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A., AND VARIANT RN(-) GLN-200.
                                              Fatty acid biosynthesis; Repeat; CBS domain.
DOMAIN 228 282 CBS 2.
DOMAIN 328 CBS 2.
DOMAIN 375 428 CBS 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        464 AA.
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MEDLINE=20280150; PubMed=10818001;
Milan D., Jeon J.-T., Looft C., Am
                   InterPro; IPR000644; CBS_domain
                                                                                                                                     MM;
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HGNC:9387; PRKAG3
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282
356
428
58
164
398
                            Pfam; PF00571; CBS; 4
SMART; SM00116; CBS;
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           MIM; 604976;
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Science 288:1248-1251(2000).

1. Science 288:1248-1251(2000).

2. FUNCTION: AMPK IS RESPONSIBLE FOR THE REGULATION OF FATTY ACID SYNTHESIS BY PHOSPHORYLATION OF ACETY-COA CARBOXYLASE. ALSO REGULATES CHOLESTEROL SYNTHESIS VIA PHOSPHORYLATION AND INACTIVATION OF HYDROXYMETHYLGLUTARYL-COA REDUCTASE AND HORMONE-SENSTIVE LIPASE. THIS IS A REGULATORY SUBBUILT. IT MAY PLAY A ROLE IN THE REGULATION OF ENERGY METABOLISM IN SKELETAL MUSCLE.

2. SUBUNIT: HETEROTRIMER OF AN ALPHA CATALYTIC SUBUNIT, A BETA AND A GAMAN NOW-CATALYTIC REGULATORY SUBUNITS.

2. TISSUE SPECIFICITY: MUSCLE.

3. DISBASE: DEFECTS IN PRAGA3 (RN-) ARE ASSOCIATED WITH EXCESS GLICOGEN COMPENT GABOUT 70% IN SKELETAL MUSCLE. THIS MUTATION ORIGINATED IN THE HAMPSHIRE BREED PIGS AND HAS BENEFICIAL EFFECTS.

3. ON MEAT CONTENT BUT DETAINBUNAL BFFECTS ON PROCESSING YIELD. THUS, THIS MUTATION IS OF CONSIDERABLE ECONOMIC SIGNIFICANCE IN THE PIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Chardon P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: BELONGS TO THE 5'-AMP-ACTIVATED PROTEIN KINASE, GAMMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                    "A mutation in PRKAG3 associated with excess glycogen content in pig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 2011; DB 1; Length 464; Pred. No. 7.4e-145;
Lundstroem K., Reinsch N., Gellin J., Kalm E., Le Roy P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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17638CB12A2BA9DF CRC64;
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CBS 2.
CBS 3.
CBS 4.
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Pfam; PF00571; CBS; 4.
SMART; SM00116; CBS; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF214521; AAF73989.1; -. EMBL; AF214520; AAF73988.1; -.
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86.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BREEDING INDUSTRY.
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SEQUENCE
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Best Local
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VVNECGQVVGLYSRFDVIHLAAQQTYNHLDMSVGEALRQRTLCLEGVLSCQPHESLGEVI 444
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                                                                                                                                                                                                                                      AAKH_HUMAN STANDARD, PRT; 569 AA.
09U0510; 09UDN8; 09NU29; 09UI.X8;
16-COT-2001 (Rel. 40, Last sequence update)
116-COT-2001 (Rel. 40, Last annotation update)
5'-MMP-activated protein kinase, gamma-2 subunit (AMPK gamma-2 chain)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lang T., Yu L., Qiang T., Jiang J., Chen Z., Xin Y., Liu G., Zhao S.; Molecular clohing, genomic organization, and mapping of PRRAG2, a heart abundant gamma-2 subunit of 5'-AMP-activated protein kinase, to human chromosome 7436.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Saito T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. (ISOFORM A).
MEDLINE=20164049; PubMed=10698692;
Cheung P.C.F., Salt I.P., Davies S.P., Hardie D.G., Carling D.;
"Characterization of AMP-activated protein kinase gamma-subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDL/NE=21614537; PubMed=11748095;
Gollob M.H., Seger J.J., Gollob T.N., Tapscott T., Gonzales O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of
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                                                                                                             DRIAREQVHRLVLVDETQHLLGVVSLSDILQALVLSPAGIDALGA 489
                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 218-569 FROM N.A.
Hattori A., Seki N., Hayashi A., Kozuma S., Muramatsu M.,
"Human homolog of AMPK gamma-1 chain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (JAN-2002) to the FMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Walker C., Scott K., Bauer C., Harkins R.;
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VARIANTS HCM/WPWS LEU-350 INS AND ARG-383.
MEDLINE-21264334; Pubmed~11371514;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         isoforms and their role in AMP binding.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. (ISOFORM B).
MEDLINE-20564210; Pubmed-11112354;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. (ISOFORM B). TISSUE-Placenta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. (ISOFORM B).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 254-569 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Biochem. J. 346:659-669(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genomics 70:258-263(2000).
                                                                                                                                                                                                                                                                                                                                                                             (AMPK gamma2) (H91620p).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VARIANT WPWS GLY-531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PISSUE-Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Strausberg R.
385
                                                                                      445
                                                                                                                                                                                                                                                                                                                                                                                               PRKAG2
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INACTIVATION OF HYDROXYMETHYLGLUTARYL-COA REDUCTASE AND HORMONE-
SENSTITUE LIFASE. THIS IS A REGULATORY SUBUNIT.
SUBUNIT: HETEROYRIMER OF AN ALPHA CAPALYTIC SUBUNIT, A BETA AND A
GAMMA NON-CAPALYTIC REGULATORY SUBUNITS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         common cause of paroxysmal supraventricular tachycardia. WPWS can be associated with a form of hypertrophic cardiomyopathy (HCM), which is probably due to polysaccharide storage in the heart. Defects in PRKAG2 may not be a frequent cause of HCM where no features of pre-excitation are found in affected individuals. SIMILARITY: BELONGS TO THE 5'-AMP-ACTIVATED PROTEIN KINASE, GAMMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Z
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Blair E., Redwood C., Ashrafian H., Oliveira M., Broxholme J., Kerr B., Salmon A., Oestman-Smith I., Nakkins H.; "Mutations in the gamma(2) subunit of AMP-activated protein kinase cause familial hypertrophic cardiomyopathy: evidence for the central role of energy compromise in disease pathogenesis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-21686220; PubMed-11827995; Arad M., Benson D.W., Perez-Atayde A.R., McKenna W.J., Sparks B.A., Karter R.J., McGarry K., Scidman J.G., Seidman C.E.; "Constitutively active AMP kinase mutations cause glycogen storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -i- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A (SHOWN HERE) AND B; ARE PRODUCED BY ALTERNATIVE SPLICING.
-i- TISSUE SPECIFICITY: ISOFORM B UDBLOUITOUSLY EXPRESSED EXCEPT LIVER AND THYMUS. THE HIGHEST LEVEL IS DETECTED IN HEART WITH ABUNDANT EXPRESSION IN PLACENTA AND TESTIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -:- FUNCTION: AMPK IS RESPONSIBLE FOR THE REGULATION OF FATTY ACID SYNTHESIS BY PHOSPHORYLATION OF ACETYL-COA CARBOXXLASE. ALSO REGULATES CHOLESTEROL SYNTHESIS VIA PHOSPHORYLATION AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gollob M.H., Green M.S., Tang A.S.-L., Gollob T., Karibe A., Alma Sayegh A.H., Ahmad F., Lozado R., Shah G., Fananapazir L., Bachinski L.L., Roberts R.; New Engl. J. Med. 345:552-552(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gollob M.H., Green M.S., Tang A.S.-L., Gollob T., Karibe A., Ala Sayegh A.H., Ahmad F., Lozado R., Shah G., Fananapazir L., Bachinski L.L., Roberts R.; New Engl. J. Med. 346:300-300(2002).
                                                                                                                                                                                                                                                                                                                                                            MEDLINE-21279949; PubMed~11407343; Gollob M.H., Green M.S., Tang A.S.-L., Gollob T., Karibe A., Al Sayegh A.H., Ahmad F., Lozado R., Shah G., Fananapazir L., Bachinski L.L., Roberts R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Identification of a gene responsible for familial Wolff-Parkinson-White syndrome.";
New Engl. J. Med. 344:1823-1831(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VARIANTS WPWS GLN-302; ASN-400 AND ILE-488.
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                                                                                                                                                                                                                                   Hum. Mol. Genet. 10:1215-1220(2001).
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EMBL; BC020540; AAH20540.1;
EMBL; AB025580; BAA84695.1;
EMBL; AC006966; AAF03528.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genew; HGNC:9386; PRKAG2
                                                                                                                                                                                                                                                                                                                               VARIANT WPWS GLN-302.
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Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000644; CBS_domain.
Pfam; PF00571; CBS; 4.
SMART; SM00116; CBS; 4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fatty acid biosynthesis;
                                                          Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBUNIT FAMILY.
                                                                                                 SEQUENCE FROM N.A.
                                                                                 NCBI_TaxID=10116;
                                                                                                           STRAIN-Wistar;
                                                                                                                                                                                                                                                                                                                                                                                       SUBUNIT
                                         (AMPKg).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
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                                                  PRKAG
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 10;
                                                                                                                                                                                                                                                                                                                                                                               210
                                                                                                                                                                                                                                                                                                                                                                                              287
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                                                                                                                                                                                                                                                                                                                             RSSSKESSPNSNPATSPGGIRFFSRSRKTSGLSSSPSTPTOVTKOHTFPLESYKHEPERL 187
                                                                                                                                                                                                                                                                                                                                              -----AGVGTPPTGWDCLPSDC---TASAAGSST-----DDVELATEFPATEAWECELEG 151
                                                                                                                                                                                                                                                                                                                                                             ENRIYASSSPPDTGQRFCPSSFQSPTRPPLASPTHYAPSKAAALAAAIGPAEA----G 241
                                                                                                                                                                                                                                                                                                                                                                                                              211 EIKKAFFALVANGVRAAPUMDSKKOSFVGMLTITDFILVIHRYYRSPIVQIYEIEQHKIE 270
                                                                                                                                                                                                                                                                                                                                                                                                                                              TWREIYIQGCFKPLVSISPNDSLFEAVYTLIKNRIHRLPVLDPVSGNVLHILFHKRLLKF 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                       LHIFGSLLPRPSFLYRTIQDLGIGTFRDLAVVLETAPILTALDIFVDRRVSALPVVNECG 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QVVGLYSRFDVIHLAAQQTYNHLDMSVGEALRQRTLCLEGVLSCQPHESLGEVIDRIARE 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LLEERPALCLSPQAPFPKLGWDDE-LRKPGAQ1YMRFMQEHTCYDAMATSSKLV1FDTML
                                                                                                                                                                                                                                                                                                                                                                                       52; Gaps
                                        Repeat; CBS domain; Alternative splicing;
                                                                                                                                                                                                                                           ASPTHYAPSKAAALAA -> MLIAVLLLPLRRRWRR
                                                                                                                                                                                                                   R -> G (IN WPWS; ABSENCE OF CARDIAC HYPERTROPHY; ONSET IN CHILDHOOD). /FTId=VAR_013269.
                                                                                                                   -> RL (IN FAMILIAL HCM WITH WPWS;
                                                                                                                                           -> R (IN FAMILIAL HCM WITH WPWS;
                                                                                                                                                                                                                                                                           Length 569;
                                                                                                                                                                                                                                                                                             95; Indels
                                                                                                                                                                                  /FTId=VAR_013267.
N -> I (IN WPWS WITH CARDIAC HYPERTROPHY).
                                                                                                                                                                 -> N (IN WPWS WITH CARDIAC
                                                                                                                                                                                                                                                    (IN REF. 5).
F51C30668C294089 CRC64;
                                                                                          MISSING (IN ISOFORM B).
                                                                                                                                                                                                                                                                           43.1%; Score 1093; DB 1;
51.0%; Pred. No. 3.2e-75;
Live 75; Mismatches 95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FTId=VAR_013268.
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                                                                                                   -> Q (IN WPWS).
                                                                                                                                  /FTId-VAR_013265
                                                                                                                                                          /FTId=VAR_013266
                                                                                                          /FTId=VAR_013264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          330 AA.
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                                                                                                                                                   SEVERE)
                                                                                                                          SEVERE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
              InterPro; IPR000644; CBS_domain. Pf057; CBS; 4. SWART; SM00116; CBS; 4. Fatty acid biosynthesis; Repeat;
                                                                                                                                                                                                                                                            569 AA; 63066 MW;
                                                                                                                                                                                                                                                                                              231; Conservative
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409
483
555
302
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Best Local Similarity
                                                 Disease mutation
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      194200; -.
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                                                                                                                                                                                                                                                             SEQUENCE
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                                                                                         VARSPLIC
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                                                                                                                                                                                           VARIANT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-95050763; Pubmed=7961907; Aidher J., Mitchelhill K., Azapleton D., Gao G., Michell B.J., Widner J., Mitchelhill K., Teb T., House C.M., Witters L.A., Kemp B.E.; "Mammalian 5'-AMP-activated protein kinase non-catalytic subunits are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBDIVIT: HETEROTRIMER OF AN ALPHA CATALYTIC SUBUNIT; A BETA AND A CAMAR NON-CATALYTIC REGULATORY SUBUNITS.
TISSUE SPECIFICITY: HIGHLY EXPRESED IN HEART AND BRAIN, ALSO FOUND IN KIDNEY, WHITE ADIPOSE TISSUE, LUNG AND SPLEEN.
SIMILARITY: BELONGS TO THE 5'-AMP-ACTIVATED PROTEIN KINASE, GAMMA
01-FEB-1995 (Rel. 31, Created)
11 NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
5'-AMP-activated protein kinase, gamma-1 subunit (AMPK gamma-1 chain)
                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 homologs of proteins that interact with yeast Snfi protein kinase."; J. Biol. Chem. 269:29343-29346(1994).
-!- FUNCTION: AMPK IS RESPONSIBLE FOR THE REGULATION OF FATTY ACID SYNTHESIS BY PHOSPHORYLATION OF ACETYL-COA CARBOXYLASE. IT ALSO REGULATES CHOLESTEROL SYNTHESIS VIA PHOSPHORYLATION AND INACTIVATION OF HORMONE-SENSITIVE LIPASE AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Characterization of AMP-activated protein kinase beta and gamma subunits. Assembly of the heterotrimeric complex in vitro."; J. Biol. Chem. 271:10282-10290(1996).
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STRAIN—Sprague-Dawley; TISSUE-Liver;
MEDLINE-96224074; PubMed-8621499;
Gao G., Fernandez C.S., Stapleton D., Auster A.S., Widmer J.,
Dyck J.R.B., Kemp B.E., Witters L.A.;
Mon-catalytic beta- and gamma-subunit isoforms of the
5'-AMP-activated protein kinase.";
J. Biol. Chem. 271:8675-8681(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-96215327; Pubmed-8626596;
Woods A., Cheung P.C.F., Smith F.C., Davison M.D., Scott J.,
Beri R.K., Carling D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 48-330 FROM N.A., AND PARTIAL SEQUENCE. STRAIN-Sprague-Dawley; TISSUE-Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   domain.
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Similarity
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P58108;
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Gao G., Fernandez C.S., Stapleton D., Auster A.S., Widmer J.,
Dyck J.R.B., Kemp B.E., Witters L.A.;
"Non-catalytic beta-and gamma-subunit isoforms of the 5'-AMP-activated
                                                                                                                                                                                                                                                              9 APAPENEHSQETPESNSSVYTTFMKSHRCYDLIPTSSKLVVFDTSLQVKKAFFALVTNGV
                                                                                                                                                                                                                       165 APFPKLGWDDELRKPGAQIYMRFMQEHTCYDAMATSSKLVIFDTMLEIKKAFFALVANGV
                                                                                                                        225 RAAPLWDSKKQSFVGMLTITDFILVLHRYYRSPLVQIYEIEQHKIETWREIYLQGCFKPL
                                                                                                                                                                                                          345 YRTIQDLGIGTFRDLAVVLETAPILTALDIFVDRRVSALPVVNECGQVVGLYSRFDVIHL
                                                                                                                                                                                                                                                                                                                                                                                             01-0CT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
5'-AMP-activated protein kinase, gamma-1 subunit (AMPK gamma-1 chain)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: BELONGS TO THE 5'-AMP-ACTIVATED PROTEIN KINASE, GAMMA
                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SENSITIVE LIPASE. THIS IS A REGULATORY SUBUNIT. SUBUNIT: HETEROTRIMER OF AN ALPHA CATALYTIC SUBUNIT, A BETA AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                               0;
                                           Length 330;
                                                               Indels
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 E -> Q (IN REF. 3).
A -> P (IN REF. 3).
36031E526C1F1E97 CRC64;
                                                               63;
                                           DB 1;
                               40.5%; Score 1028; DB 1;
                                                                                                                                                                                                                                                                                                                                                                  331 AA.
                                                              56; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GAMMA NON-CATALYTIC REGULATORY SUBUNITS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A., AND PARTIAL SEQUENCE
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                      37386 MW;
                                                                                                                                                                                                                                                                                           465 LGVVSLSDILQALVLS 480
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                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
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114 1
201 2
330 AA;
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                                                   Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein kinase.
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                                                           Matches 197;
                                                                                                                                                                                                                                                                                                                                                                 AAKG_HUMAN
P54619;
 CONFLICT
                                                                                                                                             69
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                     SEQUENCE
                                         Query Match
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                                                    Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       363 LETAPILTALDIFVDRRVSALPVVNECGQVVGLYSRFDVIHLAAQQTYNHLDMSVGBALR 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    243 ITDFILVLHRYYRSPLVQIYEIEQHKIETWREIYLQGCFKPLVSISPNDSLFEAVYTLIK 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NRIHRLPVLDPVSGNVLHILTHKRLLKFLHIFGSLLPRPSFLYRTIQDLGIGTFRDLAVV 362
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40.1%; Score 1017; DB 1; Length 331; 64.8%; Pred. No. 8.4e-70;
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Benkel B., Kollers S., Fries R., Sazanov A., Yoshida E.,
Hickey D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       52; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OF22B9CAlDBD87AE CRC64;
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                      Fatty acid biosynthesis; Repeat; CBS domain.
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Pfam; PF00571; CBS; 4.
SMART; SM00116; CBS; 4.
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                                                                                                                                                                                                                      EMBL; U42412; AAC50495.1; -.
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                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        423 QRTLCLEGVLSCQPHESLGEVIDRIAREQVHRLVLVDETQHLLGVVSLSDILQALVLS 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GAMMA NON-CATALYTIC REGULATORY SUBUNITS.
SIMILARITY: BELONGS TO THE 5'-AMP-ACTIVATED PROTEIN KINASE, GAMMA SUBUNIT FAMILY.
SIMILARITY: CONTAINS 4 CBS DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
5'-AMP-activated protein kinase, gamma-1 subunit (AMPK gamma-1 chain)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Shamsadin R., Jantsan K., Adham I., Engel W.;
"Cloning, organisation, chromosomal localization and expression analysis of the mouse Prkaql gene.",
Cytogenet. Cell Genet. 92:134-138(2001).
-!- FUNCTION: AMPK IS RESPONSIBLE FOR THE REGULATION OF FATTY ACID SYNTHESIS BY PHOSPHORYLATION OF ACETYL-COA CARBOXYLASE. ALSO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 330;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  39.9%; Score 1013; DB 1;
64 4%: Pred. No. 1.7e-69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fatty acid biosynthesis; Repeat; CBS domain.

ODMAIN

48

96

CBS 1.

CBS 2.
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CBS 2.
CBS 3.
CBS 4.
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MEDLINE=21203559; PubMed=11306812;
                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR000644; CBS_domain.
Pfam; PF00571; CBS; 4.
SMART; SM00116; CBS; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     37481 MW;
                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AF329081; AAK19307.1; -.
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Matches 192; Conservative
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197 2
271 3
330 AA;
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PRKAG1 OR PRKAAC.
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SUBUNIT: HETEROTRIMER OF AN ALPHA CATALYTIC SUBUNIT, A BETA AND A GAMMA NON-CATALYTIC REGULATORY SUBUNITS.
                                                                                                                                                     SIMILARITY: BELONGS TO THE 5'-AMP-ACTIVATED PROTEIN KINASE, GAMMA SUBUNIT FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
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NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              39.3%; Score 997; DB 1; 64.1%; Pred. No. 2.7e-68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nuclear protein SNF4 (Regulatory protein CAT3).
SNF4 OR CAT3 OR YGL115W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-1989 (Rel. 12, Created)
01-OCT-1989 (Rel. 12, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fatty acid biosynthesis; Repeat; CBS domain.
DOMAIN 47 95 CBS 1.
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                                                                                                                                                                                                                         SIMILARITY: CONTAINS 4 CBS DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CBS 2.
CBS 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AF036535; AAB95475.1; -. MGD; MGI:108411; Prkag1. Interpror; IPR000644; CBS_domain. Pfam; PF00571; CBS; 4. SMART; SM00116; CBS; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CBS
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249
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A MODOD V. GWILLIAM R. RAJANGTHEAS DOUGH R., Lyne R., Stewart A., SA MCDLINE-110-1000 N., Hayles J., Baker S., Basham D., Bowman S., Sqourcs J., Peat N., Hayles J., Baker S., Basham D., Bowman S., Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M., Chillingworth T., Churcher C.M., Chillingworth T., Churcher C.M., Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G., Holrosby Y., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K., Amoney B., Moule S., Mungall K., Murphy L., Niblett D., Odell C., Money P., Moule S., Mungall K., Murphy L., Niblett D., Odell C., R. Aliver K., O'Neil S., Pearson D., Quall M.A., Rabbinowitsch E., Rutherford K., Ruther S., Saunders B., Squares K., Sharp S., Stevens K., Raylor K., Taylor R., Squares R., Squares S., Stevens K., Taylor K., Taylor R., Reger M., Schaefer M., Mueller-Auer S., Welton J., Simmonds M., Squares R., Squares B., Stewens K., Amodward J., Voltkaert G., Aert R., Robben J., Grymonprez B., Welthens I., Vanstreels E., Reger M., Schaefer M., Mueller-Auer S., Geleu B., Chiller H., Reinhardt R., Pohl T.M., Eger P., Zimmermann W., Nedler H., Reinhardt R., Pohl T.M., Eger P., Zimmermann W., Nedler H., Reinhardt R., Purnelle B., Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S., Lucas M., Rochet M., Gaillardin C., Hallardin C., Moore K., Hurst S.M., Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G., Chrift I., Towa Y., Revuelta J.L., Moreno S., Amstrong J., Forsburg S.L., Amertini M. Parakhini W. P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
        DENIITQDNMKSCQMTTPVIDVIQMLTQGRVSSVPIIDENGYLINVYEAYDVLGLIKGGI 249
                                                                                                                                                                                       110 YNHLDMSVGEALRQRTLCLEGVLSCQPHESIGEVIDRIAREQVHRLVLVDETQHLLGVVS 469
                                                                                 DLGIGTFRDLAVVLETAPILTALDIFVDRRVSALPVVNECGQVVGLYSRFDVIHLAAQQT 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 415:871-880(2002).
-!- SIMILARITY: BELONGS TO THE 5'-AMP-ACTIVATED PROTEIN KINASE, GAMMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg
Cerrutti L., Lowe T., McCombia W.R., Paulsen I., Potashkin J.,
Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.,
"The genome sequence of Schizosaccharomyces pombe.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Schizósaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YDA1_SCHPO STANDARD; PRT; 334 AA. 010343; Q9UTJ1; G1-C2T-1996 (Rel. 34, Created) 16-CCT-2001 (Rel. 40, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical protein C1F12.01c in chromosome SPAC1F12.01C OR SPAC1556.08C.
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                                                                                                                                                                                                                                                                                            470 LSDILQALVL 479
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         186 RFMQEHTCYDAMATSSKLV1FDIMLEIKKAFFALVANGVRAAPLWDSKKQSFVGMLT1TD 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FINVIOYYFSNP------DKFELVDKLQLDG-LKDIERALGVDQLDTASIHPSRPLF 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILVLHRYYRSPLVQIYEIEQHKIETWREIYLQGCFKPL------VSISPNDSLF 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EAVYTLIKNRIHRLPVLDPVSGN----VLHILTHKRLLKFLHIFGSLLPRPS-FLYRTIQ 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24 KFLNSKTSYDVLPVSYRLIVLDTSJ.LVKKSLNVILQNSIVSAPLWDSKTSRFAGLLTTTD 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION: Nuclear.
SIMILARITY: BELONGS TO THE 5'-AMP-ACTIVATED PROTEIN KINASE, GAMMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         J. Biol. Chem. 269:2361-2364(1994).
-!- FUNUTION: THIS PROTEIN GAUGES EXPRESSION OF GLUCOSE-REPRESSIBLE GENES UPON GLUCOSE DEPRIVATION. IT INTERACTS AND HAS FUNCTIONAL RELATIONSHIP TO THE PROTEIN-KINASE SNFT.
                                                                                                  Celenza J.L., Eng F.J., Carlson M.; "Molecular analysis of the SNR4 gene of Saccharomyces cerevisiae: evidence for physical association of the SNR4 protein with the SNF1 protein kinase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mitchelhill K.I., Stapleton D., Gao G., House C., Michell B., Katsis F., Witters L.A., Kemp B.E., "Mammalian AMP-activated protein kinase shares structural and functional homology with the catalytic domain of yeast Snfl protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMART; SW00116; CBS; 4. Carbohydrate metabolism; Transcription regulation; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18.0%; Score 457; DH 1; Length 322; 34.2%; Pred. No. 2e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     66; Mismatches 108; Indels
                                                                                                                                                                                                                                                                                                                                                                                                   Doi A., Doi K.;
Submitted (JUN-1993) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                            Lauguin G.;
Submitted (MAY-1996) to the FMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51B387E346EE9561 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY: CONTAINS 4 CBS DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CBS 1.
CBS 2.
CBS 3.
CBS 4.
                                                                                                                                                                                                            Mol. Cell. Biol. 9:5045-5054(1989).
                                                                               MEDLINE=90097921; PubMed=2481228;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=94131988; PubMed~7905477;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000644; CBS_domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 30-34 AND 316-322.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36401 MW;
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EMBL; M30470; AAA35061.1; -.
EMBL: 272637; CAA96823.1; -.
EMBL; D16506; BAA03958.1; -.
                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 1-21 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      89
175
246
318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00571; CBS; 4.
Gene 67:247-257(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIR; A33480; A33480.
SGD; S0003083; SNF4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR; JT0316; RGBYC3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Repeat; CBS domain.
DOMAIN 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           322 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                           [2]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBUNIT FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       192
259
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         kinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
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122
198
271
328 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-FEB-1995
                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAKG_PIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                              Query Match
                                                                                                                                                                          Best Local
                                                                                     DOMAIN
                                                                                                  DOMAIN
                                                                                                               DOMAIN
                                                                                                                         DOMAIN
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                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           QΫ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
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                                                                                                                                                             7;
                                                                                                                                                                                                                                                                                                 ELRKPGAQIYMRFMQEHTCYDAMATSSKLVIFDTMLEIKKAFFALVANGVRAAPLWDSKK 234
                                                                                                                                                                                                                                   235 QSFVGMLTITDFILVLHRYYRSPLV --QIYEIEQHKIETWREIYLQ-GCFKP-LVSISPN 290
                                                                                                                                                                                                                                                                                   291 DSLFEAVYTLIKNRIHRLPVLDPVSGN-----VLHILTHKRLLKFLHIFGSLLPRPSFLY 345
                                                                                                                                                                                                                                                                                                                                                                                                 66 NKFAGLLTMADFVNVIKYYYQSSSPPEAIAEIDKFRLLGLREVERKIGAIPPETIYVHPM 125
                                                                                                                                                                                                                                                                                                                                  346 RT-IQDLGIGTFRDLAVVLETAPILTALDIFVDRRVSALPVVNECGQVVGLYSRFDVIHL 404
                                                                                                                                                                                                                                                                                                                                                                                   405 AAQQTYNHLDMSVGEALRQRTLCLEGVLSCQPHESLGEVIDRIAREQVHRLVLVDETQHL 464
                                                                                                                                                                                                           ETQKGALKEIQAFIRSRTSYDVLPTSFRLIVFDVTLFVKTSLSLLTLNNIVSAPLWDSEA 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBCELLULAR LOCATION: Nuclear (By similarity).
SIMILARITY: BELONGS TO THE 5'-AMP-ACTIVATED PROTEIN KINASE, GAMMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tomasini L., Ferrero I., Goffrini P.;
"Molecular characterization of KISNF4 gene.";
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: THIS PROTEIN CAUSES EXPRESSION OF GLUCOSE-REPRESSIBLE
GENES UPON GLUCOSE DEPRIVATION. IT INTERACTS AND HAS FUNCTIONAL
RELATIONSHIP TO THE PROTEIN-KINASE SNF1 (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kluyveromyces lactis (Yeast).
Eukaryota; Fungi; Ascomycota; Sarcharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
                                                                                                                                                             15;
                                                                                                                                      DB 1; Length 334;
                                                                                                                                                             Indels
                                                                                                              8D32CC6CE53F7916 CRC64;
                                                                                                                                   18.0%; Score 456.5; DB 1; 32.8%; Pred. No. 2.3e-27; ive 73; Mismatches 123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       328 AA
                                                Hypothetical protein; Repeat; CBS domain.
DOMAIN 33 81
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                                                            CBS 1.
CBS 2.
CBS 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
EMBL; AL132984; CAB61219.1; -.
InterProx; IPRO00644; CBS_domain.
Pfam: PF00571; CBS; 4.
SMART; SM00116; CBS; 4.
                                                                                                            37427 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  |::||:||| ::
EGILSLADILNYII 314
                                                                                                                                                                                                                                                                                                                                                                                                                                    LGVVSLSDILQALV 478
                                                                                                                                               3est_Local Similarity 32.8
4atches 103; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nuclear protein SNF4.
                                                                                                266 3
334 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCB1_TaxID=28985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SNF4_KLULA
                                                                                                                                                                                                                                                                                                                                                                                                                                  465
                                                                                                                                                                                    175
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                                                                                                               SEQUENCE
                                                                                                                                       Query Match
                                                                       DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09P869;
                                                                                                 DOMAIN
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 QQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             80 FAGLLTSSDFINVIQYYFHNP-----DKFELVDKLQLNGLKDIERAIGIQPYDTRS 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        293 -----LFEAVYTLIKNRIHRLPVLDPVSGN----VLHILTHKRLLKFLHIFGSLLPRPS 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |:|| :|:| :|::| |:|::| |::| |::| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             248 IGLIKGGIYNDLSLSVGEALMRRSDDFBGVFTCTEKHKLSSILDTVRKSRVHRFFVVDSN 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             343 FLYRIIQDLGIGTFRDLAVVLETAPILTALDIF-VDRRVSALPVVNECGQVVGLYSRFDV 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           402 IHLAAQQTYNHLDMSVGEALRQRTLCLEGVLSCQPHESLGEVIDRIAREQVHRLVLVDET 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           237 FVGMLTITDFILVLHRYYRSPLVQIYEIEQHKIETWREIYLQGC--FKPLVSISPNDS--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-FEB-1995 (Rel. 31, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
5'-AMP-activated protein kinase, gamma-1 subunit (AMPK gamma-1 chain)
(AMPKg) (38 kDa subunit) (Fragments).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Stapleton D., Gao G., Michell B.J., Widmer J., Mitchelhill K.,
Teh T., House C.M., Witters L.A., Kemp B.E.;
"Mammalian 5'-AMP-activated protein kinase non-catalytic subunits are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SENSITIVE LIPASE. THIS IS A REGULATORY SUBUNIT. SUBUNIT: HETEROTRIMER OF AN ALPHA CATALYTIC SUBUNIT, A BETA AND A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GAMMA NON-CATALYTIC REGULATORY SUBUNITS.
SIMILARITY: BELONGS TO THE 5'-AMP-ACTIVATED PROTEIN KINASE, GAMMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      homologs of proteins that interact with yeast Snfl protein kinase.";
J. Biol. Chem. 269:29343-29346[1994).
-!- FUNCTION: AMPK IS RESPONSIBLE FOR THE REGULATION OF FATTY ACID
SYMTHESIS BY PHOSPHORYLATION OF RETYL-COA CARBOXYLASE. ALSO
REGULATES CHOLESTEROL SYNTHESIS VIA PHOSPHORYLATION AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INACTIVATION OF HYDROXYMETHYLGLUTARYL-COA REDUCTASE AND HORMONE-
EMBL; AJ277480; CAB89520.1; -.
InterPro; IPR000644; CBS_domain.
Prem; Pr00571; CBS; 4.
SMART; SW00116; CBS; 4.
Carbohydrate metabolism; Transcription regulation; Nuclear protein;
Repeat; CBS domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16.5%; Score 418.5; DB 1; Length 328; 31.0%; Pred. No. 1.7e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DC9ED3F85E46BAD3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata;
Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        72; Mismatches 121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          133 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             CBS 1.
CBS 2.
CBS 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CBS 4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                462 QHLLGVVSLSDILQALVLS 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         308 GFLTGVLTLSDILKYILFA 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Rel. 31, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          37163 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99; Conservative
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the SWISS institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 284 LVSISPNDSLFEAVYTLIKNRIHRLPVLDPVSGNVLHILTHKRLLKFL----HIFGSLLP 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---LINSSLQDLHIGVLNIQSKPTSRQSRVISIQGEEPLIMGLYKMHVERISSIAVIDKQ 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         123 ASAAGSSTDDVELATEFPATEAWECELEGLLEERPALCLS----PQAPFPKLG----W 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 AAAPGPGC----AATPAP-----LRDEKPQFKLSAVPMTQTPSQCLSCVHAQKW 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          173 DDELRKPGAQIYMRFMQEHTCYDAMATSSKLVIFDTMLEIKKAFFALVANGVRAAPLWDS 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -------QHIPLSQLIEQNKLIFVPGSISVEEAFNTLIKYHLNSIPV--- 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             233 KKQSFVGMLTITDF-----ILVLHRYYRSPLVQIYEIEQHKIETWREIYLQGCFKP 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               340 RPSFLYRTIQDLGIG-----TFRDLAV--VLETAPILTALDIFVDRRVSALPVVNEC 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GOVVGLYSRFDVIHLAAQQTYNHLDMS----VGEALRQRTLCLE----GVLSCQPHESLG 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GNLLGNISVTDVKHVTRTSQYPLLHKTCRHFISVILNSRGLETGKDSFPIFHVYPSSSLA 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PPGQGEGPRSRPAAESTGL -- EATFPKTTPLAQADPAG-----VGTPPTGWDCLPSDCT 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --ESFPGDMNCFTFDYNDLNSYLLLVLNKITVSNKQLTADCQNGKPVPVGEMYKLTPKNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              204 FYKLPENESL-STVMGILGSGVHRVAITNEEMTKVKGILSQRRLIKYLWDNARSFTSLEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PPSQSNSSNNLPTSRHASIVEMLSTPPLLPHVQVNDTDDKEQPEESTPPT-----AT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 527;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63; Mismatches 182; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                   DC2741550A69C154 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Archaea; Euryarchaeota; Methanococci; Methanococcales; Methanocaldococcaceae; Methanocaldococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6.2%; Score 158; DB 1; 1.5%; Pred. No. 0.00018;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Rel. 36, Created)
(Rel. 36, Last sequence update)
(Rel. 40, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein; Repeat; CBS domain.
DOMAIN 196 251 CBS 1.
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STRAIN-JAL-1 / DSM 2661 / ATCC 43067;
MEDLINE-96337999; PubMed=8688087;
                                                                                                                                                                                                                                                                                                                                                                                                              CBS
                                                                                                                                                                                               EMBL; 236083; CAA85178.1; -. PIR; S46088; S46088. SGD; S0000418; SDS24. InterProc; IPR000644; CBS_domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EVIDRIAREQVHRLVLV 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     380 RTLAKLVATKSHRLWIV 396
                                                                                                                                                                                                                                                                                                                                                                                   196 251 C
283 335 C
527 AA; 57187 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein MJ1225
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                                                                                                                                                                                                                                                                                                       Pfam; PF00571; CBS; 4.
SMART; SM00116; CBS; 2.
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15-JUL-1998
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Q58622;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local S:
Matches 94,
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                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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     STAMPHARA MARKETS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       203 LVIFDTMLEIKKAFFALVANGVRAAPLWDSKKQSFVGMLTITDFILVLHRYYRSPLVQIY 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EIEQHKIETWREIYLQGCFKPLVSISPNDSLFEAVYTLIKNRIHRLPVLDPVSGNVLHIL 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           THKRLLKFLHIFGSLLPRPSFLYRTIQDLGIGTFRDLAVVLETAPILTALDIFVDRRVSA 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LPVVNECGQVVGLYSRFDVIHLAAQQTYNHLDMSVGEALRQRTLCLEGVLSCQPHESLGE 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --- 102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TXK------LFITEFPKPEFMSKSLEELQIGTYANIAMV--------RVSA 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AIOAT.----
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Dubois E., el Bakkoury M., Glansdorff N., Messenguy F., Pierard A.,
Scherens B., Vierendeels F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LPVV-----IYSKFDVINLAAEKSH-------YFEGVL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10.5%; Score 267.5; DB 1; Length 133; 28.1%; Pred. No. 1.3e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (Rel. 30, Last sequence update)
(Rel. 36, Last annotation update)
57.2 kDa protein in MET8-HPC2 intergenic region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rieger M.;
Submitted (AUG-1994) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (AUG-1994) to the EMBL/GenBank/DDBJ databases -!- SIMILARITY: TO YEAST YGL056C AND S.POMBE SDS23.-!- SIMILARITY: CONTAINS 2 CBS DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14763 MW; 84C0C3D41E845CEF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Saccharomycetales; Saccharomycetaceae; Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             443 VIDRIAREQVERLVLVDETQHLLGVVSLSDILQALVLS 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fatty acid biosynthesis; Repeat; CBS domain.
NON_TER 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     32; Mismatches
                       -!- SIMILARIȚY: CONTAINS 4 CBS DOMAINS.
InterPro; IPR000644; CBS_domain.
Pfam; PF00571; CBS; 1.
                                                                                                                                                                            CBS 1.
CBS 2.
CBS 3.
CBS 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
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01-OCT-1994 (Rel. 30, Last seq
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LVVFDTSLQVKSA-----
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127
                                                                                                SMART; SM00116; CBS; 1
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P38314;
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NCBI_TaxID=2269;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   243 ---ITDFI-----LVLHRYYRSPLVQIYEIEQHKIETWREIYLQGCFKPLVSISPNDS 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               54 SMDIVDFMGGGSKYNLIREKHERNFLAAINEPVREIME------ENVITLKENAD 102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                410 YNHLDMSVGEA-----LRQRTLCLEGVLSCQPHESLGEVIDRIAREQVHRLVLVDETQHL 464
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D., Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D., Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I., Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A., Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D., Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C., Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M., Klank H.-P., Fraser C. M., Smith H.O., Woese C.R., Venter J.C., "Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical protein; Repeat; CBS domain; Complete proteome. DOMAIN 7 62 CBS 1. DOMAIN 88 141 CBS 2.
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01-APR-1990 (Rel. 14, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypotherical 33.4 kDa protein in ribosomal RNA operon.
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Archaea; Crenarchaeota; Thermoprotei; Thermoproteales;
Thermofiliaceae; Thermofilum.
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                                                                                                                                                                                                                                 Science 273:1058-1073(1996).
-!- SIMILARITY: CONTAINS 4 CBS DOMAINS.
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CBS 2.
CBS 3.
CBS 4.
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Pfam; PF00571; CBS; 4.
SMART; SM00116; CBS; 4.
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P15889;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     279 GCFKPLVSISPNDSLFEAVYTLIKNRIHRLPVLDPVSGNVLHILTHKRLLKFL--HIFGS 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       337 LLPR--PSFLYRTIQDLGIGTFR-DLAVVLETAPILTALDIFVDRRVSALPVVNECGQVV 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 68 VVEARFNGDVYKALEQTGVEFLKYDPPYVYTRSDLREVIELMVERGIGALAVVDEDLRVV 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              394 GLYSRFDVIHLAAQQTYNHLDMSVGEALRQRTLCLEGVLSCQPHESLGEVIDRIAREQVH 453
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STRAIN-ALI-1 / DSM 2661 / ATCC 43067;
MIDDLINE-96337999; PUDMed-8688087;
Bult C.J., White O.O. Olsen G.J., Zhou L., Fleischmann R.D.,
Sutton G.G., Blake J.A., Fitzderald L.M., Clayton R.A., Gocayne J.D.,
Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
SEQUENCE FROM N.A.
STRAIN-HVV3 / DSW 2475;
Krjems J., Leffers H., Olesen T., Ingelore H., Garrett R.A.;
"Sequence, organisation and transcription of the ribosomal RNA operon and the downstream tRNA and protein genes in the archaebacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5.5%; Score 139; DB 1; Length 300 23.4%; Pred. No. 0.0022; tive 52; Mismatches 86; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            D811A313D37A4293 CRC64;
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01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical protein; Repeat; CBS domain.
                                                                                                                                                                                          Microbiol. 13:117-127(1990)
                                                                                                                                                                                                                       !- SIMILARITY: CONTAINS 4 CBS DOMAINS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; X14835; CAA32944.1; -.
PIR; S08244; S08244.
InterPro, IPR000644; CBS_domain.
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150 202 CBS
224 276 CBS
300 AA; 33437 MW; I
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Methanococcus jannaschii.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00571; CBS; 4.
SMART; SM00116; CBS; 4.
                                                                                                                                                             Thermofilum pendens.
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Q58799;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     282 KPLVSISPNDSLFEAVYTLIKNRIHRLPVLDPVSGNVLHILTHKRLLKFLHIFGSLLPRP 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             342 SFLYRTIQDLGIGTFRDLAV-----VLETAPILTALDIFVDRRVSALPVVNECGQV 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  52 EYYLISMRDLLLASSTDEEVRSLMYKAHCVHEDT-PFLDAVCEMLDSGQRAAPIVNNVGKM 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    393 VGLYSRFDVIHLAAQQTYNHLDMSVGEALRQRTLCLEGVLSCQPHESLGEVIDRIAREQV 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D., Ulterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C., Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M., Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C., "Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5.5%; Score 138.5; DB 1; Length 421; 21.2%; Pred. No. 0.0039; tive 48; Mismatches 73; Indels 39
                                                                                                                                                                                                                                                                                                                                             InterPro: IPR000644; CBS_domain.
Pfam; PF00571; CBS; 4.
SMART: SM00116; CBS; 4.
Hypothetical protein; Repeat; CBS domain; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FF89C9E64060202F CRC64;
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                                                                                                         Science 273:1058-1073(1996).
-!- SIMILARITY: CONTAINS 4 CBS DOMAINS.
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CBS 2.
CBS 3.
CBS 4.
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186 CB
264 CB
47609 MW;
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Matches 43; Conservative
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421 AA;
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Search completed: June 6, 2004, il:01:28 Job time : 19.9842 secs

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June 6, 2003, 10:58:04; Search time 63.373 Seconds (without alignments) 1589.904 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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sp_unclassified:*
sp_rvirus:*
sp_bacteriap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	091w95 mus musculu 096613 drosophila 098642 drosophila 08848 drosophila 08848 drosophila 08848 drosophila 08548 drosophila 09516 caenorhabdi 08501 caenorhabdi 09159 arabidopsis 091v59 arabidopsis 091v9 arabidopsis 091v9 arabidopsis 091v9 arabidopsis 095210 caenorhabdi 09520 mus musculu
SUMMARIES	091WG5 096613 098DD2 088XT8 088XS7 09BHL6 09BHL6 091168 0914A6 094A6 09174 09174 09174 09178 09178 09178 09178 09178
DB	111 110 100 110 110 110 110
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Score	1085.5. 1085.5. 871.5. 869.5. 869.5. 736.5.
Result No.	100 100 100 100 100 100 100 100 100 100

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RRC STRAIN—BERKELEY.

RA Adams N.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Adams N.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Adams N.D., Celniker S.E., Holt R.A., Hoskins R.A., Galle R.F.,

Recorge R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA Gutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,

Brandon R.C., Rogers Y.-H.C., Blazel R.G., Champe M., Pfeiffer B.D.,

RA Bardon R.C., Basen D.A., Baxendale J., Bayraktaroju L., Beasley E.M.,

RA Ballew R.M., Basu A., Baxendale J., Bayraktaroju L., Beasley E.M.,

RA Ballew R.M., Basu D.A., Baxendale J., Bayraktaroju L., Beasley E.M.,

RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Clandra I.,

RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Clandra I.,

RA Cherry J.M., Cawley S., Dahlke C., Davemport L.B., Davies P.,

RA Cherry J.M., Cawley S., Dahlke C., Davemport L.B., Davies P.,

RA Dodson K., Doule L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA Barris M.C., Busam D.A., Hennan T.J., Hernandez J.R., Houck J.,

RA Glodek A., Gong P., Gorrell J.H., Cu Z., Guan P., Harris M.,

RA Harris M.L., Harvey D., Hennan T.J., Hernandez J.R., Houck J.,

RA Harris M.L., Harvey D., Hennan T.J., Hernandez J.R., Mouck J.,

RA Harris M., Moult S.M., Murphy L., Muzny D.M., Nelson D.L.,

RA Moult S.M., Moy, W., Wurphy B., Murphy L., Muzny D.M., Nelson D.L.,

RA Moult S.M., Wow, W., Wurphy B., Wurphy L., Muzny D.M., Nelson D.L.,

RA Reiner K., Semington K.A., Nisokern D., Scheeler F., Shen H.,

RA Reiner K., Semington K.A., Siapson M., Stubs R., Palazzolo M., Pittman G.S., Pan S., Pollar G., Wassenbard J.,

RA Milliams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,

RA Shier S.W., Spier E., Spradling A.C., Stapleton M., Stubskin M., Stubskin M., Shibs H.,

RA Shier S.M., Share E.W., Stapleton M., Stand S., Shu K., Shih H.,

RA Sheng X.H., Zhong F.N., Zhon S., Zhan M., Zhan S., Zhan S., Zhan M., Zhan S., Z
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                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster (Fruit fly).
Makaryota; Metazos, Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 5; Length 634;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              71; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       70174 MW; 3FFD0D53E54BBE7C CRC64;
                                                                                                                                                                                                         01-MAY-2000 (TrEWBLrel. 13, Created)
01-MAY-2000 (TrEWBLrel. 13, Last sequence update)
01-JUN-2002 (TrEWBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34.3%; Score 869.5; DB 5
53.1%; Pred. No. 3.1e-62;
ive 73; Mismatches 71.
                                                                                                                                                            634 AA.
                                                                                                                                                                                                                                                                                            SNF4AGAMMA protein.
SNF4A-GAMMA OR SNF4AGAMMA OR CG17299.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AE003733; AAF55864.1; FlyBase; FBgn0025803; SNF4A-gamma.
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Pfam; PF00571; CBS; 4.
SMART; SM00116; CBS; 4.
SEQUENCE 634 AA; 70174 MW; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Science 287:2185-2195(2000).
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                                                                                                                                                            PRELIMINARY;
||| |:|
461 LYLVLRPSG 469
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-BERKELEY;
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Matches l
                                                                                                                                                                                        Q9VDD2
                                                                                                                                                            09VDD2
                                                                                                       RESULT 3
                                                                                                                                      Q9VDD2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QSFVGMLTITDFILVLHRYYRSPLVQIYEIEQHKIETWREIYLQGCFKPLVSISPNDSLF 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EAVYTLIKNRIHRLPVLDPVSGNVLHILTHKRLLKFLHIFGSLLPRPSFLYRTIQDLGIG 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  355 TFRDLAVVLETAPILTALDIFVDRRVSALPVVNECGQVVGLYSRFDVIHLAAQQTYNHLD 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  341 TYNNIETADETTSIITAEKKFVERRVSALPLVDSDGRLVDIYAKFDVINLAAEKTYNDLD 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          415 MSVGEALRQRTLCLEGVLSCQPHESLGEVIDRIAREQVHRLVLVDETQHLLGVVSLSDIL 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      248 LVLHRYYRSPLVQIYEIEQHKIETWREIYLQGCFKPLVSISPNDSLFEAVYTLIKNRIHR 307
                                                                                                                                   308 LPVLDPVSGNVLHILTHKRLLKFLHIFGSLLPRPSFLYRTIQDLGIGTFRDLAVVLETAP 367
                                                                                                                                                                                                                                                                                                                        368 ILTALDIFVDRRVSALPVVNECGQVVGLYSRFDVIHLAAQQTYNHLDMSVGEALRQRTLC 427
188 MQEHTCYDAMATSSKLVIFDTMLEIKKAFFALVANGVRAAPLWDSKKQSFVGMLTITDFI 247
                              501
                                                                                                                                                                                                                                                428 LEGVLSCOPHESLGEVIDRIAREQVHRLVLVDETQHLLGVVSLSDILQALVLSPAG 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34.3%; Score 871.5; DB 5; Length 647; 53.1%; Pred. No. 2.2e-62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               70; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
Yoshida E.N., Benkel B.F., Fong Y., Hickey D.A.;
Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF094704; AAC95306.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE 647 AA; 71592 MW; B792BE1089730B52 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
SNF4/AMP-activated protein kinase gamma subunit.
SNF4-GAMMA OR CG17299.
Drosophila melanogaster (Fruit fly).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        647 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               74; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FlyBase; FBqn0025803; SNF4A-gamma. Interpro; IPR000644; CBS_domain. Pfam. Profest.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00571; CBS; 4.
SMART; SM00116; CBS; 4.
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Caenorhabditis elegans.
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                              720 LYLVLRPSG 728
          QALVLSPAG
                                                                                                                                                                                                                                                                                                                                                                  Similarity
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SEQUENCE FROM N.A.
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Y111B2A.8.
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Matches 16
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Q9внц6;
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                                                                                                                                                             DLEEDDSQIFVKFFRFHKCYDLIPTSAKLVVFDTQLLVKKAFYALVYNGVRAAPLWDSEK 208
                               EAVYTLIKNRIHRLPVLDPVSGNVLHILTHKRLLKFLHIFGSLLPRPSFLYRTIQDLGIG 354
                                                                        TFRDLAVVLETAPILTALDIFVDRRVSALPVVNECGQVVGLYSRFDVIHLAAQQTYNHLD 414
                                                                                                                   MSVGEALRQRILCLEGVLSCQPHESLGEVIDRIAREQVHRLVLVDETQHLLGVVSLSDIL 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MSVGEALRQRILCLEGVLSCQPHESLGEVIDRIAREQVHRLVLVDETQHLLGVVSLSD11, 474
                   QSFVGMLTITDFILVLHRYYRSPLVQ1YEIEQHKIETWREIXLQGCFKPLVSISPNDSLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ELRKPGAQIYMRFMQEHTCYDAMATSSKIVIFDTMLEIKKAFFALVANGVRAAPLWDSKK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        500 TYNNIETADETTSIITALKKFVERRVSALPLVDSDGRLVDIYAKFDVINLAAEKTYNDLD
                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster (Fruit fly).
Rkaryota, Metazoa, Arthropoda, Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophillade; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                              Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise B., George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G., Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S., Patel S., Phouanenavong S., Man K., Yu C., Lewis S.E., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 5; Length 906;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (MAR-2002) to the EMBL/GenBank/UDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL: AYO84138; AAL69876.1; -
SEQUENCE 906 AA; 99970 MW; C867D9556F42D57F CRC64;
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Last annotation update)
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73; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34.3%; Score 869.5; 53.1%; Pred. No. 5e-
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hes 164; Conservative
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                                                                                                                                                                                          QALVLSPAG 483
                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=7227;
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Celniker S.;
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RE22690p.
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EAVYTLIKNRIHRLPVLDPVSGNVLHILTHKRLLKFLHIFGSLLPRPSFLYRTIQDLGIG 354
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Eukaryota; Neoptera; Endopterygota; Diptera: Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophilia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ELRKPGAQIYMRFMQEHTCYDAMATSSKLVIFDTMLEIKKAFFALVANGVRAAPLWDSKK
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                                                                                                                                                                                                                                                                                                                                                                        Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E., George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G., Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S., Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1400;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 869.5; DB 5; Leuge...
Pred. No. 9e-62;
'-----hes 71; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases. 
EMBL; AY070541; AAL48012.1; -. SEQUENCE 1400 AA; 152380 MW; 411B93CC6B9EC7AF CRC64;
                                         21, Created)
21, Last sequence update)
21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Pred. No. 9e-6273; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        372 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
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53.1%;
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                                                                   01-JUN-2002 (TrEMBLrel. 01-JUN-2002 (TrEMBLrel.
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01-JUN-2001 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
                                              01-JUN-2002 (TrEMBLrel.
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|214 LYLVLRPSG 1222
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RLPVVDKKDTNSILHILTHSRILAFMMKSFPQLPE-KLLSIPIGSLGIGTFATVVTVMTH 450
                                                                                                                                                                                                             252 RYYRSPLVQ--IYEIEQHKIET-WREIYLQGCFKP--LVSISPNDSLFEAVYTLIKNRIH 306
                                                                                                                                                                                                                              RLPVLDPVSGN-VLHILTHKRLLKFLHIFGSLLPRPSFLYRTIQDLGIGTFRDLAVVLET 365
                                                                                                                                                                                                                                                                                                                                                                                                                         163 LPSTDNKSSTNTNNNNNENPLKQTISSSPSKSTTTTTTSTSTTTTPSLSSLSSNNNNSN 222
                                                                                                           223 SNNNYINHSSISTVSEGLEN-----LNLKSGIKKI--DSETEKYIEEGKQVFVNFLKGH 274
                                                                                                                                             192 TCYDAMATSSKLVIFDTMLEIKKAFFALVANGVRAAPLWDSKKQSFVGMLTITDFILVLH 251
                                                                                                                                                                                                                                                                                                                                                                        451 TPLVEVLELLSEKKISAVPIIDSETSKIVDVYSKSDVTLMSKQGILSPSDLNLPVHQVLS 510
                                                                                                                                                                                                                                                                                                                                                                                                        417 VGEALRORTLCLEGVLSCOPHESLGEVIDRIAREOVHRLVLVDETOHLLGVVSLSDILQA 476
                -----PLAQ----ADPA-GVGTPPTGWDCLPSDCTASAAGSSTDDVE 134
                                                                               LATEFPATEAWECELEGLLEERPALCLSPQAPFPKLGWDDELRK---PGAQIYMRFWQEH 191
                                                                                                                                                                                                                                                                                                                                          366 APILTALDIFVDRRVSALPVV-NECGQVVGLYSRFDVIHLAAQQTYN-----HLDMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBL_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "The sequence of C. elegans cosmid T20F7.";
Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Waterston R.; "Direct Submission."; Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases. EMBL; U97550; AAK18981.2; ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical protein.
SEQUENCE 423 AA; 47451 WW; 6997065D515E7B21 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUL-1997 (TrEMBLrel. 04, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    423 AA.
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STRAIN-BRISTOL N2;
MEDLINE-99069613; PubMed-9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000644; CBS_domain.
Pfam; PF00571; CBS; 4.
SMART; SM00116; CBS; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical 47.5 kDa protein. T20F7.6.
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Science 282:2012-2018(1998).
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STRAIN-BRISTOL N2;
Miller N., Gattung S.;
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                LEATFPKTT----
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                                                                                                                                                                                                                                                                                                                                                                        188 MQEHTCYDAMATSSKLVIFDTMLEIKKAFFALVANGVRAAPLWDSKKQSFVGMLTITDFI 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                           248 LVLHRYY - - RSPLVQIYEIEQHKIETWREIY - LQGCFKPLVSISPNDSLFEAVYTLIKNR 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     305 IHRLPVLOPVSGNVLHILTHKRLLKFLHIFGSLLPRPSFLYRTIQDLGIGTFRDLAVVLE 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     365 TAPILTALDIFVDRRVSALPVVNECGQVVGLYSRFDVIHLAAQQTYNHLDMSVGEALRQR 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NSIEQPSPSFISSSQ--DGVLTVDPLAVDGEKGNKESQSPPNGDNQILNNNMFFKDITS 162
                                                                                                                                                                                                                                                                                                                                                                                         33 NSSSWPSPAVISSSERIRGKRRAKALRWIRQKSVEEGEPPGQGEGP----RSRPAAESTG 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gloeckner G., Eichinger L., Szafranski K., Pachebat J., Dear P., Lehmann R., Baumgart C., Parra G., April J.F., Guigo R., Kumpf K., Tunggal B., Cox E., Quail M.A., Platzer M., Rosenthal A., Noegel A.A.; "Sequence and Analysis of Chromosome 2 of Dictyostellum."; Submitted (MAR-2002) to the EMBL/Genbank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEMFEGVQTCLETDSLFQVLEAIVKAEVHRLIVTDQDKKVVGVVSLSDILKNLVLDP 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TLCLEGVLSCQPHESLGEVIDRIAREQVHRLVLVDETQHLLGVVSLSDILQALVLSP 481
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                                                                                                                                                                                                                                                                                                        29.0%; Score 736.5; DB 5; Length 372; 49.8%; Pred. No. 1e-51;
                                                                                                                                                            'Genome sequence of the nematode C.elegans: A platform for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 151; Conservative 100; Mismatches 178; Indels
                                                                                                                                                                                                                                                                                                                                          Indels
                                                                               to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                   EMBL; AL1320.25.35.1; -.
InterPort; 1PR000644; CBS_domain.
Pfam; PF00571; CBS; 4.
SMART: SM00116; CBS; 4.
SEQUENCE 372 AA; 41376 MW; 81A39670877167DF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64209 MW; 3FBC56EA649B25A9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
SNF4/AMPP activated protein kinase gamma subunit.
Dictyostelium discoideum (Slime mold)
Eukaryota: Myeetozoa; Dictyosteliida; Dictyostelium.
                                                                                                                                                                                                                                                                                                                                          83;
                                                                                                                                                                                                                                                                                                                                        63; Mismatches
 Rhabditidae; Peloderinae; Caenorhabditis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                            MEDLINE-99069613; PubMed-9851916;
                                                                                                                                                                             investigating biology.";
Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                              Sulston J.E.;
Submitted (SEP-2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                577 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                           Similarity
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                                               SEQUENCE FROM N.A.
                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                        Matches 148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-AX4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  241
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                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                           Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 7
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183 IYMRFWQEHTCYDAMATSSKLVIFDTMLEIKKAFFALVANGVRAAPLWDSKKQSFVGMLT 242
                                                                                                                                   SPNDSLFEAVYTLIKNRIHRLPVLDPVSGNVLHILTHKRLLKFLHIFGSLLPRPSFLYRT 347
                                                                                                                                                                                                 IQDLGIGTFRDLAVVLETAPILTALDIFVDRRVSALPVVNE-CGQVVGLYSRFDVIHLAA 406
                                                                                                                                                                                                                                                                 QQTYNHLDMSVG--EALRQRT----LCLEGVLSCQPHESLGEVIDRIAREQVHRLVLVDE 460
                                                                                                                                                                                                                                                                                               354 AAFSDHIDLSVSVTRAIQERDYQNGIRRDGVVTANYTTTLWSLIEIFIDKNVHRIFMVDD 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----KPLVSISPNDSLFEAVYTLIKNRIHRLPVL----DPVSGNVLHILTHKRLLK- 329
                                                                   243 ITDFILVLHRY--YRSPLVQI------YBIEQHKIETWRE-IYLQGCFKPLVSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      102 TGPDMVPAGFSPETLGRSNMDVDDVFLRTADPSOEA-------VP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KL-GWDDELRKPGAQIYMRFMQEHTCYDAMATSSKLVIFDTMLEIKKAFFALVANGVRAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGWDCLPSDCTASAAGSS---TDDVELATEPATEAWECELEGLLEERPALCLSPQAPFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassitales; Brassitaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PLWDSKKQSFVGMLTITDFILVLHRY - - YRSPLVQIYEIEQHKIETWRE - - IYLQGCF - -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.

Shinn P., Chen H., Cheuk R., Kim C.J., Koesema E., Meyers M.C.,
Banh J., Bowser L., Carninci P., Dale J.M., Goldsmith A.D.,
Hayashizaki Y., Ishida J., Jiang P.X., Jones T., Kamiya A.,
Karlin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Liu S.X.,
Miranda M., Narusaka M., Nguyen M., Onodera C.S., Palm C.J.,
Pham P.K., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A.,
Tang C.C., Toriumi M., Yamada K., Yamanura Y., Yu G., Yu S.,
"Arabicopsis cond."
"Arabicopsis cond."
Submitted (CCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AR439826; AAL27498.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 374.5; DB 10; Length 487; Pred. No. 4.3e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR000644; CBS_domain.
Pfam; PF00571; CBS; 4.
SEQUENCE 487 AA; 53466 MW; 4545FE3BF2C4EBEC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Pred. No. 4.3e-22; 77; Mismatches 140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                487
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                                                                                                                                                                                                                                                                                                                               481
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                                                                                                                                                                                                                                                                                                                               TOHLLGVVSLSDILQALVLSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14.8%;
29.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=3702;
                                                                                                                                   288
                                                                                                                                                                                                 348
                                                                                                                                                                                                                                                                 407
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7;
                                                                 182 QIYMRFMQEHTCYDAMATSSKLVIFDTMLEIKKAFFALVANGVRAAPIWDSK-KQSFVGM 240
                                                                                                                                                                                                                                                            347 TIQDLGIGTFRDLAVVLETAPILTALDIFVDRRYSALPVY-NECGQVVGLYSRFDVIHLA 405
                                                                                                                               241 LIITDFILVLHRYYRS------PLVQI--YEIEQHKIETWRE-IYLQGCFKPLVS 286
                                                                                                                                                                 157
                                                                                                                                                                                               287 ISPNDSLFEAVYTLIKNRIHRLPVLDPVSGNVLHILTHKRLLKFLHIFGSLLPRPSFLYR 346
                                                                                                                                                                                                               :::|||||:::||
218 SPKELGIGTWSGIRVVFPDTQLVDCLDILLINKGVSGLPVVERETFKVVDMYSRFDAVGIA 277
                                                                                                                                                                                                                                                                                                                            406 AQQTYNHLDMSVGEALRQRTLCLEG-----VI,SCQPHESLGEVIDRIAREQVHRLVL 457
                                                                                                                                                                                                                                                                                                                                                  97
                                                                                    98 LSVIDFIKVMLKIYRERIKCEKESTELDMIQIANEEIGNLSIRQYRELVKKEGNLRPLVS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25;
                                   30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18.5%; Score 470.5; DB 5; Length 448; 33.0%; Pred. No. 5.9e-30; Live 79; Mismatches 111; Indels 25
   Length 423;
                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases. EMBL. AC006761, AAR60550.1; -.
InterPro: IPRO00644, CBS_domain.
Pfam: PF00571; CBS; 4.
SMART; SMO0116; CBS; 3.
Hypothetical protein.
SEQUENCE 448 AA; 51514 MW; B689218979299479 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ryan E., Wohldman P., Walker C., Fielder T.;
"The sequence of C. elegans cosmid Y41G9A.";
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-2000 (TrEMBLrel. 15, Created)
01-CCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypotherical 51.5 KDa protein.
                                   106;
   DB 5;
cch 19.2%; Score 488; DB 5
il Similarity 36.7%; Pred. No. 2e-31;
119; Conservative 69; Mismatches 1º
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             448 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rhabditidae, Peloderinae, Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                            458 VDETQHLLGVVSLSDILQALVLSP 481
                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN~BRISTOL N2;
MEDLINE=99069613; PubMed=9851916;
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Matches 106; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'Direct Submission.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-BRISTOL N2;
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 Query Match
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                  Best Loca
Matches
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Q9N501
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17;

Gaps

168

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ILVLHRY -- YRSPLVQIYEIEQHKIETWREIXLQGC -- -- -- FKPLVSISPNDSLFE 295
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       286 IAVKLLLNDISTVPVIYSSSSDGSFPQLLHLASLSGILKCIFRYFKNSTGNLPILNQPVC 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -LPRPSFLYRTIQDLGIGTFRDLAVVLETAPILTALDIFVDRRVSALPVVNECGQVVGLY 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SRFDVIHLAAQQTYNHL---DMSVGEALR------QR-TLCLEGVLSCQPHE 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIPLGSW----VPKIGDPNSRPLAMLRPNASLSSALNMLVQAGVSSIPIVDENDSLLDTY 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SRSDITALAKAKVYTHVRLDEMAIHQALQLGQDANTPFGFFNGQRCQMCLRS-----D 454
                                                                                                                                                                                                                                                                                                                         Zea mays (maize).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         187 FMQEHTCYDAMATSSKLVIFDIMLEIKKAFFALVANGVRAAPLWDSKKQSFVGMLTITDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AVYTLIKNRIHRLPVLDPVSGN-----VLHILTHKRLLK-----FLHIFGSL-----
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
Panicoideae; Andropogoneae; Zea.
  GORCHMCLRSDSLVKVMERLANPGVRRLVIVEAGSKRVEGIISLSDVFQFLL 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 10; Length 497;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Victoria L., Mar A., Tatjana K., Csaba K., Montserrat P.;
"Domain fusion between Snfl related kinase subunits during
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF276085; AAG31751.1; -
Interpro; IPR00644; CBS_domain.
Pran; PR00771; CBS; 3.
SWART; SM00116; CBS; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    497 AA; 54938 MW; B9EF06A530C1AD8B CRC64;
                                                                                                                                                                                                          01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Protein kinase AKINbetagamma-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Protein kinase AKINbetagamma-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SLGEVIDRIAREQVHRLVLVDE-TQHLLGVVSLSDILQALV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PLLKVMERLANPGVRRVFIVEAGSKRVEGIISLSDIFKFLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13.7%; Score 346.5; DB 10; 29.0%; Pred. No. 8.5e-20; Live 72; Mismatches 109;
                                                                                                                                                            Ā
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                                                                                                                                                          497
                                                                                                                                                          PRT;
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                                                                                                                                                                                                                                                                                                                                                               Spermatophyta; Magnoliophyta; Li
Panicoideae; Andropogoneae; Zea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity 29.0%
99; Conservative
                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=4577;
                                                                                                                                                                                                                                                                                                                 Zea mays (Maize)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    evolution.
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Matches 9
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                                                                                                                                                       Q9FUY5
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                                                                                                         RESULT 12
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                                                                                                                                                                                  431
SGRPYPRPLVQVGPYDNLKDVALKILQNKVAAVPVIYSSLQDGSYPQLLHLASLSGILKC 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----FLHIFGSLLPRPSFLYRTIQDLGIGTF------RDLAVVLETAPILTALDIFV 376
                                                                                                              316 ICRYFRHSSSSL----PILQQPICSIPLGTWVPRIGESSSKPLATLRPHASLGSALALLV 371
                                                                                                                                                                                                                                   431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           111 PTGWDCLPSDCTASAAGSSTOPVELATEPATEAMECELEGILLEERPALCLSPQAPFPKL 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -GWDDELRKPGAQIYMRFMQEHTCYDAMATSSKLVIFDTMLEIKKAFFALVANGVRAAPL 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----KPLVSISPNDSLFEAVYTLIKNRIHRLPVL----DPVSGNVLHILTHKRLLK--- 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RDLAVVLETAPILTALDIFVDR 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 213 RYFRHSSSSL----PILQQPICSIPLGTWVPRIGESSSKPLATLRPHASLGSALALLVQA 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RVSALPVVNECGQVVGLYSRFDVIHLAAQQTYN--HL-DMSVGEALR--QRTLCLEGVLS 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EVSSIPVVDDNDSLIDIYSRSDITALAKDKAYAQIHLDDMTVHQALQLGQDASPPYGIFN 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | | | | | : : : | | : : | | : : | | : : | | | SGVDLELSRHRISV---LLSTRTAYELL, PESGKVIALDVNLPVKQAFHILYEQGIPLAPL 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 PAGF----SPETLGRSNMDVDDVFLRTADPSQEA------VPRM 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-20387008; PubMed-10929106; Kleinow T., Bhalerao R., Breuer F., Umeda M., Salchert K., Koncz C.; "Functional identification of an arabidopsis snf4 ortholog by screening for heterologous multicopy suppressors of snf4 deficiency in
                                                                                                                                                                                                             WDSKKQSFVGMLTITDFILVLHRY --YRSPLVQIYEIEQHKIETWRE--IYLQGCF----
                                                                                                                                                                                  DRRVSALPVVNECGQVVGLYSRFDVIHLAAQQTYN--HL-DMSVGEALR--QRTLCLEGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                   LS-----CQPHESLGEVIDRIAREQVHRLVLVDE-TQHLLGVVSLSDILQALV 478
                                                                                                                                                                                                                                                                                                              432 FNGQRCHMCLRSDSLVKVMERLANPGVRRLVIVEAGSKRVEGIISLSDVFQFLL 485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----CQPHESLGEVIDRIAREQVHRLVLVDE-TQHLLGVVSLSDJLQALV 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Putative activator subunit of SNF1-related protein kinase SNF4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 382;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    382 AA; 41800 MW; A9E7A4D5E1A3CB53 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-2001 (TrEMBLrel. 16, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          140;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --FLHIFGSLLPRPSFLYRTIQDLGIGTF----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              yeast.";
Plant J. 23:115-122(2000).
Plant J. AF2S0335; AAG10141.1;
InterPro; IPR000644; CBS_domain.
Pfam; PF00571; CBS; 4.
SMART; SM00116; CBS; 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          [1]
SEQUENCE FROM N.A.
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NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                   432
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9FV59
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12; 246

Gaps

61;

47;

Length Indels

Matches

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RP RT RT DR DR DR KW

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156 RPALCLSPQAPFPKLGWDDELRKPGAQIYMRFMQEHTCYDAMATSSKLVIFDTMLEIKKA 215
                                                                                                                                                                                              279 GCF-----KPLVSISPNDSLFEAVYTLIKNRIHRLPVL-----DPVSGNVLHILTHK 325
                                                                                                                                                                                                                                                                           326 RLLK-----FLHIFGSLLPRPSFLYRTIQDLGIGTF------RDLAVVLETAPILTA 371
                                                                                                                                                                                                                                                                                                                                                       372 I,DIFVDRRVSALPVVNECGQVVGLYSRFDVIHLAAQQTYN--HL-DMSVGEALR--QRTL 426
                                                                                                                                                                                                                                                                                                                                                                            223 GVRAAPLWDSKKQSFVGMLTITDFILVLHRY--YRSPLVQIYEIEQHKIETWRE--IYLQ
                                                                                                                                                                                                                                                                                                      240 GILKCICRYFRHSSSSL----PILQQPICSIPLGTWVPRIGESSSKPLATLRPHASLGSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8.9%; Score 227; DB 5; Length 423;
Llarity 25.9%; Pred. No. 3.7e-10;
Conservative 61; Mismatches 135; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Direct Submission.";
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; U67950; AAK84564.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL/GenBank/DDBJ databases.
26D6D08280587B74 CRC64;
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SEQUENCE 423 AA; 47571 MW; C38F5C7D18DDB167 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
                                    DB 10;
                                    ; Score 243.5; DB 10;
; Pred. No. 1.5e-11;
53; Mismatches 89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          423 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cosmid T01B6.";
                                                                                                                                                                                                                                                                                                                                                                                                                                   427 CLEGVLS-----CQPHESLGEVIDRIA 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                           |::|:|:|
356 PPYG1FNGQRCHMCLRSDSLVKVMERLA 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-DEC-2001 (TrEMBLrel. 19, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-BRISTOL N2;
MEDLINE-99069613; PubMed-9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR000644; CBS_domain.
391 AA; 43032 MW;
                                      9.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-DEC-2001 (TrEMBLrel. 19, I
01-JUN-2002 (TrEMBLrel. 21, I
Hypothetical protein T01B6.3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "The sequence of C. elegans
Submitted (SEP-1996) to the
                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Caenorhabditis elegans.
                  Query Match
Best Local Similarity
T9; Conservat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
Matches 90; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. STRAIN=BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        [3]
SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Waterston R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Johnson D.;
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                          247 ILVLHRY--YRSPLVQIYE1FQHKIETWREIYLQ-----GCFKP---LVSISPNDSLFE 295
                                                                                                                                                                                                                                                                                                                                                                                                                296 AVYTLIKNRIHRLPVLDPVSGN-----VLHILTHKKLLK-----FLHIFGSLLPRPSFLY 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               285 IAVKLLONGISTVPVIYSSSBUGSFPQLLHLASLSGILKCICRXFKNSTGNL----PILN 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     346 RTIQDLGIGTF-----RDLAVVLETAPILTALDIFVDRRVSALPVVNECGQVVGLY 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                34] QPVCSIPLGSWVPKIGDLNSRPLAMLRPNASLSSALNMLVQAGVSSIPIVDDNDSLLDTY 400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Arabidopsis thallana (Mouse-ear cress). Makaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae: eurosids II; Brassicales; Brassicaceee; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=CV. COLUMBIA;
OSDORNE B.I., VYSOKSKala V.S., Toriumi M., Yu.G., Oji, O, Buehler E.,
COGWAY A.B., COGWAY A.R., Dewar K., Feng J., Kim C., Kurtz D., Li Y.,
Shinn P., Sun H., Davis R.W., Ecker J.R., Federspiel N.A.,
                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "The sequence of BAC F7G19 from Arabidopsis thaliana chromosome 1."; Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
                Victoria L., Mar A., Tatjana K., Csaba K., Montserrat P.;
"Domain fusion between Snfl related kinase subunits during plant
                                                                                                                                                                                                                                                                           61;
                                                                                                                                                                                                                                     Length 496;
                                                                                                                                                                                                                              13.6%; Score 345; DB 10; Length 49 28.7%; Pred. No. 1.1e-19; ive 77; Mismatches 105; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
EMBL: AC000106; AAB70406.1; -.
InterPro; IPR000644; CBS_domain.
PFdan; PF00571; CBS; 2.
SWART; SM00116; CBS; 1.
                                                                         Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                              496 AA; 54799 MW; 316F8282B3B55D8A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SLGEVIDRIAREQVHRLVLVDE-TQHLLGVVSLSD1LQALV 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
F7G19.11.
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                                                                                            EMBL, AF276086, AAG31752.1; -...
InterProx; IPRO00644, CBS_domain.
Pfam; PF00571; CBS; 3.
SMART; SM00116; CBS; 3.
                                                                                                                                                                                                                                                                         98; Conservative
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STRAIN=CV. COLUMBIA;
Theologis A.;
SEQUENCE FROM N.A.
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                                                     evolution.";
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RESULT 14

004028

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216 FFALVANGVRAAPLWDSKKQSFVGMLTITDFILVLHRYRKSPLVQIYEJEQHKI 269	90 VHALSQHGHIAAVVTNTDKYQAECVFNMGHCLTAILLVAAGNREVASKTLV 140	270 ETWREIYLQGCFKPLVSISPNDSLFEAVYTLIKNRIHRLPVLDPVSGNVLHILTHKR 326	SGN	327 LLKFIHIFGSLLPRPSFLYRTIQDLGIGTFRDLAVVLETAPILTA 371	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	372 LDIFVDRRVSALPVVNECCQVVGLYSRFDVI-HLAAQQTYVHLDMSVGEALRQRTLCLEG 430	246 IKLMSERKMSTIPVVNDFKQIVNMLARKDIILEIMSHQGGNFHDMLKEPVKILQS 300	431 VLSCQPHESLGEVIDRIAREQVHRLVLVDETQHLLGVVSLSDIL 474	301 LOSRLVYGRSSYTVFETVAKWMTSDKSSLPIIDEGKRILAVYSCSDIL 348
216	06	270	141	327	197	372	246	431	301
ζŌ	QQ	QY	qq	δy	qq	Qy	qq	δλ	q Q

Search completed: June 6, 2003, 11:02:49 Job time: 66.373 secs

Sequence 12, Appl Sequence 12, Appl Sequence 2, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli

Sequence 2 Sequence 2 Sequence 2

Sequence 4, Sequence 4, Sequence 4, Sequence 4,

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APPLICANT: Guegler, Karl G.
APPLICANT: Lal, Preeti
APPLICANT: Goli, Surya K.
TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN
TITLE OF INVENTION: KINASES
TITLE OF INVENTION: KINASES
CORRESPONDENCE: 21
CORRESPONDENCE ADDRESS:
             US-09-448-868-4
US-07-853-913-4
US-08-764-870-12
US-08-980-115-12
US-08-465-746-2
US-08-467-85A-3
US-08-247-491A-3
US-08-319-795-2
US-08-312-949-2
US-08-312-949-2
US-08-312-949-2
US-08-312-948-2
US-08-312-948-2
US-08-312-948-2
US-08-214-22-2
US-08-214-22-2
US-08-214-22-2
US-08-214-22-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E: Incyte Pharmaceuticals, Inc. 3174 Porter Drive
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                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 7, Application US/08878989 Patent No. 5885803
                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Bandman, olga
APPLICANT: Hillman, Jennifer L.
APPLICANT: Corley, Neil C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Billings, Lucy J J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 328 amino acids
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MEDIUM TYPE: Diskette
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
 STRANDEDNESS: single
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TYPE: amino acid
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STREET:
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2538
1 MEPGLEHALRRTPSWSSLGG......LSDILQALVLSPAGIDALGA 489
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/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
               GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-272-796-7
US-09-273-796-7
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US-08-101-146-64
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Maximum Match 100%
Listing first 45 summaries
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GENERAL INFORMATION:
APPLICANT: Bradford, Kent J.
APPLICANT: Dahal, Peetambar
APPLICANT: Dahal, Michael
APPLICANT: Yang, Hong
APPLICANT: Cooley, Michael
APPLICANT: Downle, Bruce
APPLICANT: Develey, Michael
APPLICANT: Gee, Oliver
APPLICANT: Gee, Oliver
APPLICANT: Gee, Oliver
APPLICANT: Geo, Oliver
TITLE OF INVENTION: Regulation of Source-Sink Relationships and Responses
TITLE OF INVENTION: Costress Conditions in Plants
FILE REPRENCE: 023070-095900US
CURRENT FILING DATE: 1999-07-21
NUMBER OF SEQ ID NOS: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64 PLWESKKQSFVGMLTITDFINILHRYYKSPWVQIYELEEHKIETWRELYLQETFKPLVNI 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      169 KLGWDDE-LRKPGAQIYMRFMQEHTCYDAMATSSKLVIFDTMLEIKKAFFALVANGVRAA 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             228 PLWDSKKQSFVGMLTITDFILVLHRYYRSPLVQIYEIEQHKIETWREIYLQGCFKPLVSI 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    288 SPNDSLFEAVYTLIKNRIHRLPVLDPVSGNVLHILTHKRLLKFLHIFGSLLPRPSFLYRT 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         408 QTYNHLDMSVGEALRQRTLCLEGVLSCQPHESLGEVIDRIAREQVHRLVLVDETQHLLGV 467
                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                               ; Score 1080.5; DB 4; Length 328; Pred. No. 2.3e-111; 67; Mismatches 48; Indels 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 40.5%; Score 1028; DB 4;
62.3%; Pred. No. 1.6e-105;
tive 56; Mismatches 63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 6, Application US/09359161A Patent No. 6342656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   468 VSLSDILQALVLSPAG 483
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                                                          328 amino acids
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Best Local Similarity 62.39
Matches 197; Conservative
                                                                                                                                                                                                                                  Query Match
Best Local Similarity 63.33
Matches 200; Conservative
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                    INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                            TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                     LIBRARY: PENITUT01
CLONE: 1452972
                                                                                                                 TOPOLOGY: linear IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-359-161-6
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                                                                                                                                                                               ; CLONE: US-09-272-796-7
                                                          LENGTH:
                                                                                                                                                                             CLONE:
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                                                                                                                                                                                                                                                                                                                165 KLGWDDE-LRKPGAQIYMRFMQEHTCYDAMATSSKLVIFDTMLEIKKAFFALVANGVRAA 227
                                                                                                                                                                                                                 228 PLWDSKKQSFVGMLTITDFILVLHRYYRSPLVQIYEIEQHKIETWREIYLQGCFKPLVSI 287
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                                                                                                                                                                                                                                                                                                                                                                                                                                               408 QTYNHLDMSVGEALRQRILCLEGVLSCQPHESLGEVIDRIAREQVHRLVLVDETQHLLGV 467
                                                                                                                                                             Gaps
                                                                                                1;
                                                        42.6%; Score 1080.5; DB 2; Length 328; 63.3%; Pred. No. 2.3e-111; tive 67; Mismatches 48; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN TITLE OF INVENTION: KINASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATES: TSPERM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Billings, Lucy J J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0321 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEPAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/09/272,796 FILING DATE:
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Hillman, Jennifer L.
Corley, Neil C.
Guegler, Karl G.
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/878,989
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 7, Application US/09272796
Patent No. 6207148
GENERAL INFORMATION:
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Goli, Surya K.
Shah, Purvi
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                                                                          Best Local Similarity 63.3%
Matches 200; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
; CLONE: 1452972
US-08-878-989-7
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APPLICANT:
APPLICANT:
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APPLICANT:
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183 IYMRFWQEHTCYDAMATSSKLVIFDTMLEIKKAFFALVANGVRAAPLWDSKKQSFVGMLT 242
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                                                                                                                                                                                                                                                                                            303 NRIHRLPVLDPVSGNVLHILTHKRLLKFLHIFGSLLPRPSFLYRTIQDLGIGTFRDLAVV 362
                                                                                                                                                                                                                                                                                                                                                                                                                                         363 LETAPILTALDIFVDRRVSALPVVNECGQVVGLYSRFDVIHLAAQQTYNHLDMSVGEALR 422
                                                                                                                                                                                                           28 VYTSFMKSHRCYDLIPTSSKLVVFDTSLQVKKAFFALVTNGVRAAPLWDSKKQSFVGMLT 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                208 RTTTPVYVALGIFVQHRVSALPVVDEKGRVVDIYSKFDVINLAAEKTYNNLDVSVTKALQ 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         423 QRTLCLEGVLSCQPHESLGEVIDRIAREQVHRLVLVDETQHLLGVVSLSDILQALVLS 480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 64, Application US/09101146
Patent No. 6144125
Patent No. 6144125
Patent Description:
APPLICANT: Dartmouth College, St. Vincents Institute of APPLICANT: Medical Research, Kemp et al.
TTYLE OF INVENTION: No. 6124125el AMP Activated Protein Kinase NUMBER OF SEQUENCES: 64
                                                                                                                                            ;
0
                                                                                                     Length 331;
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                                                                                                                                            Indels
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MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
                                                                                                                                            52;
                                                                                                 40.1%; Score 1017; DB 2;
64.8%; Pred. No. 2.7e-104;
live 53; Mismatches 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: WORDPERFECT 6.0 FOR WINDOWS CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/101,146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Jane Massey Licata, Esq. STREET: 66 E. Main Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DC-0050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: October 7, 1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PN7450
FILING DATE: 8 JAN 1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: WINDOWS 95
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TELEPHONE: (856) 810-1515
TELEFAX: (856) 810-1454
INFORMATION FOR SEQ ID NO: 64:
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                                                                                                     Query Match
Best Local Similarity 64.89
Matches 193; Conservative
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                   ; LIBRARY: GenBar
; CLONE: 1335856
US-08-878-989-21
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
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US-09-101-146-64
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                                                                                                                                                                                                                                                                                                                                                        285 VSISPNDSLFEAVYTLIKNRIHRLPVLDPVSGNVLHILTHKRLLKFLHIFGSLLPRPSFL 344
                                                                                                                                                                                                                                                345 YRTIQDLGIGTFRDLAVVLETAPILTALDIFVDRRVSALPVVNECGQVVGLYSRFDVIHL 404
165 APFPKLGWDDELRKPGAQIYMRFMQEHTCYDAMATSSKLVIFDTMLEIKKAFFALVANGV 224
                                                                                225 RAAPLWDSKKQSFVGMLTITDFILVLHRYYRSPLVQIYEIEQHKIETWREIYLQGCFKPL 284
                                       68
                                       9 APAPENEHSQETPESNSSVYTTFMKSHRCYDLIPTSSKLVVFDTSLQVKKAFFALVTNGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN
TITLE OF INVENTION: KINASES
NUMBER OF SEQUENCES: 21
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US/08/878,989
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Patent No. 5885803
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Hillman, Jennifer L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Billings, Lucy J J REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                     LGVVSLSDILQALVLS 480
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APPLICANT: Guegler, Karl G.
APPLICANT: Lal, Preeti
APPLICANT: Goli, Surya K.
APPLICANT: Shah, Purvi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
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LENGTH: 331 amino acids
TYPE: amino acid
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TELEFAX: 415-845-4166
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INFORMATION FOR SEQ ID NO:
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TOPOLOGY: linear
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CLASSIFICATION: 435
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                                                                                                                         69
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                                                                          Length 331;
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                                                                                                         Indels
                                                                         40.1%; Score 1017; DB 4; 64.8%; Pred. No. 2.7e-104;
                                                                                                         53; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/359,161A CURRENT FILING DATE: 1999-07-21 NUMBER OF SEQ ID NOS: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: kinase subunit (SNF1) US-09-359-161-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 7, Application US/09359161A; Patent No. 6342656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Saccharomyces cerevisiae
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Best Local Similarity 34.28
Watches 106; Conservative
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APPLICANT: Bradford, Kent J.
APPLICANT: Dahal, Peetambar
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                                                                                                       Matches 193; Conservative
           LIBRARY: GenBank
                                                                                          Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION:
                       1335856
             ; LIBRARY:
; CLONE: 1
US-09-272-796-21
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                                                                         Query Match
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SEQ ID NO 7
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                                                      183 IYMRFMQEHTCYDAMATSSKLVIFDTMLEIKKAFFALVANGVRAAPLWDSKKQSFVGMLT 242
                                                                                                                      243 ITDFILVLHRYYRSPLVQIYEIEQHKIETWREIYLQGCFKPLVSISPNDSLFEAVYTLIK 302
                                                                                                                                         303 NRIHRLPVLDPVSGNVLHILTHKRILKPLHIFGSILPRPSFLYRTIQDLGIGTFRDLAVV 362
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64.8%; Pred. No. 2.7e-104;
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3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/09/272,796
                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 21, Application US/09272796
Patent No. 6207148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bandman, Olga
Hillman, Jennifer L.
Corley, Neil C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Billings, Lucy J J REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 21: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Guegler, Karl G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lal, Preeti
Goli, Surya K.
Shah, Purvi
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COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
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TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                       193; Conservative
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        Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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CLASSIFICATION:
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APPLICANT: Cooley, Michael
APPLICANT: Cooley, Michael
APPLICANT: Downie, Bruce
APPLICANT: Gee, Oliver
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Regulation of Source-Sink Relationships and Responses
FILE REFERENCE: 023070-0959000S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              423 QRTLCLEGVLSCQPHESLGEVIDRIAREQVHRLVLVDETQHLLGVVSLSDILQALVLS 480
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186 RFMQEHTCYDAMATSSKLVIFDTMLEIKKAFFALVANGVRAAPL------ 230
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SALPVVNECG-------QVVGLYSRFDVIHLAAQQTYNHLDMSVGEALRQRT 425
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Lycopersicon esculentum sucrose non-fermenting protein OTHER INFORMATION: kinase activation subunit 4 (LesNF4)
                                                                                            APPLICANT: Bradford, Kent J.
APPLICANT: Dahal, Peetambar
APPLICANT: Yang, Hong
APPLICANT: Yang, Hong
APPLICANT: Cooley, Michael
APPLICANT: Cooley, Michael
APPLICANT: Geo, Oliver
APPLICANT: Of Regents of the University of California
TITLE OF INVENTION: Regulation of Source-Sink Relationships and Responses
TITLE APPLICATION UNMER: US/09/359,161A
CURRENT FILING DATE: 1999-07-21
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Pred. No. 2.9e-12;
66; Mismatches 126; Indels
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                                      Sequence 3, Application US/09359161A Patent No. 6342656 GENERAL INFORMATION:
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Matches 82; Conserv
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APPLICANT: Dahal, Peetambar
APPLICANT: Dahal, Peetambar
APPLICANT: Cooley, Michael
APPLICANT: Cooley, Michael
APPLICANT: Gee, Oilver
APPLICANT: Gee, Oilver
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Regulation of Source-Sink Relationships and Responses
TITLE OF INVENTION: to Stress Conditions in Plants
TITLE OF INVENTION: O559000US
CURRENT APPLICATION NUMBER: US/09/359,161A
CURRENT FILING DATE: 1999-07-21
NUMBER OF SEQ. ID NOS: 7
SOFTWARE: Patentin Ver. 2.1
                      DLGIGTFRDLAVVLETAPILTALDIFVDRRVSALPVVNECGQVVGLYSRFDVIHLAAQQT 409
                                                                         410 YNHLDMSVGEALRQRTLCLEGVLSCQPHESLGEVIDRIAREQVHRLVLVDETQHLLGVVS 469
                                                                                                188 MQEHTCYDAMATSSKLVIFDTMLEIKKAFFALVANGVRAAPL-----W-----DS 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          77 DKQTGAVRKHYIGMVTMLD1LAHIAGDDHLSCGDNITQ--DLDQRMSDSVSSIIGHSFEG 134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               325 KRILKFLHIFGSLLPRPSFLYRTIQDLGIGTFRDLAVVLETAPILTALDIFVDRRVSALP 384
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     233 KKQS-----FVGMLTITDFILVL----HRYYRSPLVQIYEIEQHKIETWREIY---LQG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Phaseolus vulgaris L. Pv42
                                                                                                                                                                                                                                                                        US-09-359-161-5; Sequence 5, Application US/09359161A; Patent No. 6342656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23.5%;
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Matches 85; Conserv
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US-09-359-161-5
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76 EGPRSRRAAEST-GLEAT-----FPKTTPLAQAD------PAGVGTPPTGWD---C 116
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                                                                                                                                                                                                                                                                                                                                                                                                                        38 PSPAVTSS-----KSVEEGEPPGQG 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19 PAPCTIRSCPPRSGRGRGISRSAGSDR-RGRRANGARRWIRRLPPRPGRSLADAAPAPCA 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              117 LPSD----CTASAAGSSTDDVELATEFPATEAWECELEGLLEERPALCLSPQAPFP 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         138 APCSRGRPCAAP------PPSPAW------PARSSAGSAPSP 167
                                                                                                                                                                                                                                                                                                                                                                               72;
                                                                                                                                                                                                                                                                                                                                  4.0%; Score 101; DB 4; Length 187; 25.0%; Pred. No. 0.0069; Live 14; Mismatches 46; Indels
      TITLE OF INVENTION: VIRULENCE-ASSOCIATED NUCLEIC ACID
TITLE OF INVENTION: SEQUENCES AND USES THEREOF
FILE REPERBACE: 00786/3611002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Childyal, Namit
TITLE OF INVENTION: Human B3 Ubiquitin Protein
TITLE OF INVENTION: Ligase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/070,060
FILING DATE: 30-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: ZENECA Pharmaceuticals, Inc. STREET: 1800 Concord Pike
                                             FILE REFERENCE: 00786/361002
CURRENT APPLICATION NUMBER: US/09/199,637A
CURRENT FILING DATE: 1998-11-25
PRIOR APPLICATION NUMBER: 60/066,517
PRIOR FILING DATE: 1997-11-25
                                                                                                                                                        NUMBER OF SEQ ID NOS: 437
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PHM.70312
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; Patent No. 5976849
                                                                                                                                                                                                                                                                  ORGANISM: Pseudomonas aeruginosa
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 302.886.4889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : Diskette
IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 05-FEB-1998 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Higgins, Patrick H
REGISTRATION NUMBER: 39,7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 852 amino acids TYPE: amino acid
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Matches 44; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 11 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
PRIOR APPLICATION DATA:
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COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM:
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                                                                                                                                                                                                   SEQ ID NO 287
LENGTH: 187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : | | | | | | : | : | : | : | | 1224 ADDEGNLSKGERVRAWIRARLPACCLERDS-----WSAYIFPPQSRFRLLCHRIITHKM 1277
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          114 ------WDCLPSDC-----TASAAGSSTDDVE------LATEFPATEAWE 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           147 CELEGLIE--ER------PALCLSPQAPFPKLGWDDELRKPGA--QIYMRFMQEHTC 193
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                                                                                                                                                                                                                                              4.0%; Score 102; DB 4; Length 2273;
19.5%; Pred. No. 0.4;
tive 77; Mismatches 194; Indels 234; Gaps
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FILE REFERENCE: ORT-1057
CURRENT APPLICATION NUMBER: US/09/426,998
CURRENT FILING DATE: 1999-10-26
NUMBER OF SEQ ID NOS: 5
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Patent No. 6355411
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APPLICANT: Ausubel, Frederick
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Rahme, Laurence G.
                                                                                                                                                                                                                                Query Match 19.58.
Best Local Similarity 19.58.
Matches 122; Conservative
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                                                                                      SOFTWARE: PATENTIN VER. 2.0
SEQ ID NO 5
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Cao, Hui
                                                                                                                                                                            ; ORGANISM: HOMO SAPIENS
US-09-426-998-5
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APPLICANT:
                                                                                                                                                          TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 EPGLEHALRRTPSWSSLGGSEHQEMSFLEQENSSSWPSPAVTSSSERIRGKRRAKALRWT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   48; Gaps
329 FTRTTTWQRPTLESVRNYEQWQLQ---RSQLQGAMQQFNQRFIYGNQDLF 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic , OTHER INFORMATION: Sequence US-09-562-737-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 4; Length 830; 0.32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                74; Indels
                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Herz, Joachim
APPLICANT: Gotthardt, Michael
TITLE OF INVENTION: LDL Receptor Signaling Pathways
FILE REFRENCE: UTSW0708
CURRENT APPLICATION NUMBER: US/09/562,737
CURRENT FILING DATE: 2000-05-01
NUMBER OF SEO ID NOS: 132
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/582,945
FILING DATE: 19901012
CLASS.FICGATION: 424
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 3.8%; Score 96; DB Best Local Similarity 24.5%; Pred. No. 0.32 Matches 46; Conservative 20; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: TAKKER FOGED, Niels
APPLICANT: PETERSON, Svend
TITLE OF INVENTION: A PASTEURELLA VACCINE
NUMBER OF SEQUENCES: 2
CORRESSPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                    ; Sequence 33, Application US/09562737; Patent No. 6428967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-07-582-945-2; Sequence 2, Application US/07582945; Patent No. 5369019
                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                PatentIn Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                      : | : : | : : | : : | : | : | 193 SNGGFKPSRPPRPRPASVNGSPSA----TSESDGSSTGSLPPTNTNTSE 248
                                                                                                                                                                                                                                                                                                                                                                                                      LATE---FPATEAWECELEGLLEERPALCLSP--QAPFPKLGWDDELRKPGAQIYMRFMQ 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ------RPEPLPPGWERRVDN-MGRIYYVDH 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         85 ESTGLEATFP----KTTPLAQADPAGVGTPPTGWDCLPSDCTASAAGS-----STDDVE 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  193 SNGGFKPSRPPRPSRPPPTPRRPASVNGSPSA----TSESDGSSTGSLPPTNTNTSE 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   135 LATE---FPATEAWECELEGLI, EERPAI, CLSP--QAPFPKLGWDDELRKPGAQIYMRFMQ 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   249 GAISGLIPLT-----ISGGSGPRP---LNPVTQAPLPP-GWEQRVDQHGRVYYVDHVE 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              190 EHTCYDAMATSSKLVIFDTMLEIKKAFFALVANGVRAAPL---WDSKKQSFVGMLTITUF 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             134 LESEVVINGETICSESASQNDDGSRSKDETRVSTNGS-DDPEDAGAGENRRVSGNNSPSL 192
                                                                                                                                                                                                                                                                                                         ESTGLEATFP----KTTPLAQADPAGVGTPPTGWDCLPSDCTASAAGS-----STDDVE 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                249 GAISGLIIPLT----ISGGSGPRP---LNPVTQAPLPP-GWEQRVDQHGRVYYVDHVE 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EHTCYDAMATSSKLVIFDTMLEIKKAFFALVANGVRAAPL --- WDSKKQSFVGMLTITDF 246
                                                                                                                                                                                                              29 LEQENSSSWPSPAVTSSSERIRGKRRAKALRWTRQKSVEEGEPPGQGEGPR----SRPAA 84
                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29 I.EQENSSSWPSPAVTSSSERIRGKRRAKALRWTRQKSVEEGEPPGQGEGPR----SRPAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FTRITTWORPILESVRNYEQWQLQ---RSQLQGAMQQFNQRFIYGNQDLF 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            247 ILVLHRYYRSPLVQIYEIEQHKIETWREIYLQGCFKPLVS--ISPNDSLF 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         247 ILVLHRYYRSPLVQIYEIEQHKIETWREIYLQGCFKPLVS--ISPNDSLF 294
                                                                                                                                                                  72;
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                                                                                                                                         ; Pred. No. 0.26;
40; Mismatches 114; Indels
                                                                                                                   DB 2; Length 852;
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GENERAL INCORATION:
TITLE OF INVENTION: HUMAN E3 UBIQUITIN PROTEIN LIGASE
FILE REFERENCE: PHM. 70312.N1
CURRENT APPLICATION NUMBER: US/09/357,746
CURRENT FILING DATE: 1999-07-21
EARLIER APPLICATION NUMBER: US NO. 6087122 60/073,839
EARLIER FILING DATE: 1998-03-05
EARLIER FILING DATE: 1998-04-30
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                   Score 97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3, Application US/09357746 Patent No. 6087122
                                                                                                                3.8%; 22.1%;
                                                                                                                                                               64; Conservative
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  unknown
                      TOPOLOGY: unknown MOLECULE TYPE: peptide
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Best Local Similarity (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Homo sapiens
                                                                                                                Query Match
Best Local Similarity
Matches 64; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               299 KRTTWD----
STRANDEDNESS:
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US-09-357-746-3
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179 PGAQIYMRFMQEHTCYDAMATSSKLVIFDTMLEIKKAFFALVANGVRAAPLWDSKKQSFV 238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               :| :| | ::| ::| 322 GIDKALQYIAEESPEWPANKYILYNPTH---LETENLFNIMMKRTE--QRMLEDSDVQIR 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---QALA 486
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  239 GML------PLVQIYEIEQH 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                262 GLPTPKVILYIPGGTQPFVEFLNTDDLKQWIAMHLKDNKHWYRFRKHFSLKQRQEGETFT 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           311 -LD------PVSGNVLHILTHKRLLKFLHIFGSLLPRPSFLYRTIQDLGI--- 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            354 ---GTFRDLAV-VLET-APILTALDIFV------DRR 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      377 SNSEATRDYALSLLETFISQLSAIDMLVPAVGIPINFALSATALGLSSDIVVNGDSYEKR 436
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 3.7%; Score 94.5; DB 1; Length 1285;
Best Local Similarity 19.9%; Pred. No. 1;
Matches 81; Conservative 58; Mismatches 109; Indels 159; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            :: :||::| :: :| |:: | |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |
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qq
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Search completed: June 6, 2003, 11:04:13 Job time: 31.1173 secs

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GenCore version 5.1.6
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OM protein - pr	OM protein - protein search, using sw model
Run on:	June 6, 2003, 11:02:59; Search time 40.2504 Seconds (without alignments) 1254.259 Million cell updates/sec
Title: Perfect score: Sequence:	US-09-826-581-6 2538 1 MEPGLEHALRRTPSWSSLGGLSDILQALVLSPAGIDALGA 489

1 MEPGLEHALRRTPSWSSLGG......LSDILQALVLSPAGIDALGA 392085 segs, 103240269 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table: Searched:

Total number of hits satisfying chosen parameters: Minimum DB seq length: 0 Maximum DB seq length: 2000000000

392085

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

1: //ggnl_c/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*
2: //ggnl_c/ptodata/2/pubpaa/NCS_NEW_PUB.pep:*
3: //ggnl_c/ptodata/2/pubpaa/NCS_NEW_PUB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Sequence 6, Appli Sequence 11, Appl Sequence 195, Appl Sequence 33979, Appl Sequence 50, Appl Sequence 6006, Appl Sequence 12, Appl Sequence 12, Appli Sequence 1, Appli Sequence 1, Appli Sequence 3, Appli Sequence 10, Appli Sequence 11, Appli Sequence 12, Appli Sequence 13, Appli Sequence 13, Appli Sequence 13, Appli Sequence 13, Appli Sequence 13, Appli
SUMMARTES ID	US-09-826-581-6 US-10-108-605-71 US-10-108-605-71 US-10-108-605-19 US-09-864-761-33979 US-09-975-719-287 US-09-975-719-287 US-09-738-626-6006 US-09-738-626-6006 US-09-738-626-6006 US-10-052-092-12 US-10-052-092-12 US-10-052-093-12 US-10-077-89-33 US-10-211-962-33 US-10-273-8626-4919 US-10-273-8626-4919 US-10-273-962-33 US-10-273-962-33 US-10-273-962-33 US-10-273-962-33 US-10-273-8626-4919 US-10-273-962-33 US-10-273-962-33
DB	000000000000000000000000000000000000000
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Score	2538 1017 892.5 114 105.5 100 99.5 97.5 97.5 97.5 97.5 97.5 97.5 97.5
Result No.	100 8 4 5 5 7 7 8 6 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8

Sequence 5, Appli Sequence 24, Appl Sequence 31, Appl Sequence 31, Appl Sequence 4, Appli Sequence 4, Appli Sequence 4, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 4, Appli Sequence 1, Appli	Sequence 5, Appli Sequence 2, Appli Sequence 14028, A Sequence 6, Appli Sequence 12, Appli Sequence 12, Appl
12 US-10-819-104A-5 US-10-042-417-44 9 US-10-072-02-4 10 US-10-052-092-31 10 US-09-813-013-4 9 US-10-26-103-4 9 US-10-26-296-4 9 US-10-26-318-4 9 US-10-26-318-4 9 US-10-26-81-136-93 10 US-09-81-242-13693 10 US-09-81-242-13693 10 US-09-81-26-91-2 9 US-09-81-26-91-2 9 US-09-81-26-91-2 9 US-09-81-26-91-2 9 US-09-81-26-91-2 10 US-09-81-26-91-2 9 US-09-81-26-91-2 9 US-09-81-774-1 9 US-09-81-774-1	9 US-00-044-539-5 9 US-09-819-104A-2 10 US-09-815-242-14028 10 US-09-815-033-6 9 US-09-388-221-4 9 US-09-388-221-12 9 US-10-028-392-11
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ALIGNMENTS

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N N	489;	RGKRR RGKRR	PPTGW PPTGW	CGWDD	WDSKK WDSKK
PROT	Length 489 ndels 0	SSERI	AGVGT AGVGT	APFPK APFPK	RAAPL RAAPL
VATED	Н	PAVTS	AQADP, AQADP	CLSPQ CLSPQ	VANGV VANGV
-ACTI	DB 10 e-209 0;	SSWPS SSWPS	KTTPL KTTPL	ERPAL ERPAL	AFFAL AFFAL
N AMP 1	Score 2538; DB 10; Pred. No. 1.5e-209; Mismatches 0;	EQENS - - EQENS	eatep Eatep	EGLLE EGLLE	LEIKK LEIKK
HUMA. 26,58 ,665	ore 2538; ed. No. 1. Mismatches	EMSFL EMSFL	ESTGL ESTGL	WECEL WECEL	IFDTM FDTM
25581 SY09/8 105 105 105 105 105 105 105 105	0;	GSEHQ GSEHQ	SRPAA SRPAA	PATEA PATEA	SSKLV
-6 Application US/09826581 ORMATION: Andersson, Leif Luthman, L. Holger Marklund, Stefan NVENTION: VARIANTS OF THE HUMAN NVENTION: VARIANTS OF THE HUMAN PLICATION NUMBER: US/09/826,581 LING DATE: 2001-04-05 SEQ ID NOS: 14 FastSEQ for Windows Version 4.0 R9 Homo sapiens -6	.0%;	WSSLG WSSLG	GEGPR GEGPR	LATEF LATEF	DAMAT DAMAT
on US 310A1 , Lei b. H. 7 Ste 7 Ste 7 Ste 8 Ste	/at	RRTPS RRTPS	EPPGQ EPPGQ	TDDVE TDDVE	EHTCY EHTCY
LT 1 quence 6, Application US/0982 tent No. US20020142310A1 WRRAL INFORMATION: PPLICANT: AnderSson, Leif PPLICANT: AnderSson, Leif PPLICANT: Marklund, Stefan ITLE OF INVENTION: VARIANTS OF ILE REPERENCE: 11145-007001 URRENT FILING DATE: 2001-04- RROR PPLICATION NUMBER: US 6 RIOR FILING DATE: 2000-04-07 OWHERDER OF SEQ ID NOS: 14 OWHER OF SEQ ID NOS: 14	100 1 Similarity 100 489; Conservative	LEHAL LEHAL	SVEEG SVEEG	AAGSS AAGSS	MRFMQ
-6 US200 ORMATO ORMATO Ande Lut MAT NVENT ENCE: PLICA LING LING LING LING FESTS SEQ I FESTS	Simil 9; C				
LT 1 quence 6, 4 quence 6, 5 tent No. 6, 5 tent No. 6, 5 PPLICANT: 1 PPLICANT: 1 PPLICANT: 1 PPLICANT: 1 IT R. 60 INV URRENT APPLI. URRENT APPLI. RIOR APPLICANT RIOR FILING URMERO 6 SE OUTHARE: Fat	Match ocal s 48		61	121	181
RESULT 1 US-09-826-581-6 Sequence 6, Application US/09826581 Patent No. US20020142310A1 GENERAL INFORMATION: APPLICANT: Andersson, Leif APPLICANT: Luthman, L. Holger APPLICANT: Marklund, Stefan TITLE OF INVENTION: VARIANTS OF THE HUMAN FILE REPERENCE: 11145-007001 CURRENT APPLICATION NUMBER: US/09/826,581 CURRENT FILING DATE: 2001-04-05 PRIOR FILING DATE: 2000-04-07 NUMBER OS SEQ ID NOS: 14 SEQ ID NO 6 SEQ ID NO 6 LENGTH: 489 TYPE: PAT ORGANISM: Homo sapiens	Query Match Best Local Similarity Matches 489; Conser				
RESULT (18-09-18-0	OMX	QĀ	QY Db	QY GB	Qy

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93; Mismatches
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Patent No. US20020160934A1
GENERAL INFORMATION:
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               APPLICANT: Stam, Lynn
APPLICANT: Bachmann, Jane
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                                                    IKNRIHRLPVLDPVSGNVLHILTHKRLLKFLHIFGSLLPRPSFLYRTIQDLGIGTFRDLA 360
                                                                 VVLETAPILTALDIFVDRRVSALPVVNECGQVVGLYSRFDVIHLAAQQTYNHLDMSVGEA 420
                                                                                                                   LRQRTLCLEGVLSCQPHESLGEVIDRIAREQVHRIJULVDETQHLLGVVSLSDILQALVLS 480
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TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA105
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64.8%; Pred. No. 3.6e-79;
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CURRENT APPLICATION NUMBER: PCT/US00/0599
PRIOR APPLICATION NUMBER: PCT/US00/0599
PRIOR TILING DATE: 2000-03-08
PRIOR PILING DATE: 1999-03-12
NUMBER OF SEO ID NOS: 928
SOFTWARE: PATENTIN VET. 2.0
                                                                                                                                                                                                                                                                                                    ; Sequence 461, Application US/09925297
; Patent No. US20020091659A1
; GENERAL INFORMATION:
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Patent No. US20020160934A1
GENERAL INFORMATION:
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US-10-108-605-71
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APPLICANT: Kandar, Vance
APPLICANT: Kandar, Vance
APPLICANT: Kandar, Kim
TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FROM DROSOPHILA MELANOGASTER THAT E
TITLE OF INVENTION: PROTEINS ESSENTIAL FOR LARVAL VIABILITY AND USES THEREOF
FILE REFERENCE: 31133B
CURRENT APPLICATION NUMBER: US/10/108,605
CURRENT FILING DATE: 2002-03-27
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2000-01-14
NUMBER OF SEQ ID NOS: 361
SOFTHARE: PALENTIN VANCE: 21
SOFTHARE: PALENTIN VANCE: 21
LENGTH: 1207
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APPLICANT: Stam, Lynn
APPLICANT: Bachmann, Jane
APPLICANT: Mandar, Jane
APPLICANT: Admidar, Nim
TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FROM DROSOPHILA MELANOGASTER THAT F
TITLE OF INVENTION: PROTEINS ESSENTIAL FOR LARVAL VIABILITY AND USES THEREOF
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APPLICANT: Chen, Sei-Yu
APPLICANT: Sun, Yongming
APPLICANT: Liu, Chenghua
APPLICANT: Liu, Chenghua
APPLICANT: Turner, Leah
TITLE OF INVENTION: Compositions and Methods Relating to Lung Specific Genes and I
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NN: EXPRESSED IN PLACENTA, SIGNAL = 7.8

NN: EXPRESSED IN BY474, SIGNAL = 5.2

NN: EXPRESSED IN BY474, SIGNAL = 5.2

NN: EXPRESSED IN HOLIOO, SIGNAL = 6.5

NN: EXPRESSED IN HOLIOO, SIGNAL = 6.5

NN: EXPRESSED IN HOLIOO, SIGNAL = 4.8

NN: EXPRESSED IN ADULT LIVER, SIGNAL = 4.7

NN: EXPRESSED IN ADULT LIVER, SIGNAL = 5.4

NN: EXPRESSED IN BRAIN, SIGNAL = 5.4

NN: EXPRESSED IN HEART, SIGNAL = 5.4

NN: EXPRESSED IN HEART, SIGNAL = 5.9

NN: EXPRESSED IN HEART, SIGNAL = 5.9
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Pred. No. 0.018;
8; Mismatches 3; Indels
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PRIOR PAPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SECTION NOS: 49117
SECTION NOS: 49117
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                                                                                                                                                       FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00667
FILING DATE: 2001-01-30
                                                                                                                                                                                                                                FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00664
                                                                                                                                                                                                                                                                                                    FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00669
       2000-10-04
IUMBER: US 60/236,359
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Patent No. US20020160388A1
GENERAL INFORMATION:
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Best Local Similarity 65.6%;
Matches 21; Conservative E
                                                                                   2000-09-27
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APPLICANT: Recipon, Herve
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ORGANISM: Homo sapiens
FEATURE:
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TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: AGOMICA'-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PLVQIYEIEQHK-----IETWREIYLQGCFKPLVSISPNDSLFEAVYTLI-KNRIHR 307
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FILE REFERENCE: 31133B
CURRENT APPLICATION NUMBER: US/10/108,605
CURRENT FILING DATE: 2002-03-27
PRIOR APPLICATION NUMBER: US 09/761,142
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2000-01-14
PRIOR FILING DATE: 2000-01-14
NUMBER OF SEQ ID NOS: 361
SOFTWARE: Patentin Ver. 2.1
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PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
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APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
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              341 PSFLYRTIQDLGIGTFRDLAVVLETAPILTALDIFVDRRVSALPVVNE-CGQVVGLYSRF 399
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                                                                                                                 117 LPSD----CTASAAGSSTDDVELATEFPATEAWECELEGLLEERPALCLSPQAPFP 168
                                                                                                                                                                                 138 APCSRGRPCAAP------PARSSAGSAPSP 167
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19.8%; Pred. No. 2.6;
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CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-08-03
NUMBER: PRIOR PLING DATE: 2000-08-03
SOSTWARE: PATENTING NOS: 7059
SEQ ID NO 6006
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304 ILVDEYGGVAGLISIEDILEEIV 326
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ANDO, SEIKO
HAYASHI, MIKIRO
OCHIAI, KEIKO
YOKOI, HARUHIKO
TATEISHI, NAOKO
SENOH, AKHIRO
                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: NAKAGAWA, SATOSHI
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OZAKI, AKIO
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Best Local Similarity
Matches 64; Conservat
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US-09-738-626-6006
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    88 GLEATFPKTTPLAQADP--AGVGTPPTGWDCLPSDCTASAAGSSTDDVELATEFPATEAW 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 124 GVQLT-PETLVEAKEEPVEVPVGVPVV--EAVPEEGLAQVAPSESQ------PTLEMS 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        146 ECELEGILEERPALCLSPQAPFPKLGWDDELRKPGAQIYMRFMQEHTC-YDAMATSSKL- 203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           204 -----VIFDTMLEIKKAFFALVANGVRAAPLWDSKKQSFVGMLTITDFILVLHRYY 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              255 RSPLVQIYEIEQHKIETWREIYLQGCFKPLVSISPNDSLFEAVYTLIKNRIHRLPVLDPV 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19 PAPCTIRSCPPRSGRGRGTSRSAGSDR-RGRRANGARWTRRLPPRPGRSLADAAPAPCA 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           231 QARPLPSPGAAGAQALEKLEAAESLVL-------EQSFLHGITL-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              71; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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APPLICANT: Rahme, Laurence G.
TITLE OF INVENTION: VIRULENCE-ASSOCIATED NUCLEIC ACID
TITLE OF INVENTION: SEQUENCES AND USES THEREOF
FILE REFERENCE: 00786/361003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         46;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4.0%; Score 101; DB 9 ilarity 25.0%; Pred. No. 0.68; Conservative 14; Mismatches
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CURRENT FILING DATE: 2001-10-10
PRIOR APPLICATION NUMBER: US 09/199,637
PRIOR FILING DATE: 1998-11-25
PRIOR FILING DATE: 1997-11-25
NUMBER OF SEQ ID NOS: 437
SOCTWARE: FastSEQ for Windows Version 4.0
FILE REFERENCE: DEX-0275
CURRENT APPLICATION NUMBER: US/10/001,873
CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: 60/252,055
PRIOR FILING DATE: 2000-11-20
PRIOR FILING DATE: 2000-11-22
NUMBER OF SEO ID NOS: 55
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 105.5;
Pred. No. 4;
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Publication No. US20030022349A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 23.3%
Matches 70; Conservative
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; ORGANISM: Homo sapien
US-10-001-873-50
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Best Local Similarity
Matches 44, Conserva
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                                                                                                                                                                                                                                                                                                                                                       LENGTH: 1134
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APPLICANT: CELL SIGNALING TECHNOLOGY, INC.
APPLICANT: CELL SIGNALING TECHNOLOGY, INC.
APPLICANT: CENSEY, Katherine
APPLICANT: CROSSY, Katherine
APPLICANT: CROSSY, Katherine
APPLICANT: WJ. Jiong
TITLE OF INVENTION: Monoclonal Antibodies Specific for Phosphorylated Estrogen Re-
TITLE OF INVENTION: (Ser 118) and Uses Thereof
FILE REPRENUE: CST-202
CURRENT APPLICATION NUMBER: US/10/211,613
CURRENT APPLICATION NUMBER: US 60/310,066
PRIOR FILING DATE: 2001-08-03
NUMBER: OF SEQ ID NOS: 2
SOFTWARE: Patentin version 3.1
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94 PKTIPLAQADPAGVGTPPTGWDCLPSDCTASAAGSSTDDVELATEFPATEAWECELEGLL 153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 38 -MNLQGEEFVCLKSIILLN-----SGVYFFLSSTLKSLEEKDHIHR--VLDKIIDTLIH 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           321 ILT------HKRLLKFLHIFGSLLPRPSFLYRTIQDLGIGTFRDLAVVLETAPILTA 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       372 LDIFVDRRVSALPVVNECGQVVGLYSRFDVIHLAAQQTYNHLDMSVGEALRQRTLCLEGV 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                522 ------KC--VEGMVEIFDML-LATSSRFRMMNLO-GEEF----VCLKSI 557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           37 WPSPAVTSSSERIRGKRAKALRWTRQKSVE---EGEPPGQGEGPRSRPAAESTGLEATF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           214 KAFFALVANGVRAAPLWDSKKQSFVGMLTITDFILVLHRYYRSPLVQIYEIEQHKIETWR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      410 ------LDRNQGKCVEGMVEIFDMLLATSSRFRM----------
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                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                               66; Mismatches 126;
                            CURRENT FILING DATE: 2002-01-18
PRIOR APPLICATION NUMBER: US 60/262,990
PRIOR FILING DATE: 2001-01-19
PRIOR FILING DATE: 2001-01-19
PRIOR FILING DATE: 2001-07-09
NUMBER OF SEQ ID NOS: 49
SCHWARE PatentIn version 3.1
SEQ ID NO 12
LENGTH: 701
            CURRENT APPLICATION NUMBER: US/10/052,092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 1, Application US/10211613; Publication No. US20030099641A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: human
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Matches E
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APPLICANT: Allred, D.
APPLICANT: HOPP, Torsten A.
APPLICANT: O'Connell, Peter
TITLE OF INVENTION: Methods and Composition in Breast Cancer Diagnosis and Therapeuti
                                                                                                                                                                                                                                                                                                                                                                                                                                                  34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             276 RGQPSAAMEPMAAVQSTWEKPRPFTSVAP----LPPT--NCVPHGYTLGELEQRSDWIAP 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        450 TL-----ALL------DALYEGK---MYGVL-----VIAMDRFKRINESFGHKTGDGLLQ 490
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        704 ARQFQDEKWINSVLECLKRTGMPPEDLELEITESLAMEDIKGTVVLLHRLREGVQVAID 763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              79 RSRPAA---ESTGLEATFPKTTPLAQADPAGVGTPPTGWDCLP-----SDCTAS 124
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                                                                                                                                                                                                                                                                                                                                                                                               Query Match 3.9%; Score 100; DB 10; Length 1276; Best Local Similarity 20.3%; Pred. No. 14; Matches 115; Conservative 72; Mismatches 165; Indels 214; Gaps
                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Description of Unknown Organism:cph2 Locus SLL0821US-09-272-809-2
Patent No. US20020022339al
GENERAL INFORMATION:
APPLICANT: Lagarias, John C.
TITLE OF INVENTION: Phytofluors as fluorescent labels
FILE REFERENCE: 2500.118USO
CURRENT APPLICATION NUMBER: US/09/272,809
CURRENT FILING DATE: 1998-03-19
NUMBER OF SEQ ID NOS: 24
SOSTWARE: Patentin Ver, 2.0
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US-10-052-092-12
; Sequence 12, Application US/10052092
; Publication No. US20030027778A1
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                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Unknown
                                                                                                                                                                                                             SEQ ID NO 2
LENGTH: 1276
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                                                                                                                                                                                                                                                                                                           FEATURE:
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                                                                       514 PLTSSRSSMEM-PSQPAPRTVTDEEINFVKTCLQRWRSEIEQDIQDLKTCIASTTQTIEQ 572
                                                                                                                                                                                204 VIFDTMLE------WDS-KKQ 235
                                                                                                                                                                                                   151 GLLEERPALCLSPQAPFPKLGWDDE-----LRKPGAQIYMRFMQEHTCYDAMATSSKL 203
                                                                                                                                                                                                                                                                 94 PKTTPLAQADPAGVGTPPTGWDCLPSDCT---ASAAGSSTDDVELATEFPATEAWECELE 150
                                                                                                                                                                                                                                                -----OHKI 269
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LATE---FPATEAWECELEGELEERPALCLSP--OAPFPKLGWDDELKKPGADIYMRFMQ 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         136 GAISGLIIPLT-----ISGGSGPRP---LNPVTQAPLPP-GWEQRVDQHGRVYYVDHVE 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --- RPEPLPPGWERRVDN-MGRIYYVDH 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  85 ESTGLEATFP----KTTFLAQADPAGVGTPPTGWDCLPSDCTASAAGS-----STDDVE 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29 LEQENSSSWPSPAVTSSSERIRGKRRAKALRWTRQKSVEEGEPPGQGEGPR----SRPAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EHTCYDAMATSSKLVIFDTMLEIKKAFFALVANGVRAAPL---WDSKKQSFVGMLTITDF
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                                                                                                                                                                                                                                               236 SFVGMLTITDFILVLHR----YYRSPLV----QIYEIE-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 9; Length 739;
11;
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tive 40; Mismatches 114; Indels
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                                                                                                                                                                                                                                                                                                             270 ETWREIYLQGCFKPLVSISPNDS 292
                                                                                                                                                                                                                                                                                                                                          693 EEWEE--EOSCKIPOMESSTNSS 713
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 64; Conserv
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                                                                                                                               ----ILYSEY 331
                                                                                                                                                             94 PKTTPLAQADPAGVGTPPTGWDCLPSDCTASAAGSSTDDVELATEFPATEAWECELEGLL 153
                                                                                                                                                                                            332 DPTRPFSEASMMGLLT------NADRELVHMI----NWAKRVPGFV 368
                                                                                                                                                                                                                              EERPALCLSPQAPFPKLGWDDELRKPGAQIYMRFWQEHTCYDAMATSSKLVIFDTMLEIK 213
                                                                                                                                                                                                                                                         214 KAFFALVANGVRAAPLWDSKKQSFVGMLTITDFILVLHRYYRSPLVQIYEIEQHKIETWR 273
                                                                                                                                                                                                                                                                                                                                                          274 EIYLQG----CFKPLVSISPNDSLFEAVYTLI------KNRIHRLPVLDPVSGNVLH 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                          521
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                                                                                                                                                                                                                                                                                                                                                                                                                        ILT------HKRLLKFLHIFGSLLPRPSFLYRTIQDLGIGTFRDLAVVLETAPILTA 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KRRA------KALRWIRQKSVEEGEPPGQGEGP------RSRPAAESTGLEATF 93
                                                                                           37 WPSPAVTSSSERTRGKRRAKALRWTRQKSVE---EGEPPGQGEGPRSRPAAESTGLEATF
                                                                                                                                                                                                                                                                                                                        -----LDRNQGKCVEGMVEIFDMLLATSSRFRM-------
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APPLICANT: Curtis, Rory A. J.
APPLICANT: Curtis, Rory A. J.
APPLICANT: Bandaru, Rajasekhar
TITLE OF INVENTION: 48120, 23479 AND 46689, NOVEL HUMAN HYDROLASES
TITLE OF INVENTION: 48120, 23479 AND 46689, NOVEL HUMAN HYDROLASES
TITLE OF INVENTION: 48120, 23479 AND 46689, NOVEL HUMAN HYDROLASES
TITLE OF INVENTION: 48120, 23479 AND 46689, NOVEL HUMAN HYDROLASES
TITLE OF INTERPRETATION OF THE CONTROL OF THE COURRENT FILLING DATE: 2001-10-05
PRIOR FILLING DATE: 2000-10-05
PRIOR FILLING DATE: 2000-10-05
PRIOR FILLING DATE: 2000-10-05
NUMBER OF SEQ. ION NOSS: 20
NUMBER OF SEQ. ION NOSS: 20
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                                   Length 701;
                                                                                                                     292 WPSPLMIK-----RSKKNSLALSJ.TADQMVSALLDAEPP-----
                            3.9%; Score 99.5; DB 9;
17.2%; Pred. No. 6.4;
rative 66; Mismatches 126;
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Best Local_Similarity 19.8%; Pred. No. 19
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; Publication No. US20030032091A1
; GENERAL INFORMATION:
                                                                Conservative
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                            Query Match
Best Local Similarity
Matches 81; Conserv
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603 GPGPDIPCLPELQFGFITIFVGAFLLAPLFTLLNNRVE------IGLDAHKFLC 650
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                                                                                                                                                                                              389 TVFFSIFMSFWGHGLPGALEAGSATLAHHWDCSDFQDQEAMPSSAPHHWDC-----SDF 442
                                                                                                                                                                                                                                          DDVELATEPPATEAWECELEGLLEERP----ALCLSPQAPFPKLGWDDELRKPGAQIYM 185
                                                                                                                                                                                                                                                                                443 QDQEVMPS-SALHHWDCSDFQDQEECPHLQFAALALQ-MTQNPVTG----LKEP---- 490
                                                                                                                                                                                                                                                                                                                                             229 LWDSKKQSFVGMLTITDFILV-----LHRYYRSPLVQIYEIEQHKIETWREIYLQG 279
                                                                                                                                                                                                                                                                                                                                                                                                                                           548 LWGNG-----GPKALSKVLCVCQQQCGPGGCHIQVTQQLIIIMVGKQLLNHMEEFVGLGG 602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----CFKPL----VSISPNDSLFEAVYTLIKNRIHRLPVLDPVSGNVLHILTHKRLL 328
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                                       ---EAATPAAA-----GERRLRORRWRENFORN 333
  12 TPSW----SSLGGSEHQEMSFLEQENSSSWPSPAVTSSSERIRGKRRAKALRWTR--QKS 65
                                                                               ---KTTPLAO---
                                                                                                                                                                                                                                                                                                                      186 RFMQEHTCYDAMATSSKLVIFDTMLEIKKAFF--ALVANGV----
                                                                               66 VEEG--EPPGQGEGPRSRPAAESTGLEATFP----
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                                       296 TPRWVRLRARLGG-
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Job time: 43.2504 secs
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APPLICANT: Burgess, Catherine E.
TITLE OF INVENTION: No. US20020137202Alel Proteins and Nucleic Acids Encoding Same FILE REFERENCE: 15966-621
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | | | : : | : : | | : : | | 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RQKSVEEGEPPGQGEGPRSRPAAESTGLEATFPKTTPLAQADPAGVGTPPTGWDCLPSDC 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 EPGLEHALRRIPSWSSLGGSEHQEMSFLEQENSSSWPSPAVISSSERIRGKRRAKALRWT
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19.0%; Pred. No. 43;
ative 60; Mismatches 167; Indels 230;
FTRITTWORPILESVRNYEQWQLQ---RSQLQGAMQQFNQRFIYGNQBLF 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           48;
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                                                                                                               Sequence 33, Application US/10211962
Publication No. US20030082640A1
GENERAL INFORMATION:
APPLICANT: Joachim
APPLICANT: Gotthardt, Michael
TITLE OF INVENTION: LDL Receptor Signaling Pathways
                                                                                                                                                                                                                                    FILE REFERENCE: UTSW0708
CURRENT APPLICATION NUMBER: US/10/211,962
CURRENT FILING DATE: 2002-08-01
PRIOR APPLICATION NUMBER: US/09/562,737
PRIOR FILING DATE: 2000-05-01
NUMBER OF SEQ ID NOS: 132
SECTION 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/746,491
CURRENT FILING DATE: 2000-12-20
PRIOR APPLICATION NUMBER: USSN 60/171,329
PRIOR FILING DATE: 1999-12-21
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; Sequence 8, Application US/09746491
; Patent No. US20020137202A1
                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Artificial Sequence
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SOFTWARE: Patentin Ver. 2.0
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Best Local Similarity 19.05
Matches 107; Conservative
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US-09-746-491-8
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AAG35967 AAW71562 AAW71560 AAW71580

Drosophila melanog Drosophila melanog Drosophila melanog

ABB67322 ABB67321 ABB58729 ABG26522 AAU41694

Novel human diagno Propionibacterium Amino acid sequenc

Human native hepat

Human secreted pro Human polypeptide Thermophilus therm

AAU39054 ABB55763

AAY05940 ABG08090

AAY29189

AAY29328

Human secreted pro

Novel human diagno

polypeptide polypeptide

Human

Human

Thermophilus therm

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Human; AMP-activated protein kinase gamma 3 subunit; PRKAG3; variant; metabolic disease; diabetes; obesity; substitution; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers 71
                                                                                                                                                                                                                                                                                                                                                                                                                                AAB47679 standard; Protein; 489 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    06-APR-2001; 2001WO-SE00765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-APR-2000; 2000US-195665P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Andersson L, Luthman H,
                                                                                                 Misc-difference 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (AREX-) AREXIS AB.
Misc-difference
 WO200177305-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-JAN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 1
                                                                                                                                                                                                                                                                                                                                                                                                                      AAB47679
 Human AMPK gamma's
Pig PRKAG3 polymor
Pig AMPK gamma'sub
Pig PRKAG3 polymor
Pig PRKAG3 polymor
Sus scrofe Prkag3
Pig PRKAG3 polymor
Sus scrofe Prkag3
Pig PRKAG3 polymor
Novel human diagno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRKAG3. Homo sap
                                                                              (without alignments)
827.023 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                     2. SIDSZ/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
2. SIDSZ/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
3. SIDSZ/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
3. SIDSZ/gcgdata/geneseq/geneseqp-embl/AA1982.DAT:*
5. SIDSZ/gcgdata/geneseq/geneseqp-embl/AA1984.DAT:*
6. SIDSZ/gcgdata/geneseq/geneseqp-embl/AA1984.DAT:*
7. SIDSZ/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
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                                                                   June 6, 2003, 10:55:08 ; Search time 6.60595 Seconds
                                                                                                                                .....PGQGEGPRSRPAAESTGLEA
        GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                908470 seqs, 133250620 residues
                                                                                                                                                                                                                                                     Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAE22985
AAE00222
AAE22984
AAE22987
AAE22988
AAE00224
AAE22986
                                                protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB47679
AAE00223
                                                                                                           US-09-826-581-6_COPY_51_91
                                                                                                                                                   BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                    214
1 GKRRAKALRWTRQKSVEBGE.
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                                                                                                                                                                                                                         Minimum DB seq length: 0 Maximum DB seq length: 2000000000
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Match Length DB
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                                                                                                                     Perfect score:
                                                                                                                                                    Scoring table:
                                                OM protein
                                                                                                                                                                                  Searched:
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                                                                   Run on:
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Drosophilā melanog Novel human diagno Human osteoclast a Human osteoclast a Fbox protein FBP-Human ZPZ6 protein Human protein phos

SGP018 phosp

Human Human

AAE04836

AAY70506

polypeptide

human diagno

Amino Novel Human

acid sequenc protein phos

AAU96712 AAY83085 AAB48307 AAE14452 AAU82751 ABG27792 AAU75786

ABG03531 AAU96713

ABB64979

AAM39328 AAM41114

C glutamicum prote Human BAG-1L prote

human diagno

protein segu

ALIGNMENTS

Marklund S;

Rogel-Gaillard C;

variant

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activity, and for restoring a normal AMPK function. PRRAGS sequence and its functionally altered mutants are useful for the diagnostic evaluation, genetic testing and prognosis of a metabolic disorder, preferably a carbohydrate metabolism disorder. Primers that can detect a genetic polymorphic marker linked to a sequence encoding PRRAG3, are useful for detecting a dysfunction of carbohydrate metabolism resulting from the expression of a functionally altered allele of PRRAG3.

Transgenic animal and host cell transformed with PRRAG3 or a heterotrimeric AMPK consisting of PRRAG3 or its mutant, are useful for screening compounds able to modulate AMPK activity. Nucleic acid encoding PRRAG3 is useful for detecting mutations in a Prkag3 gene, or in a sequence encoding the first cystathione beta synthase (CBS) domain of PRRAG3 and is useful in gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence is human adenosine monophosphate (AMP)-activated Kinase (AMPK) gamma subunit muscle-specific isoform, complete PRKAG3. Mutation in Prkag3 results in an altered regulation of carbohydrate metabolism, particularly in skeletal muscle. PRKAG3 is useful as therapeutic for treating carbohydrate metabolism disorders such as diabetes, obesity, and disorders associated with muscle metabolism as diabetes, obesity, and disorders associated with muscle metabolism such as myopathy and cardiovascular diseases, to modulate AMPK
                                                                                                                                                                                                                                                                                                                                                                       New variants of the gamma subunit of vertebrate adenosine monophosphate-activated kinase for diagnosis or treatment of disorders associated with energy metabolism such as diabetes, obesity, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AMP activated protein kinase regulatory gamma subunit; PRKAG3 gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    screening; meat quality; single nucleotide polymorphism; SNP; pig;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "Wild type Asn is substituted with Thr due
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 210; DB 22; Length 464; Pred. No. 1.9e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GKRRAKALRWIRQKSVEEGEPPGQGEGPRSRPAAESTGLEA 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26 GKRRAKALRWTRQKSVEGGEPPGQGEGPRSRPTAESTGLEA 66
                                                                                                                                                                                                                              ooft C, Kalm E, Milan D, Robic A,
Gellin J, Le Roy P, Chardon P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pig PRKAG3 polymorphic variant (PRKAG3-30).
                                                                                                        INRA INST NAT RECH AGRONOMIQUE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAE22985 standard; Protein; 464 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 5; Fig 3; 71pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98.1%;
97.6%;
                              10-SEP-1999; 99EP-0402236.
18-MAY-2000; 2000EP-0401388.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 97.6
ses 40; Conservative
                                                                                                                                                                                                                              Looft C,
                                                                                                                                                                                                                                                                                                  WPI; 2001-244810/25.
N-PSDB; AAD03320.
                                                                                                                             ANDERSSON 1
LOOFT C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      464 AA;
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                                                                                                                                                                             KALM E.
                                                                                                                                                                                                                                                    Tannuccelli N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-AUG-2002
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                                                                                                                                                                                                                                Andersson
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAE22985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      myopathy
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                                                                                                        (INRG)
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                                                                                                                                                                             (KALM/)
                                                                                                                               (ANDE/)
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0
                                                                    New variants of human AMP-activated protein kinase gamma3 subunit associated with a metabolic disease e.g. diabetes or obesity and method for determining a risk estimate of diseases in subject by detecting the
                                                                                                                                                                                                                                                               AMP-activated protein kinase gamma 3 subunit (PRKAG3). Detecting the presence of the PRKAG3 DNA, or a variant, is useful in determining a risk estimate of a metabolic disease, such as diabetes or obesity, in a subject. The variation may occur in exons 3, 4 or 10. In exon 3 variation may be a substitution of a G for a C at nucleotide 320, resulting in the amino acid substitution p71A; in exon 4 variation may be a substitution of a T for a C at nucleotide 130, variation may be a substitution of a T for a C at nucleotide 1037, resulting in the amino acid substitution for a T for a C at nucleotide 1037, resulting in the amino acid substitution RMA. There may also be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRRAG3; diabetes; obesity; myopathy; cardiovascular disease; anorectic; genetic testing; carbohydrate metabolism disorder; skeletal muscle; cystathione beta synthase; CBS; cardiant; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; gamma subunit; adenosine monophosphate-activated kinase; AMPK; PRKAG3; diabetes; obesity; myopathy: cardiovascular disease. anomonei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                  This sequence is encoded by the full length cDNA encoding the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human AMPK gamma subunit muscle-specific isoform, complete PRKAG3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 214; DB 22; Length 489; 100.0%; Pred. No. 6.3e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nuclectide variation in intron 6. The numbering of these variations is based on the full length cDNA, rather than on position 1 of the open reading frame.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "Cystathione beta synthase domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label= CBS
/note= "Cystathione beta synthase domain"
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/note≈ "Cystathione beta synthase domain"
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/note= "Cystathione beta synthase domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GKRRAKALRWTRQKSVEEGEPPGQGEGPRSRPAAESTGLEA 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51 GKRRAKALRWTRQKSVEEGEPPGQGEGPRSRPAAESTGLEA 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "RN- mutation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAE00223 standard; Protein; 464 AA.
                                                                                                                                                                                                 Disclosure; Fig 5; 25pp; English.
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WPI; 2001-657170/75.
N-PSDB; AAH43685.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
Matches 41; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           489 AA;
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AAE00223;

AAE00223

Domain

Domain

Domain

Domain

Sequence

Query Match

δ a ;

Gaps

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Indels

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defection of a curoupping marker linked to a sequence encoding PRKAG3 are useful for detecting a dysfunction of carbohydrate metabolism resulting from the expression of a functionally altered allele of PRKAG3.

Transgenic animal and host cell transformed with PRKAG3 or a heterotrimeric AMPK consisting of PRKAG3 or its mutant, are useful for screening compounds able to modulate AMPK activity. Nucleic acid encoding PRKAG3 is useful for detecting mutations in a prkag3 gene, or in a sequence encoding the first cystathione beta synthase (CBS) domain of PRKAG3 and is useful in gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (AMP) activated Kinase (AMPK) gamma subunit muscle-specific isoform, complete PRKAG3. Prkag3 gene is located in the RN locus of Chromosome 15. Mutation in Prkag3 gene is located in the RN locus of Chromosome 15. Mutation in Prkag3 results in an altered regulation of carbohydrate metabolism, particularly in skeletal muscle. PRKAG3 is useful as therapeuric for treating carbohydrate metabolism disorders such as diabetes, obesity, and disorders associated with muscle metabolism such as myopathy and cardiovascular diseases, to modulate AMPK activity, and for restoring a normal AMPK function. PRKAG3 sequence and its functionally altered mutants are useful for the diagnostic evaluation, genetic testing and prognosis of a metabolic disorder, preferably a carbohydrate metabolism disorder. Primers that can detect
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 monophosphate-activated kinase for diagnosis or treatment of disorders associated with energy metabolism such as diabetes, obesity, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kalm E, Milan D, Robic A, Rogel-Gaillard C;
J, Le Roy P, Chardon P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 464;
                                                                                                      /label= CBS
/note= "Cystathione beta synthase domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New variants of the gamma subunit of vertebrate adenosine
    "Cystathione beta synthase domain"
                                                                   synthase domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       present sequence is pig adenosine monophosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 142; DB 22;
Pred. No. 8.4e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3; Mismatches
                                         /label= CBS
/note=_"Cystathione beta
                                                                                                                                                                                                                                                                                                                                                              (INRG ) INRA INST NAT RECH AGRONOMIQUE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 5; Fig 3; 71pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                66.48;
68.38;
                                                                                                                                                                                                                                                       11-SEP-2000; 2000WO-EP09896.
                                                                                                                                                                                                                                                                                               10-SEP-1999; 99EP-0402236.
18-MAY-2000; 2000EP-0401388.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gellin J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 68.3
hes 28; Conservative
                     .382
                                                                                       400..453
      /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Looft C,
                                                                                                                                                                                                                                                                                                                                                                                 ANDERSSON L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-244810/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           464 AA;
                                                                                                                                                                                                                                                                                                                                                                                                   LOOFT C.
KALM E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAD03319
                                                                                                                                                                     WO200120003-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Andersson L, L
Iannuccelli N,
                                                                                                                                                                                                                                                                                            10-SEP-1999;
                                                                                                                                                                                                              22-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAE22984;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        myopathy
                                                                                                                                                                                                                                                                                                                                                                                                                      (KALM/)
                                                                                                                                                                                                                                                                                                                                                                                                       (LOOF/)
                                                                                                                                                                                                                                                                                                                                                                                   (ANDE/)
                          Domain
                                                                                       Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAE22984
    QY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AX D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pig; gamma subunit; adenosine monophosphate-activated kinase; AMPK; PRKAG3; diabetes; Obsaity; myopathy; cardiovascular disease; anorectic; genetic testing; carbohydrate metabolism disorder; skeletal muscle; cystathione beta synthase; CBS; cardiant; gene therapy; RN locus;
                                                                                                                                                                                                                                                                                                                                                                                              Screening animals to determine those likely to produce larger litters and improved meat quality traits involves assaying for the presence of polymorphisms in the AMP activated protein kinase regulatory gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a method for screening animals to determine those more likely to produce large litters and improved meat quality traits. The method involves assaying for the presence of a genotype in the sample of genetic material obtained from animal. The genotype is characterised by polymorphism(s) in the AMP activated protein share equilatory gamma subunit (PRRAG3) gene. The method is used for screening animals e.g., pigs to determine those most likely to exhibit improved meat quality traits and to produce larger litters. The present sequence is pig PRRAG3 polymorphic variant (PRRAG3-30).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pig AMPK gamma subunit muscle-specific isoform, complete PRKAG3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 144; DB 23; Length 464; Pred. No. 4.7e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "Cystathione beta synthase domain"
200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10; Indels
to single nucleotide polymorphism (SNP)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GKRRAKALRWIRQKSVEEGEPPGQGEGPRSRPAAESTGLEA 41
                                                                                                                                                                                                                                                                                          Malek M, Plastow G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 4.7e
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "RN- mutation site" 253..307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 91-93; 109pp; English.
                                                                                                                                                                                                                                                   (IOWA ) UNIV IOWA STATE RES FOUND INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67.3%;
68.3%;
                                                                                                                                                                                                                                                                                            Ciobanu DC,
                                                                                                                                                              08-SEP-2000; 2000US-231045P.
08-JAN-2001; 2001US-260239P.
18-JUN-2001; 2001US-299111P.
                                                                                                                       10-SEP-2001; 2001WO-US28283.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              172..225
/label= CBS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label= CBS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
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                                                                                                                                                                                                                                                                                                                                    WPI; 2002-393850/42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        464 AA;
                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAD36457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Misc-difference
                                                                                                                                                                                                                                                                                            Rothschild MF,
                                       WO200220850-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          chromosome 15
                                                                                                                                                                08-SEP-2000;
                                                                                                                                                                                08-JAN-2001;
                                                                              14-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sus scrofa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAE00222;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Domain
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Gaps .; 0

09-AUG-2002

Sus scrofa

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Screening animals to determine those likely to produce larger litters and improved meat quality traits involves assaying for the presence of polymorphisms in the AMP activated protein kinase regulatory gamma subunit gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a method for screening animals to determine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AMP activated protein kinase regulatory gamma subunit; PRKAG3 gene;
                                                                                                                                                                                                                                                                                      /note= "Wild type Val is substituted with Ile due to single nucleotide polymorphism (SNP)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ó:
                                                                                                                   AMP activated protein kinase regulatory gamma subunit, PRKAG3 screening; meat quality; single nucleotide polymorphism; SNP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 464;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1. GKRRAKALRWTRQKSVEEGEPPGQGEGPRSRPAAESTGLEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Malek M, Plastow G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 142; DB 23;
Pred. No. 8.4e-10;
3; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pig PRKAG3 polymorphic variant (PRKAG3-200).
                                                                               Pig PRKAG3 polymorphic variant (PRKAG3-199).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 100-102; 109pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (IOWA ) UNIV IOWA STATE RES FOUND INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66.4%;
68.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rothschild MF, Ciobanu DC,
                                                                                                                                                                                                                                                                                                                                                                                                                               10-SEP-2001; 2001WO-US28283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08-SEP-2000; 2000US-231045P.
08-JAN-2001; 2001US-260239P.
18-JUN-2001; 2001US-299111P.
                                      (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 68.3
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-393850/42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      464 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAD36459
                                                                                                                                                                                                                                                  Key
Misc-difference
                                                                                                                                                                                                                                                                                                                                                  WO200220850-A2
                                      09-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                           14-MAR-2002
                                                                                                                                                                                                       Sus scrofa
AAE22987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAE22988;
                                                                                                                                                                variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 7
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  셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Screening animals to determine those likely to produce larger litters and improved meat quality traits involves assaying for the presence of polymorphisms in the AMP activated protein kinase regulatory gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a method for screening unimals to determine those more likely to produce large litters and improved meat quality traits. The method involves assaying for the presence of a genotype in the sample of genetic meterial obtained from animal. The genotype is characterised by polymorphism(s) in the AMP activated protein kinase regulatory gamma subunit (PRKAG3) gene. The method is used for screening animals e.g., pigs to determine those most likely to exhibit improved meat quality traits and to produce larger litters.
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                                                                                              AMP activated protein kinase regulatory gamma subunit; PRKAG3 gene; screening; meat quality; single nucleotide polymorphism; SNP; pig.
                                                                                                                                                                                                                                           /note= "Wild type Asn is replaced with Thr during single nucleotide polymorphism (SNP)"
                                                                                                                                                                                                                                                                                                   /note= "Wild type Gly is replaced with Ser during single nucleotide polymorphism (SNP)"
                                                                                                                                                                                                                                                                                                                                                             /note= "Wild type Val is replaced with lle during single nucleotide polymorphism (SNP)"
                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "Wild type Arg is replaced with Gln during single nucleotide polymorphism (SNP)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GKRRAKALRWTRQKSVEEGEPPGQGEGPRSRPAAESTGLEA 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence is pig wild-type PRKAG3 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 142; DB 23;
Pred. No. 8.4e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ciobanu DC, Malek M, Plastow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (IOWA ) UNIV IOWA STATE RES FOUND INC.
                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAE22987 standard; Protein; 464 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          66.48;
                                                       Pig wild-type PRKAG3 protein.
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2001US-260239P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2001US-299111P
                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-393850/42.
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Best Local Similarity
Matches 28; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 464 AA;
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                                                                                                                                                                                                                      Misc-difference
                                                                                                                                                                                                                                                                                    Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                          Misc-difference
                                                                                                                                                                                                                                                                                                                                              Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200220850-A2
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08-SEP-2000; 08-JAN-2001; 18-JUN-2001;

14-MAR-2002

subunit gene

Sequence

RESULT 6 AAE22987 ΩX

P á

ó,

Gaps

Rogel-Gaillard C;

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The present sequence is pig adenosine monophosphate (AMP)-activated kinsse (AMPK) gamma subunit muscle-specific isoform, PRKAG3 splice variant. Prkag3 apens is located in the RN locus of chromosome 15.

Mutation in Prkag3 results in an altered regulation of carbohydrate metabolism, particularly in skeletal muscle. PRKAG3 is useful as therapeutic for treating carbohydrate metabolism disorders such as diabetes, obesity, and disorders associated with muscle metabolism such as myopathy and cardiovascular diseases, to modulate AMPK activity, and for restoring a normal AMPK function. PRKAG3 sequence and its functionally altered mutants are useful for the diagnostic evaluation, genetic testing and prognosis of a metabolic disorder. Preferably a carbohydrate metabolism disorder. Primers that can detect useful for detecting a Mysfunction of carbohydrate metabolism resulting from the expression of a functionally altered allele of PRKAG3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    heterotrimeric AMPK consisting of PRKAG3 or its mutant, are useful for screening compounds able to modulate AMPK activity. Nucleic acid encoding PRKAG3 is useful for detecting mutations in a Prkag3 gene, or in a sequence encoding the first cystathione beta synthase (CBS) domain of PRKAG3 and is useful in gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                       New variants of the gamma subunit of vertebrate adenosine monophosphate-activated kinase for diagnosis or treatment of disorders associated with energy metabolism such as diabetes, obesity, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AMP activated protein kinase regulatory gamma subunit; PRKAG3 gene; screening; meat quality; single nucleotide polymorphism; SNP; pig;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Andersson L, Looft C, Kalm E, Milan D, Robic A,
Lannuccelli N, Gellin J, Le Roy P, Chardon P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GKRRAKALRWTRQKSVEEGEPPGQGEGPRSRPAAESTGLEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 142; DB 22;
Pred. No. 9.3e-10;
3; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pig PRKAG3 polymorphic variant (PRKAG3-52).
                                                                                                                                                                                            NAT RECH AGRONOMIQUE.
L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 5; Page 70-71; 71pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAE22986 standard; Protein; 464 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66.4%;
68.3%;
                                                                             11-SEP-2000; 2000WO-EP09896.
                                                                                                                          10-SEP-1999; 99EP-0402236.
18-MAY-2000; 2000EP-0401388.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 68.3 tes 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-244810/25.
                                                                                                                                                                                            (INRG ) INRA INST
(ANDE/) ANDERSSON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          514 AA;
                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAD03321.
                                                                                                                                                                                                                                                                (KALM/) KALM E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAE22986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   myopathy
                                                                                                                                                                                                                                         LOOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAE22986
              음
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pig; gamma subunit; adenosine monophosphate-activated kinase; AMPK; PRKAG3; diabetes; obesity; myopathy; cardiovascular disease; anorectic; genetic testing; carbohydrate metabolism disorder; skeletal muscle; cystathione beta synthase; CBS; cardiant; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Screening animals to determine those likely to produce larger litters and improved meat quality traits involves assaying for the presence of polymorphisms in the AMP activated protein kinase regulatory gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a method for screening animals to determine those more likely to produce large litters and improved meat quality traits. The method involves assaying for the presence of a genotype in the sample of genetic material obtained from animal. The genotype is characterised by polymorphism(s) in the AMP activated protein kinase regulatory gamma subunit (PRKAG3) gene. The method is used for screening animals e.g., pigs to determine those most likely to exhibit improved meat quality traits and to produce larger litters.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the present sequence is pig PRKAG3 polymorphic variant (PRKAG3-200).
screening; meat quality; single nucleotide polymorphism; SNP; pig;
                                                                                                                                                           /note= "Wild type Arg is substituted with Gln due to single nucleotide polymorphism (SNP)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 464;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GKRRAKALRWIRQKSVEEGEPPGQGEGPRSRPAAESTGLEA 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Plastow G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66.4%; Score 142; DB 23;
68.3%; Pred. No. 8.4e-10;
live 3; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 105-107; 109pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Malek M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                            (IOWA ) UNIV IOWA STATE RES FOUND INC.
                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAE00224 standard; Protein; 514 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sus scrofa Prkag3 splice variant.
                                                                                                                                                                                                                                                                                                                                                                   08-SEP-2000; 2000US-231045P.
08-JAN-2001; 2001US-260239P.
18-JUN-2001; 2001US-299111P.
                                                                                                                                                                                                                                                                                                                         10-SEP-2001; 2001WO-US28283.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rothschild MF, Ciobanu DC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13-JUN-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                West Local Similarity 68.3 latches 2b; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-393850/42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                464 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAD36460
                                                                                                                                          Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200120003-A2.
                                                                                                                                                                                                                                 WO200220850-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              subunit gene
                                                                                                                                                                                                                                                                            14-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sus scrofa.
                                                                           Sus scrofa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAE00224;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                              variant.
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Gaps

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41

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Length 514; 10; Indels

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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating the polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations in cisponsible for genetic disorders or other traits to assess biodiversity amino acid sequences. AbgONOIO-Abg30377 represent novel human diagnostic amino acid sequences of the invention.

Consideration, but was obtained in electronic format directly from WIPO and sequences are seasons and the printed sequences of the formation of mutations.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence; corn.
                                                                                                                                                                                                            New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 171;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 RRAKALRWIRQKSVEEGEPPGQGEG-----PRSRPAAESTGLE 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5; Mismatches 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zea mays protein fragment SEQ ID NO: 44011.
                                                                                                                                                                                                                                                                                                                    Claim 20; SEQ ID No 34025; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 64.5;
Pred. No. 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Æ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAG35967 standard; Protein; 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30.1%;
    31-MAR-2000; 2000US-0540217.
                      2000US-0649167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-FEB-2000; 2000EP-0301439.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99US-0121825.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 30.1 Best Local Similarity 37.2 Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zea mays subsp. mays.
                                                                                                                                                2001-639362/73.
                                                                                                        Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 171 AA;
                                                                (HYSE-) HYSEQ INC
                                                                                                                                                                      N-PSDB; AAS67853
                   23-AUG-2000;
                                                                                                                                                                                                                                                                            biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-FEB-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18-OCT-2000
                                                                                                        Drmanac RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAG35967;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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  ò
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Screening animals to determine those likely to produce larger litters and improved meat quality traits involves assaying for the presence of polymorphisms in the AMP activated protein kinase regulatory gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a method for screening animals to determine those more likely to produce large litters and improved meat quality traits. The method involves assaying for the presence of a genotype in the sample of genetic material obtained from animal. The genotype is characterised by polymorphism(s) in the AMP activated protain kinase regulatory gamma subunit (PRKAG3) gene. The method is used for screening animals e.g., pigs to determine those most likely to exhibit improved meat quality traits and to produce larger litters. The present sequence is pig PRKAG3 polymorphic variant (PRKAG3-52).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                           /note= "Wild type Gly is substituted with Ser due to single nucleotide polymorphism (SNP)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           e mapping; gene mapping; gene therapy; forensic;
medical imaging; diagnostic; genetic disorder.
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Pred. No. 4.8e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GKRRAKALRWTRQKSVEEGEPPGQGEGPRSRPAAESTGLEA 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11;
                                                                                                                                                                                                                                                                                                                                                                                                      Malek M, Plastow G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3; Mismatches
                                                                                                                                                                                                                                                                                                                                                          (IOWA ) UNIV IOWA STATE RES FOUND INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 36; Page 96-97; 109pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel human diagnostic protein #3657.
                                       Location/Qualifiers
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65.98;
                                                                                                                                                                                                                                                                                                                                                                                                    Rothschild MF, Ciobanu DC,
                                                                                                                                                                                                                                                                          2000US-231045P.
                                                                                                                                                                                                                             10-SEP-2001; 2001WO-US28283
                                                                                                                                                                                                                                                                                            2001US-260239P.
2001US-299111P.
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hes 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-393850/42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        464 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             food supplement;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAD36458
                                       Key
Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200175067-A2.
                                                                                                                                              WO200220850-A2
                                                                                                                                                                                                                                                                                            08-JAN-2001;
18-JUN-2001;
                                                                                                                                                                                                                                                                        08-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          subunit gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
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                                                                                                                                                                                     14-MAR-2002
Sus scrofa.
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Sednence

Query Match Best Loc Matches ABG03666;

RESULT 10 ABG03666

qq QΫ́

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Gaps

99US-0143624. 99US-0144005. 99US-0144086. 99US-0144086. 99US-0144331. 99US-0144333. 99US-0144333. 99US-0144335. 99US-014435.	9905-0144814. 9905-0145086. 9905-0145087. 9905-0145087. 9905-0145087. 9905-0145182. 9905-014518. 9905-0145218. 9905-0145218. 9905-0145918. 9905-0145918. 9905-0145918. 9905-0145918. 9905-0145918. 9905-0145918. 9905-0145918. 9905-0145918.	9918-0147260. 9918-0147416. 9918-0147416. 9918-0147416. 9918-014793. 9918-014793. 9918-0148319. 9918-0148368. 9918-0148368. 9918-0148368. 9918-0149368. 9918-0149929. 9918-0149929. 9918-0149929. 9918-0149929.	9903-0111065. 9903-0151066. 9903-0151080. 9903-0151303. 9903-0151330. 9903-0153070. 9903-0153070. 9903-0154039. 9903-0154039. 9903-0154039. 9903-0155486. 9903-0155486.
14-7UL-1999; 16-7UL-1999; 16-7UL-1999; 19-7UL-1999; 19-7UL-1999; 19-7UL-1999; 19-7UL-1999; 19-7UL-1999; 20-7UL-1999; 20-7UL-1999;	21 - 70L - 1999; 22 - 70L - 1999; 22 - 70L - 1999; 22 - 70L - 1999; 23 - 70L - 1999; 23 - 70L - 1999; 23 - 70L - 1999; 24 - 70L - 1999; 27 - 70L - 1999; 27 - 70L - 1999; 27 - 70L - 1999; 28 - 70L - 1999; 27 - 70L - 1999; 28 - 70L - 1999; 29 - 70L - 1999; 20 - 7	05-A0G-1999; 06-A0G-1999; 06-A0G-1999; 09-A0G-1999; 10-A0G-1999; 11-A0G-1999; 13-A0G-1999; 13-A0G-1999; 16-A0G-1999; 16-A0G-1999; 20-A0G-1999; 20-A0G-1999; 23-A0G-1999; 23-A0G-1999; 23-A0G-1999; 23-A0G-1999; 23-A0G-1999; 23-A0G-1999;	27 - AuG - 1999; 27 - AuG - 1999; 30 - AuG - 1999; 31 - AuG - 1999; 31 - AuG - 1999; 31 - AuG - 1999; 31 - SEP - 1999; 31 - SEP - 1999; 32 - SEP - 1999; 22 - SEP - 1999; 24 - SEP - 1999; 28 - SEP - 1999; 29 - SEP - 1999; 29 - SEP - 1999; 20 - SEP - 1999; 21 - SEP - 1999; 22 - SEP - 1999; 23 - SEP - 1999; 24 - SEP - 1999; 26 - SEP - 1999; 27 - SEP - 1999; 28 - SEP - 1999;
9905-0123180 9905-0123548 9905-0125788 9905-0126785 9905-0127462 9905-0128234 9905-0128234 9905-0130077 9905-0130677	9905-0131449. 9905-0132048. 9905-0132485. 9905-0132486. 9905-0132486. 9905-0132863. 9905-0134218. 9905-0134218. 9905-0134218. 9905-013421. 9905-013421. 9905-013421. 9905-013421. 9905-013421. 9905-013421.	9905-013724-9905-013724-9905-013724-9905-0138047-0905-0139119-9905-0139455-9905-0139455-9905-0139456-9905-0139460-9005-0139460-9005-013	9905-0139763. 9905-0139817. 9905-013989. 9905-0140353. 9905-0140695. 9905-0140695. 9905-0141287. 9905-0141287. 9905-014280. 9905-014280. 9905-0142803. 9905-0142803.
05-MAR-1999; 09-MAR-1999; 23-MAR-1999; 29-MAR-1999; 01-APR-1999; 08-APR-1999; 16-APR-1999; 16-APR-1999; 21-APR-1999; 21-APR-1999; 21-APR-1999;	28 APR 1999; 30 APR 1999; 30 APR 1999; 30 APR 1999; 04 WAY 1999; 05 WAY 1999; 07 WAY 1999; 07 WAY 1999; 08 WAY 1999; 09 WAY 1999; 00 WAY 1999;	04-70N-1999; 08-70N-1999; 08-70N-1999; 10-70N-1999; 14-70N-1999; 16-70N-1999; 18-70N-1999; 18-70N-1999; 18-70N-1999; 18-70N-1999; 18-70N-1999; 18-70N-1999; 18-70N-1999; 18-70N-1999; 18-70N-1999; 18-70N-1999; 18-70N-1999;	18 JUN 1999; 22 - JUN 1999; 22 - JUN 1999; 23 - JUN 1999; 24 - JUN 1999; 26 - JUN 1999; 27 - JUN 1999; 28 - JUN 1999; 30 - JUL 1999; 01 - JUL 1999; 06 - JUL 1999; 06 - JUL 1999; 07 - JUL 1999; 08 - JUL 1999; 08 - JUL 1999; 13 - JUL 1999;

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                                                                                                                                                                                                                         heptocyte nuclear factor I alpha (HNF-1 alpha, see also AAW1559)
that arises from a frameshift mutation at codon Pro-379 of the
coding region of the HNF-1 alpha gene (see AAV5265). The mutation
has been detected in patients with the MODY3 (maturity onset
diabetes of the young) form of diabetes. The invention concerns
the identification of genes responsible for non-insulin dependent
diabetes mellitus (NIDDM) for use in diagnostics and therapeutics.
It demonstrates that the MODY3 locus is the HNF-1 alpha gene, the
MODY4 locus is the HNF-1 beta gene (see AAV52730) and the MODY1 locus
is the HNF-4 alpha gene (see AAV52867). Analysis of mutations in
these HNF genes can be diagnostic for diabetes. The invention also
contemplates methods of screening for modulators being
utilising HNF nucleic acids or polypeptides, the modulators being
custilising HNF nucleic acids or polypeptides, the modulators being
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                           Isolated nucleic acid encoding hepatocyte nuclear factor 1-alpha and 1-beta - useful for detecting susceptibility for non-insulin dependent diabetes, especially maturity-onset diabetes of the young
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ï
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hepatocyte nuclear factor 1 alpha; HNF-1 alpha; WODY3; human; transcription factor; maturity onset diabetes of the young; diabetes; NIDDM; diagnosis; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 19; Length 415;
                                                                                                                                                                                                                  This is the amino acid sequence of a truncated form of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "DNA binding domain with POU-like and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                      ŝ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human hepatocyte nuclear factor 1 alpha (R131Q mutant).
                                                                      Kaisaki PJ, Menzel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        271 RRKEEAFRHKLAMDTYSGPPGPGPGP-ALPAHSSPGL 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    homeodomain-like motifs"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "transactivation domain"
322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 KRRAKALRWIRQKSVEEGEPPGQGEGPRSRPAAESIGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "dimerisation domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 13;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 61.5;
                                                                                                                                                                                          Disclosure; Page 180-181; 363pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "encoded by TNT"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW71560 standard; Protein; 630 AA.
                                                                       Horikawa Y,
96US-0029679.
96US-0025719.
96US-0028056.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
28.7%;
Best Local Similarity 39.5%;
Matches 15; Conservative 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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                                             (ARCH-) ARCH DEV CORP.
                                                                                                       WPI; 1998-271667/24.
N-PSDB; AAV52628.
                                                                      GI, Furuta H,
N, Yamagata K;
                                                                                                                                                                                                                                                                                                                                                                                                                           415 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Misc-difference
30-OCT-1996;
10-SEP-1996;
02-OCT-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW71560;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Key
Domain
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                                                                                  oda N,
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                                                                                                                                                                                                                                                                                                                                                                                                               Score 63.5; DB 21; Length 61; Pred. No. 0.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human hepatocyte nuclear factor 1 alpha (truncated mutant).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        150..280
/note= "DNA binding domain"
23..415
/note= "truncated transactivation domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 RRAKALRWTROKSV--EEGEPPGOGEGPRSRPAAESTGLEA 41
                                                                                                                                                                                                                                                                                                                                                                                                                                       17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "dimerisation domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                       3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW71562 standard; Protein; 415 AA
990s-015753.
990s-0157865.
990s-0158029.
990s-0158369.
990s-0159293.
990s-0159294.
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99US-0160815.
99US-0160980.
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99US-0160989.
99US-0161404.
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99US-0161406.
99US-0161359.
                                                                                             99US-0159329.
99US-0159330.
99US-0159331.
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43.9%;
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                                                                                                                                                                                            990S-0160768
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                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 43.9
nes 18; Conservative
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                                                                                                                                                                                                                                                                                        25-OCT-1999;
25-OCT-1999;
26-OCT-1999;
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21-0CT-15
21-0CT-15
21-0CT-15
22-0CT-15
                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                            14-0CT-1
18-0CT-1
21-0CT-1
                                                                                                            14-0CT-1
14-0CT-1
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Domain
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Menzel S;

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oda N,

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1 beta (HNF-1 beta), deduced from a partial gene sequence (see AAV52729). HNF-1 beta is a homeodomain-containing transcription factor. Mutations in HNF are indicative of a propensity to diabetes mellitus. The invention concerns the identification of genes responsible for non-insulin dependent diabetes mellitus (NIDDM) for use in diagnostics and therapeutics. It demonstrates that the WODY3 locus is the HNF-1 alpha gene (see AAV52632), the WODY4 locus is the HNF-1 beta gene (see also AAV52730) and the MODY1 locus is the HNF-4 alpha gene (see AAV52687). Analysis of mutations in these HNF genes can be diagnostic for diabetes. The invention also provides
                                                                                                                                                                                                                                                                                                                         Isolated nucleic acid encoding hepatocyte nuclear factor 1-alpha and 1-beta - useful for detecting susceptibility for non-insulin dependent diabetes, especially maturity-onset diabetes of the young
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      genes can be diagnostic for diabetes. The invention also provides methods of utilising HNF nucleic acids and polypeptides in screens for modulators of HNF function, the modulators being useful for treating diabetes by modulating HNF function in an animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         This is the amino acid sequence of human hepatocyte nuclear factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hepatocyte nuclear factor 1 alpha; HNF-1 alpha; MODY3; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "DNA binding domain with POU-like and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        transcription factor; maturity onset diabetes of the young;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           homeodomain-like motifs"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 KRRAKALRWIRQKSVEEGEPPGQGEGPRSRPAAESTGL
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Misc-difference 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human native hepatocyte nuclear factor 1 alpha.
                                                                                                                                                                                            , Furuta H, Horikawa Y, Kaisaki PJ,
Yamagata K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "dimerisation domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 61.5; 1
Pred. No. 20;
                                                                                                                                                                                                                                                                                                                                                                                                             Claim 94; Page 228-230; 363pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cocation/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28.78;
39.58;
                                                                96US-0029679.
96US-0025719.
96US-0028056.
                        97WO-US16037.
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Best Local Similarity 39.5
Matches 15, Conservative
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                        10-SEP-1997;
                                                                  30-OCT-1996;
                                                                                                          02-OCT-1996
                                                                                        10-SEP-1996
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AAW71559
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     concerns the identification of genes responsible for non-insulin dependent diabetes mellitus (NIDDM) for use in diagnostics and therapeutics. It shows that the NODY3 locus is the HNF-1 alpha gene, the MODY4 locus is the HNF-1 beta gene (see AAV52780) and the MODY1 locus is the HNF-1 beta gene (see AAV52687). Analysis of mutations these HNF genes can be diagnostic for diabetes. The invention also contemplates methods of screening for modulators of HNF function utilising HNF nucleic acids or polypeptides, the modulators being useful for treating diabetes by modulating HNF function in an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This is the amino acid sequence of a mutant (R131Q) form of human hepatocyte nuclear factor 1 alpha (HNF-1 alpha, see also AAW71559) that arises from a missense mutation (G to A) of codon 131 of the coding region of the HNF-1 alpha gene (see AAV52656). The mutation has been detected in a patient with the MODY3 (maturity onset human, rat, mouse, hamster, chicken, Kanopus and salmon HNF-1 alpha suggesting this residue to be functionally important. The invention
                                                                                                                                                                                                                                                                                                                                                                                  Isolated nucleic acid encoding hepatocyte nuclear factor 1-alpha and 1-beta - useful for detecting susceptibility for non-insulin dependent diabetes, especially maturity-onset diabetes of the young
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                      Horikawa Y, Kaisaki PJ, Menzel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 KRRAKALRWIRQKSVEEGEPPGQGEGPRSRPAAESIGL 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4; Mismatches 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 169-172; 363pp; English
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                                                                                                                          96US-0029679.
96US-0025719.
96US-0028056.
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39.5%;
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                                                                                                                                                                                                                                                        , Furuta H,
Yamagata K;
                                                                                                                                                                                                                                                                                                                    WPI; 1998-271667/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              630 AA;
                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAV52626
W09811254-A1
                                                                                  10-SEP-1997;
                                                                                                                            30-OCT-1996;
                                                                                                                                                10-SEP-1996;
02-OCT-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO9811254-A1
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                                          19-MAR-1998.
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Sequence

animal

Query Match

Matches

ŏ qq AAW71580;

RESULT 14 AAW71580

ä

Gaps

1;

33

Length 631;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This is the amino acid sequence of human hepatocyte nuclear factor I alpha), a homeodomain-containing sequence-specific DNA bidding protein. A cDNA sequence (see AAV52624) encoding HNF-1 alpha is provided. Mutations in this transcription factor are indicative of a propensity to diabetes mellitus. The HNF-1 alpha gene is located on human chromosome 12q, which is the location site of the NDD3 (maturity onset diabetes of the young) locus. The invention concerns the identification of genes responsible for non-insulin dependent diabetes mellitus (NIDDM) for use in diagnostics and therapeutics. It demonstrates that the MODY3 locus is the HNF-1 alpha gene (see AAV55730) and therapeutics. It demonstrates that the MODY3 locus is the HNF-1 beta gene (see AAV55730) and that one in these HNF genes can be diagnostic for diabetes. The invention also contemplates methods of screening for modulators of mutations in these HNF genes can be diagnostic for diabetes. The invention also contemplates methods of screening for modulators being useful for treating diabetees by modulating HNF contention in an animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                           Isolated nucleic acid encoding hepatocyte nuclear factor 1-alpha and 1-beta - useful for detecting susceptibility for non-insulin dependent diabetes, especially maturity-onset diabetes of the young
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match 28.7%; Score 61.5; DB 19; Length 631; Best Local Similarity 39.5%; Pred. No. 20; Matches 15; Conservative 4; Mismatches 18; Indels 1;
                                                                                                                                                                                                                                                Horikawa Y, Kaisaki PJ, Menzel S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 KRRAKALRWTRQKSVEEGEPPGQGEGPRSRPAAESTGL 39
                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 14; Fig 11; 363pp; English.
                                                                                                                            96US-0029679.
96US-0025719.
96US-0028056.
                                                                                          97WO-US16037.
                                                                                                                                                                                                           (ARCH-) ARCH DEV CORP.
                                                                                                                                                                                                                                            , Furuta H,
Yamagata K;
                                                                                                                                                                                                                                                                                                  WPI; 1998-271667/24.
N-PSDB; AAV52625.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     631 AA;
                 WO9811254-A1.
                                                                                          10-SEP-1997;
                                                                                                                              30-OCT-1996;
                                                                                                                                                  10-SEP-1996;
02-OCT-1996;
                                                     19-MAR-1998
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δy
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Search completed: June 6, 2003, 11:01:02 Job time: 8.60596 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - Run on:	OM protein - protein search, using sw model	June 6, 2003, 10:58:29 ; Search time 2.65674 Seconds (Without alignments) 1483.588 Million cell updates/sec
	OM protein -	Run on:

	4 3
	1 GKRRAKALRWTRQKSVEEGEPGQGEGPRSRPAAESTGLEA 41
11_91	
US-09-826-581-6_COPY_51_91 214	1 GKRRAKALRWTRQKSVEEGE
Title: Perfect score:	Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283224 seqs, 96134422 residues Searched:

283224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 10% Maximum Match 100% Listing first 45 summaries

1: pir1:* 2: pir2:* 3: pir3:* 4: pir4:* PIR_73:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	cription	hypothetical prote	ption	41			transcription fact	synapsin I splice	id	ribosomal protein	Ω	at	scri			synapsin Ia - rat	hypothetical prote		ubiquitin thiolest	anion exchange pro	mucin - human (fra		phenylalanine ammo	probable potassium	hypothetical prote	antigen (C-termina	interleukin-2 rece	rotea	protein C36C5.13 [protein
SUMMARIES	ID	T05105	839607	839608	A39262	A33333	A36749	A35463	AF3639	RSMXE	H87516	A75634	\$36336	T34847	A25704	A30411	F96712	S54307	S68227	S21086	S55461	D69378	S06475	T31100	S76108	B48441	JC1113	T51975	E88990	S16318
	DB																		7											7
	Length	493	494	542	628	628	631	705	565	149	435	696	673	943	691	704	1085	1980	828	1240	171	396	701	1087	203	206	275	277	303	323
ф	Query Match	29.0	28.7	28.7	28.7	28.7	28.7	27.6	26.9	26.6	26.2	26.2	25.9	25.9	25.7	25.7	25.7	25.7	25.5	25.5	25.2	25.2	25.2	25.0	24.8	24.5	24.5	24.5	24.5	24.5
	Score	62			61.5			S	57.5	57	99	S	55.5	5.	55	52	52	LO.	54.5		54			53.5	53	ä	ς.	52.5	Ċ,	ς.
	Result No.	Н	2	٣	₩	S	9	7	ω	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

C; Species: Homo sapiens (man)
C; Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 29-Aug-1997
EMBO J. 12, 4229-4242, 1993
A; Title: More potent transcriptional activators or a transdominant inhibitor of the 1 A; Title: More potent transcriptional activators or a transdominant inhibitor of the 1 A; Accession: 539607
A; Molecule type: mRNA
A; Ascession: 539607
A; Coss-references: EMBL: X71347
B; Bach, I.
R; Bach, I.

A; Reference number: S39752
A; Accession: S39752
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 118 494 < CBA2>
A; Cross-references: EMBL: X71347

transcription factor HNF-1A, splice form C - human

homeotic protein H	BHLF1 protein - hu	hypothetical prote	probable membrane-	Y4cC protein - Rhi	probable dinitrifi	hypothetical prote	band 3-related pro	band 3-related pro	band 3-related pro	hypothetical prote	NADH2 dehydrogenas	hypothetical prote	circumsporozoite p	hypothetical prote	
WJHU2H	QQBE3	C95995	C70666	T28630	S53714	T46517	A34911	A31789	A56764	T00365	S14277	T34536	OZZQAK	T34036	S01393
Н	Н	7		7	7	7	7	7	~	7	~	7	7	7	_
356	099	78	369	517	612	751	1234	1237	1237	1280	200	259	363	1359	1530
24.5	. 24.5	24.3	24.3	24.3	24.3	24.3	24.3	24.3	24.3	24.3	24.1	24.1	24.1	24.1	24.1
	'n.	25	52	52	52	25	25	25	52	25	51.5	51.5	51.5	51.5	1.5
52.5	52.5													•	٠,

ALIGNMENTS

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hypothetical protein F28M20.160 - Arabidopsis thaliana (Species: Arabidopsis thaliana (mouse-ear cress) (5pecies: Arabidopsis thaliana (mouse-ear cress) (5.5pecies: Arabidopsis thaliana (mouse-ear cress) (5.5pace: 23.4pr. 1999 #sequence_revision 23.4pr. 1999 #text_change 01-Mar-2002 (5.5ccession: T05105 R:Bevan, M.; Rieger, M.; Mueller-Auer, S.; Zipp, M.; Schaefer, M.; Hoheisel, J.; Mew Bubmitted to the Protein Sequence Database, November 1998 A;Reference number: 215398 A;Accession: T05105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14;
                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Map position: 4
A;Introas: 26/3; 105/1; 146/3; 296/3; 406/3
A;Note: F28X0.160
C;Superfamily: Arabidopsis thaliana hypothetical protein F28M20.180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 29.0%; Score 62; DB 2; Length 493; Best Local Similarity 35.6%; Pred. No. 9.1; Matches 16; Conservative 7; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 RRAKALRWT------RQKSVEEGEPPGQGEGPRSRPAAESTG 38
                                                                                                                                                                                                                                                                            A;Molecule type: DNA
A;Residues: 1-493 <BEV>
A;Cross_references: EMBL;AL031004
A;Cross_reference: cultivar Columbia; BAC clone F28M20
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
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91.rpr

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Query Match 28.7%
Best Local Similarity 39.5%
Matches 15; Conservative
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A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA A; Residues: 1-628 < CHC
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C; Genetics:
A; Gene: GDB:TCET; HNF1; LFB1
A; Cross-references: GDB:125297; OMIM:142410; OMIM:600496
A; Cross-references: GDB:125297; OMIM:142410; OMIM:600496
A; Map position: 12434.3-12424.3
C; Complex: homodimer; can also form heterodimers with, for example, HNF-1A form A; C; Complex: homodimer; can also form heterodimers with, for example, HNF-1A form A; Description: transcription activator required for the expression of a number of liver-A; Note: this form is a more potent transcriptional activator than the A form C; Superfamily: transcription factor HNF-1; homeobox homology
C; Superfamily: transcription factor HNF-1; homeobox homology
C; Superfamily: increase alternative splicing; DNA binding; homeobox; liver; nucleus; transcription received.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  transcription factor HNF-1A, splice form B - human
N,Alternate names: hepatic nuclear factor 1-alpha; transcription factor 1, hepatic; tran
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A:Map position: 12924.3-12924.3
C:Complex: homodimer; can also form heterodimers with, for example, HNF-IA form A
C:Function:
A:Description: transcription activator required for the expression of a number of liver-A:Note: this form is a more potent transcriptional activator than the A form
C:Superfamily: transcription factor HNF-I; homeobox homology
C:Keywords: alternative splicing; DNA binding; homeobox, liver; nucleus; transcription r
F:1-33/Region: dimerization
F:222-27//Domain: homeobox homology <HOX>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     transcription factor HNF-1A - mouse
NyAlternate names: hepatic nuclear factor 1-alpha; transcription factor APF; transcription (Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: A39262; S70436
R;Kuo, C.J.; Conley, P.B.; Hsieh, C.L.; Francke, U.; Crabtree, G.R.
Proc. Natl. Aacad Sci. U.S.A. 87, 8938-9842, 1990
A;Title: Molecular cloning, functional expression, and chromosomal localization of mouse A;Reference number: A39262; MuID:91088607; PMID:2263635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HNF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 29-Aug-1997
C;Accession: S39608
K;Bach, I.; Yaniv, M.
EMBO J. 12, 4229-4242, 1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Cross-references: GDB:125297; OMIM:142410; OMIM:600496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 KRRAKALRWTRQKSVEGGEPPGQGEGPRSRPAAESTGL 39
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                                                                                                                                                                                                                                                                                                                                                                                                                         28.7%; Score 61.5; D
39.5%; Pred. No. 10;
tive 4; Mismatches
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                                                                                                                                                                                                                                                                                                                                                         F:222-277/Domain: homeobox homology <HOX>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  222-277/Domain: homeobox homology <HOX>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 39.5
les 15; Conservative
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A;Gene: GDB:TCFl; HNFl; LFBl
                                                                                                                                                                                                                                                                                                                              F;1-33/Region: dimerization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
A; Residues: 1-542 <BAC>
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A; Status: preliminary
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transcription factor HNF-1A - rat
N.Alternate names: hepatic nuclear factor 1-alpha; transcription factor APF; transcri
C.Species: Rattus norvegious (Norvay rat)
C.Species: Rattus norvegious (Norvay rat)
C.Species: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C.Accession: A33333, A34590; S11568; S70435
C.Frain, M.; Swart, G.; Monaci, P.; Nicosia, A.; Staempfli, S.; Frank, R.; Cortese, R
C. A.Title: The liver-specific transcription factor LF-B1 contains a highly diverged hom
A.Reference number: A33333; MUID:90003224; PMID:2571419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A Description: transcription activator required for the expression of a number of liv A:Note: also expressed in other tissues (kidney, stomach, intestine), where it may pl C:Superfamily: transcription factor HNF-1; homeobox homology C:Keywords: DNA binding; heterodimer; homeobox; homodimer; liver; nucleus; transcript F:1-33/Region: dimerization F:222-277/Domain: homeobox homology <HOX>
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A;Residues: 'R',166-628 <BAU>
A;Cross-references: GB:X53297; NID:957867; PIDN:CAA37387.1; PID:957868
A;Cross-references: GB:X53297; NID:957867; PIDN:CAA37387.1; PID:957868
A;Note: the authors translated the codon GAG for residue 616 as Asp
R;Chouard, T.; Blumenfeld, M.; Bach, I.; Vandekerckhove, J.; Cereghini, S.; Yaniv, M.
Nucleic Acids Res. 18, 5853-5863, 1990
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A; Molecule type: mRNA
A; Residues: 1-628 «KUO>
A; Cross-references: 1-628 «KUO>
A; Cross-references: 1-628 will will b; Yaniv, M.
B; Cross-references: 20, 4199-4204, 1992
A; Title: Structure of the gene encoding hepatocyte nuclear factor 1 (HNF1).
A; Accession: S70436
A; Reference number: S70435
A; Accession: S70436
A; Reference number: S70436
A; Reference number: S70436
A; Reference number: S70436
A; Residues: 199-279 «BAC>
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Nucleic Acids Res. 20, 4199-4204, 1992
A;Title: Structure of the gene encoding hepatocyte nuclear factor 1 (HNF1).
A;Reference number: S70435; MUID:92375726; PMID:1354855
A;Accession: S70435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A.Note: only a part of the nucleic acid sequence is shown c.genetics:
A.Gene: Hnf-1
A.Introns: 238/2
A.Note: the list of introns is incomplete
C.Complex: homodimer; can also form heterodimers with, for example, HNF-1B
C.Function:
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A, Status: preliminary
A, Molecule type: mRhA
A, Residues: 1-628 < FRAA
A, Residues: 1-628 < FRAA
A, Cruss-references: GB:J03170; NID:g205164; PIDN:AAA41524.1; PID:g205165
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28.7%; Score 61.5; DB 1; Length 6 39.5%; Pred. No. 13; ive 4; Mismatches 18; Indels
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A; Molecule type: DNA*
A; Molecule type: DNA*
A; Residues: 1.659, KASPAQAQP' <SU2>
A; Cross-references: GB:M58378; GB:J05431
R; Sauerwald, A.; Hoesche, C.; Oschwald, R.; Kilimann, M.W.
D BAOL. Chen. 265, 14932-14937, 1990
A; Title: The 5'-flanking region of the synapsin I gene. A G+C-rich, TATA- and CAAT-1 A; Reference number: A35805; MUID:90368667; PMID:2118519
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A.Title: The genome sequence of the facucitative intracellular pathogen Brucella meli A; Reference number: AD3252; PMID:11756688
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pseudouridylate synthase (EC 4.2.1.70) [imported] - Brucella melitensis (strain 16M)
C.Species: Brucella melitensis
C.Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 19-Apr-2002
C.Accession: AF3639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A:Cross-references: GB:M55301; NID:g338655; PIDN:AAA60608.1; PID:g553654; GB:J05630
C;Genetics:
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A;Experimental source: strain 16M
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A:Map position: Xp11.23-Xp11.23
C:Keywords: actin binding; alternative splicing; phosphoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 705;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ribosomal protein L19.eR - Methanococcus vannielii N;Alternate names: ribosomal protein E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 59; DB 2
Pred. No. 29;
4; Mismatches
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C:Keywords: carbon-oxygen lyase; hydro-lyase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13 OKSVEEGEPPGQGEGPRSRPAAESTG 38
                                                                                            A; Cross-references: GB:M58371; GB:J05431
A; Accession: B35363
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Best Local Similarity 42.3%;
Matches 11; Conservative
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A;Molecule type: DNA
A;Residues: 1-565 <KUR>
                             A; Molecule type: DNA
A; Residues: 1-705 <SUE>
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                                                                                                                                                              A; Status: preliminary
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A; Molecule type: DNA
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A; Accession: A35363
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                   A.Molecule type: DNA
A.Residues: 199-279 CARC>
A.Note: only a part of the nucleic acid sequence is shown
G.Genetics:
A.Genetics:
A.Genetics:
A.Genetics:
A.Thirons: 238/2
A.Inhirons: 238/2
A.Note: the list of introns is incomplete
C.Complex: homodimer; can also form heterodimers with, for example, HNF-1B
C.Function:
A.Note: also expressed in other tissues (kidney, stomach, intestine), where it may play
C.Superfamily: transcription factor HNF-1; homeobox homology
C.Superfamily: heterodimer; homeobox homology
C.Superfamily: nucleus; transcription
F.1-33/Region: dimerization
F.22-277/Domain: homeobox homology <a href="https://domain.nucleus">https://domain.nucleus</a>; transcription
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A; Residues: 1:631 < BAC>
A; Wolecule type: mRNA
A; Residues: 1:631 < BAC>
A; Cross-references: GB:M57732; NID:g184264; PIDN:AAA88077.1; PID:g184265
C; Genetics: A; Genetics: GB:M577329; OMIM:142410; OMIM:600496
A; Gross-references: GB:B122297; OMIM:142410; OMIM:600496
A; Map position: 12q24.3-12q24.3
C; Complex: homodimer; can also form heterodimers with, for example, HNF-1B
C; Function: transcription activator required for the expression of a number of liver-A; Note: also expressed in some other tissues, where it may play other roles
C; Superfamily: transcription factor HNF-1; homeobox homology
C; Keywords: DNA binding; heterodimer; homeobox homology
C; Keywords: DNA binding; heterodimer; homeobox; homodimer; liver; nucleus; transcription
F; 222-277/Domain: homeobox homology < HOX>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N'Alternate names: hepatic nuclear factor 1-alpha; transcription factor 1, hepatic; tran C;Species: Homo sapiens (man)
C;Bate: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
R;Bate: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
R;Bach, I.; Galcheva-Gargova, Z.; Mattei, M.G.; Simon-Chazottes, D.; Guenet, J.L.; Cereg Genonics 8, 155-164, 1990
A;Title: Cloning of human hepatic nuclear factor 1 (HNF1) and chromosomal localization A;Reference number: A56749; MUID:91184801; PMID:1707031
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C.Date: 17-Any-1990 #sequence_revision 17-Any-1990 #text_change 01-Dec-2000
C.Accession: A35363; B35363; A35805
R.Suedhof, T.C.
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Pred. No. 13;
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A;Title: The structure of the human synapsin I gene and protein.
A;Reference number: A35363; MUID:90243651; PMID:2110562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4; Mismatches 18; Indels
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A;Status: not compared with conceptual translation
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39.5%;
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Matches 15; Conservative
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C,Accession: A25704
R:MCCaffery, C.A.; DeGennaro, L.J.
EMBO J. 5, 3167-3173, 1986
A;Title: Determination and analysis of the primary structure of the nerve terminal sy A;Reference number: A25704; MUID:87133474; PMID:3028773
                                                                                                                                                                                                                                                                                                                                                                   A.Title: Fusion between a novel Krueppel-like zinc finger gene and the retinoic acid A.Reference number: S36336; MUID:93209216; PMID:8384553
A.Accession: S36336
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C.Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 05-Nov-1999
C.Accession: T34847
R.O.Liver, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream,
submitted to the EMBL Data Library, February 1999
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            3
                                                                                                                                                                                                                                                        C.Species: Homo sapiens (man)
C.Species: Jal-Dec-1993 #text_change 05-Nov-1999
C.Accession: S36336; S31989
C.Accession: S36336; S31989
R.Chen, Z.; Brand, N.J.; Chen, A.; Chen, S.J.; Tong, J.H.; Wang, Z.Y.; Waxman, EMBO J. 12, 1161-1167, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Rattus norvegicus (Norway rat)
C;Date: 21-May-1988 #sequence_revision 21-May-1988 #text_change 05-Nov-1999
                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Cross-references: EMBL:219002; NID:938517; PIDN:CAA79489.1; PID:938518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1;
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               14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 673;
               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                         ::| | | | | :1:1|| | | :1| :1| 320 TLEAGLPDGRGDGPRQALQEPARQHILLTALNAPLPAGLEA 360
                                                             15 SVEEGEPPGQGEGPR---SRPAAEST-----GLEA 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      probable transcription regulator - Streptomyces coelicolor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 RRAKALRWIRQKSVEEGEPPGQGEGPRSRPAAESIGL 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 55.5; Pred. No. 97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 55.5;
Pred. No. 71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 AKALRWTRQKSVEEGEPPGQ-GEGPRSRP 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Superfamily: POZ domain homology
C;Keywords: zinc finger
F;20-118/Domain: POZ domain homology <POZ>
                                                                                                                                                                                                                                   probable transcription factor PLZF - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3;
            5:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25.9%;
milarity 40.5%;
Conservative 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25.9%;
37.9%;
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Matches 11; Conservative
            15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Reference number: Z21559
A;Accession: T34847
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Genetics:
A;Gene: SCOEDB:SC2G5.14c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Residues: 1-943 <OLI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Residues: 1-673 <CHE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15;
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               Matches
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Cispecies: Debinococcus radiodurans
Cispecies: Debinococcus radiodurans
Cibace: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
Cibacesion: A75634
Riwhite, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-969 <WHI>
A; Rosidues: 1-969 <WHI>
A; Cross-references: GB:AE001826; NID:g6460827; PIDN:AAF12568.1; PID:g6460864; TIGR:DRB01
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C.Species: Caulobacter crescentus
C.Species: Caulobacter crescentus
C.Species: Caulobacter crescentus
C.Species: Caulobacter crescentus
C.Species: 20-Apr-2001
B.Scession: H87516
R.Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Duckin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
D. J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1. A;Reference number: A75250; MUID:20036896; PMID:10567266
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                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
S ribosomes.
A;Reference number: S05611; MUID:90040717; PMID:2530355
A;Accession: S05622
A;Accession: S05622
A;Molecule type: DNA
A;Residues: 1-149 <AUB;
A;Cross-references: EMBL:X16720; NID:9444754; PIDN:CAA34698.1; PID:944766
C;Superfamily: rat ribosomal protein Li9
C;Keywords: protein biosynthesis; ribosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 10
H87516
D-alanyl-D-alanine carboxypeptidase [imported] · Caulobacter crescentus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26.2%; Score 56; DB 2; Length 435.
41.2%; Pred. No. 41;
                                                                                                                                                                                                                                 1; Length 149
                                                                                                                                                                                                                                                                               9; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11;
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                                                                                                                                                                                                                                                                                                                                                            2 KRRAKALRWTRQKSVEEGEPPGQGEGPRSRPAAE 35
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87;
                                                                                                                                                                                                                      DB 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5; Mismatches
                                                                                                                                                                                                                              Score 57;
Pred. No. i
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Pred. No. 8
                                                                                                                                                                                                                              26.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26.2%;
36.6%;
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Matches 12; Conservative
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Best Local Similarity
Matches 14; Conserv
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A; Residues: 1-435 <STO>
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A; Status: preliminary
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A;Gene: CC2161
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Synapsin Ia - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 23-Oct-1990 #sequence_revision 23-Oct-1990 #text_change 01-Dec-2000
C;Accession: A30411; B30411
R;Suedhof, T.C.; Czernik, A.J.; Kao, H.T.; Takei, K.; Johnston, P.A.; Horiuchi, A.; Kana Science 245, 1474-1480, 1989
A;Title: Synapsins: mosaics of shared and individual domains in a family of synaptic ves A;Reference number: A30411; MUID:89383265; PMID:2506642
A;Recension: A30411
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-704 <SUE>
A;Accession: B3041
A;Accession: B3041
A;Accession: B3041
A;Accession: B3041
A;Residues: 1-659, KA, 662, PAQAQP' <SUE>
A;Cross-references: GB:M27924; NID:9206933; PIDN:AAA42148.1; PID:9206933
C;Kcywords: actin binding; alternative spllcing; phosphoprotein
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A,Accession: A25704
A;Molecule type: mRNA
A;Residues: 1-691 <mcc
A;Cross-references: GNZQ4655; NID:g57181; PIDN:CAA28353.1; PID:g57182
A;Experimental source: brain
C;Keywords: actin binding; alternative splicing; phosphoprotein
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                                                                                                                                                                                                                   Query Match 25.7%; Score 55; DB 2; Length 691; Best Local Similarity 42.3%; Pred. No. 83; Matches 11; Conservative 4; Mismatches 11; Indels
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GenCore version 5.1.6
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OM protein - protein search, using sw model

6, 2003, 10:57:04; Search time 1.50788 Seconds June Run on:

(without alignments) 1127.761 Million cell updates/sec

US-09-826-581-6_COPY_51_91

Perfect score:

214 1 GKRRAKALRWTRØKSVEEGE......PGQGEGPRSRPAAESTGLEA 41 Sequence:

BLOSUM62 Scoring table:

Gapop 10.0 , Gapext 0.5

112892 seqs, 41476328 residues Searched:

112892 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMAPTES

	Description	Ognaig homes	Sus			P20823 homo sapien	drosc	P57796 homo sapien		metha	Q12980 homo sapien	homod	homod	mus n	P09951 rattus norv	P26221 thermomonos	ratte	homo	homo	mus m	_	homo	homo	homo	ovis	023712 arabidopsis	Q9xsk0 bos taurus	O54751 mus musculu	P23813 mus musculu	\sim	P03181 epstein-bar	5	ď	P55385 rhizobium s
SUMMARIES	ID	AAKI HUMAN	AAKI_PIG	HNFA_MOUSE	HNFA_RAT	HNFA_HUMAN	HIG_DROME	CAB4_HUMAN	SYN1_HUMAN	RL19_METVA	U171_HUMAN	Z145_HUMAN	SLBP_HUMAN	SYN1_MOUSE	SYN1_RAT	GUN4_THEFU	MY9B_RAT	CRX_HUMAN	UBP5_HUMAN	UBP5_MOUSE	PAL1_ORYSA	CHD2_HUMAN	Y514_HUMAN	SREC_HUMAN	IL2A_SHEEP	PS12_ARATH	CRX_BOVIN	CRX_MOUSE	HXDB_MOUSE	HXB2_HUMAN	YHL1_EBV	MODC_MYCTU	SYN1_CANFA	Y4CC_RHISN
	° Query Match Length DB	1	464	628	628 1	631	928	275	705															830	275	277	568	299		356	099	369	415	
ď	Query Score Match	10	7	۲.	61.5 28.7	ς.	'n.		27	57 26	5.5 25	5.5 25	25		25	25	55 25	'n.		'n				23	2.5	2.5	2.5	2.5	2.5	2.5	2.5		24.	
	Result No. Sc	:			4 6			7	ω,		10 5		12	13	14	15					20	21	22						28 5			31	32	33

Q96i34 homo sapien O51484 pseudomonas	P23347 rattus norv P13808 mus musculu	P48746 oryctolagus	204320 nomo sapien 095180 homo sapien	024705 synechococc	P25710 neurospora	P02894 plasmodium	Q9nzm5 homo sapien	Q9u7e0 caenorhabdi
PPGA_HUMAN Y525 PSEAE	B3A2_RAT B3A2_MOUSE	B3A2_RABIT	CCAH_HUMAN	RS5_SYNP6	NUJM_NEUCR	CSP_PLAKH	GSR2_HUMAN	ATRX_CAEEL
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528 612	1234	1237	2373	180	200	363	478	1359
24.3	24.3	24.3	24.3	24.1	24.1	24.1	24.1	24.1
52	52 52	52	5.2	51.5	51.5	51.5	51.5	51.5
34 35	36	38	v 4 v 0	4.	42	43	44	45

ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -:- FUNCTION: AMPK IS RESPONSIBLE FOR THE REGULATION OF FATTY ACID SYNTHESIS BY PHOSPHORYLATION OF ACETYL-COA CARBOXYLASE. ALSO REGULATES CHOLESPEROL SYNTHESIS VIA PHOSPHORYLATION AND INACTIVATION AND FATOXYMETHYLELUTARYL-COA REDUCTASE AND HORMONE-INCTIVATION OF HYDROXYMETHYLELUTARYL-COA REDUCTASE AND HORMONE-IN THE REGULATION OF ENERGY METABOLISM IN SKELETAL MUSCLE.

-:- SUBUNIT: HETEROTRINER OF ALPHA CATALYLIC SUBUNIT, A BETA AND A GAMMA NON-CATALYLIC REGULATORY SUBUNITS.

-:- TISSUE SPECIFICITY: SKELETAL MUSCLE, WITH WEAK EXPRESSION IN HEART AND PANCREAS.

-:- SIMILARITY: BELONGS TO THE 5'-AMP-ACTIVATED PROTEIN KINASE, GAMMA SUBUNIT FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-Skeletal muscle;
MEDLINE-20280150; PubMed-10818001;
Milan D., Jeon J.-T., Looft C., Amarger V., Robic A., Thelander M.,
Rogel-Gaillard C., Paul S., Tannuccelli N., Rask L., Ronne H.,
Lundstroem K., Reinsch N., Gellin J., Kalm E., Le Roy P., Chardon P.,
                                                                                                        16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
5'-AMP-activated protein kinase, gamma-3 subunit (AMPK gamma-3 chain)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "A mutation in PRKAG3 associated with excess glycogen content in pig
                                                                                                                                                                                                        Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID=9606;
                                                                                                                                                                                                                                                                                                                      MEDLINE=20164049; PubMed=10698692; Cheung P.C., Salt I.P., Davies S.P., Hardie D.G., Carling D.; Cheung P.C., Salt I.P., Davies S.P., Hardie D.G., Carling D.; "Characterization of AMP-activated protein Kinase gamma-subunit isoforms and their role in AMP binding."; Biochem. J. 346:659-669(2000).
                                         464 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -! - SIMILARITY: CONTAINS 4 CBS DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AJ249977; CAB65117.1; ALT_INIT.
EMBL; AF214519; AAF73987.1; -.
                                                           09UGI9; 09NRL1;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last seq
16-OCT-2001 (Rel. 40, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              skeletal muscle.";
Science 288:1248-1251(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                               [2]
SEQUENCE FROM N.A.
                                                                                                                                                                        (AMPK gamma3).
PRKAG3 OR AMPKG3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Andersson L.;
                                         AAKI_HUMAN
RESULT 1
AAKI_HUMAN
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us-09-826-581-6_copy_51_91.rsp

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Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                 VARIANT
                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HNFA_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- FUNCTION: AMPK IS RESPONSIBLE FOR THE REGULATION OF FATTY ACID SYNHHESIS BY PHOSPHORYLATION OF ACETYL-COA CARBOXYLASE. ALSO REGULATES GHOLESTEROL SYNTHESIS VIA PHOSPHORYLATION AND INACTIVARION OF HYDROXYMETHYLGLUTARYL-COA REDUCTAGE AND HORMONE-SENSITIVE LIPASE. THIS IS A REGULATORY SUBUNIT. IT MAY PLAY A ROLE IN THE REGULATION OF ENDERGY METABOLISM IN SKELETAL MUSCLE.
-!- SUBBNIT: HETEROTRIME OF AN ALPHA CATALYTIC SUBUNIT, A BETA AND A GAMMA NON-CATALYTIC REGULATORY SUBUNITS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORIGINATED IN THE HAMPSHIRE BREED PIGS AND HAS BENEFICIAL EFFECTS ON MEAT CONTENT BUT DETRIMENTAL EFFECTS ON PROCESSING YIELD. THUS, THIS MUTATION IS OF CONSIDERABLE ECONOMIC SIGNIFICANCE IN THE PIG
                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5'-AMP-activated protein kinase, gamma-3 subunit (AMPK gamma-3 chain)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Milan D., Jeon J.-T., Looft C., Amarger V., Robic A., Thelander M., Rogel-Gaillard C., Paul S., Iannuccelli N., Rask L., Ronne H., Lundstroem K., Reinsch N., Gellin J., Kalm E., Le Roy P., Chardon P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY: BELONGS TO THE 5'-AMP-ACTIVATED PROTEIN KINASE, GAMMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "A mutation in PRKAG3 associated with excess glycogen content in pig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- TISSUE SPECIFICITY: MUSCLE.
-!- DISEASE: DEFECTS IN PRKAG3 (RN-) ARE ASSOCIATED WITH EXCESS GLYCOGEN CONTENT (ABOUT 70%) IN SKELETAL MUSCLE. THIS MUTATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                                                                           ÷
                                                                                                                                                                                                                                                                                                                                                           Score 210; DB 1; Length 464;
Pred. No. 1.1e-16;
                                                                                                                                                                                                                     T -> A (1N REF. 1).
MQ -> IE (IN REF. 1).
Q -> K (IN REF. 1).
ALGA -> PSGPEKI (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                         1; Indels
                                                                                                                                                                                                                                                                                                               51514 MW; 53985C2C77003A63 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GKRRAKALRWTRQKSVEEGEPPGQGEGPRSRPAAESTGLEA 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26 GKRRAKALRWTRQKSVEGEPPGQGEGPRSRPTAESTGLEA 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A., AND VARIANT RN(-) GLN-200.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Rel. 40, Last sequence update)
(Rel. 40, Last annotation update)

      Fatty acid biosynthesis; Repeat; CBS domain.

      DOMAIN
      147
      201
      CBS 1.

      DOMAIN
      228
      282
      CBS 2.

      DOMAIN
      303
      356
      CBS 3.

      DOMAIN
      375
      428
      CBS 4.

                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SIMILARITY: CONTAINS 4 CBS DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=20280150; PubMed=10818001;
                                         InterPro; IPR000644; CBS_domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-OCT-2001 (Rel. 40, Created)
                                                                                                                                                                                                                                                                                                                                                           98.1%;
97.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Science 288:1248-1251(2000)
    HGNC:9387; PRKAG3.
                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                  Pfam; PF00571; CBS; 4.
SMART; SM00116; CBS; 4.
                                                                                                                                       201
282
356
428
428
164
464
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BREEDING INDUSTRY
                                                                                                                                                                                                                                                                                                               464 AA;
                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBUNIT FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sus scrofa (Pig).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           skeletal muscle.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (AMPK gamma3).
PRKAG3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Andersson L.;
Genew; HGNC: > wTM; 604976;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                         40;
                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                           Query Match
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                                                                                                                                                                                                                        CONFLICT
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or send an email to license@isb-sib.ch).
                       (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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"Molecular cloning, functional expression, and chromosomal localization of mouse hepatocyte nuclear factor 1.";
Proc. Natl. Acad. Sci. U.S.A. 87.9838-9842(1990).
-!- FUNCTION: REQUIRED FOR THE EXPRESSION OF SEVERAL LIVER SPECIFIC GENES. BINDS TO THE INVERTED PALINDROME 5'-GTTAATNATTAAC-3'.
-!- SUBGELLULAR LOCATION: Nuclear.
-!- SUBCELLULAR LOCATION: Nuclear.
-!- SIMILARITY: BELONGS TO THE HNF1 HOMEOBOX FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00027; HOMEOBOX_1; 1.
PROSITE; PS50071; HOMEOBOX_2; 1.
Transcription regulation; DNA-binding; Homeobox; Nuclear protein; Activator; Trans-acting factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ő
                                                                                                                                                                                                                                                    CBS domain; Disease mutation.
                                                                                                                                                                                                                                                                                                                                                                                                                      ; 1/oc..
Score 142; DB 1; Lenge..
-4 No. 5.3e-09;
10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 464;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hepatocyte nuclear factor 1-alpha (HNF-1A) (Liver specific transcription factor LF-B1) (LFB1).
TCF1 OR HNF1A OR HNF-1A OR HNF-1.
                                                                                                                                                                                                                                                                                                                                                                                         R -> Q (IN RN-).
17638CB12A2BA9DF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26 GDQGNKASRWTRQEDVEEGGPPGPREGPQSRPVAESTGQEA 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GKRRAKALRWIRQKSVEEGEPPGQGEGPRSRPAAESTGLEA 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-AGG-1991 (Rel. 19, Created)
01-AGG-1991 (Rel. 19, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      628 AA
modified and this statement is not removed.
                                                    or send an email to license@isb-sib.ch).
                             entities requires a license agreement
                                                                                                                                                                                                                                                                                                     CBS 2.
CBS 3.
CBS 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=91088607; PubMed=2263635;
                                                                                                     EMBL; AF214521; AAF73989.1; -.
EMBL; AF214520, AAF73988.1; -.
Interpro; IPR000644; CBS_domain.
Pfam; PF00571; CBS; 4.
SMART; SM00116; CBS; 4.
                                                                                                                                                                                                                                                    Fatty acid biosynthesis, Repeat;
DOMAIN 172 226 CBS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MGD; MGI 98504; Tcf1.
InterPro; IPR001356; Homeobox.
SMART; SM00389; HOX; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                         51308 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66.4%;
68.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; M57966; AAA37821.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR; A39262; A39262.
                                                                                                                                                                                                                                                                                                                               328
400
200
464 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSSP; P15257; 1LFB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity 28; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRANSFAC; T01211;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10090;
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ij
                                                                                                                                                                                                                                                                         Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                              NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 166-628 FROM N.A.
MEDLINE-90249741; PubMed=1970973;
MEDLINE-90249741; PubMed=1970973;
Mendel D.B., Conley P.B., Kuo C.J., Turk C.,
Graves M.K., Edwards C.A., Courtois G., Crabtree G.R.;
"HNF-1 shares three sequence motifs with the POU domain proteins and is identical to LF-B1 and APF.";
                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                           Chouard T., Blumenfeld M., Bach I., Vandekerckhove J., Cereqhini S.,
                                                   21 AMINO ACID LOOP BETWEEN HELIX 2 AND
                                                                                                                                                                                                                                                                                                                                               MEDLINE-90003224; PubMed-2571419;
Frain M., Swart G., Monaci P., Nicosia A., Staempfli S., Frank R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=91105074; pubMed=1988016;
Pastore A., de Francesco R., Barbato G., Castiglione Morelli M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 homeodomain of the transcription factor LF-B1 has a 21 amino loop between helix 2 and helix 3.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                               "A distal dimerization domain is essential for DNA-binding by the atypical HNF1 homeodomain.";
                                                                                                                                                                                                                                                                                                                                                                               "The liver-specific transcription factor LF-Bl contains a highly
                                                                                                       ij
           ASP/GLU-RICH (ACIDIC) (POTENTIAL
                                                                                 DB 1; Length 628;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=Sprague-Dawley;
Tomei L., Piaggio G., Toniatti C., Lazzaro D., de Francesco
Pozzi L., Gerstner J., Cortese R.;
                     INVOLVEMENT WITH TRANSCRIPTION)
                                                                                                                                                                                                              01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Hepatocyte nuclear factor 1-alpha (HNF-1A) (Liver specific transcription factor LF-B1) (LFB1).
                                                                                                    18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pozzi L., Gerstner J., Cortese R.;
Submitted (AUG-1992) to the EMBL/GenBank/DDBJ databases
                                                               CRC64;
                                                                                                                                   2 KRRAKALRWTRQKSVEGGEPPGQGEGPRSRPAAESTGL 39
                                                             737920D1A369B9DD
                                                                                                                                                                                              628 AA.
                                                                                Score 61.5; DE
Pred. No. 8.9;
                                                                                                      4; Mismatches
  DIMERIZATION
                                        HOMEOBOX
                                                                                                                                                                                                                                                                                                                                                                                         diverged homeobox DNA binding domain."
Cell 59:145-157(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic Acids Res. 18:5853-5863(1990).
                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-91016926; PubMed=2216777;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=90106643; PubMed=1967225;
                                                             67237 MW;
                                                                                28.7%;
39.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genes Dev. 4:372-379(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 1-12 FROM N.A.
                                                                            Query Match
Best Local Similarity 39.55
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRUCTURE BY NMR OF 1-32.
                                                                                                                                                                                              STANDARD;
                             205
279
258
 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HOMEOBOX
                                                            628 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POSITION OF
                                                                                                                                                                                                                                                                                                                                                                      Cortese R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Finney M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Yaniv M.;
                                        DNA_BIND
                                                            SEQUENCE
                                                                                                                                                                                             HNFA_RAT
DOMAIN
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                "IH resonance assignment and secondary structure determination of the dimerization domain of transcription factor LFB1."; Biochemistry 30:148-153(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21 AMINO ACID LOOP BETWEEN HELIX 2 AND 3.
                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-97272000; PubMed-9126845; Schott O., Billeter M., Leiting B., Wider G., Wuethrich K.; The NMR solution structure of the non-classical homeodomain from the
                                                                                                                                                                                                                                                           from rat liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ASP/GLU-RICH (ACIDIC) (POTENTIAL INVOLVEMENT WITH TRANSCRIPTION).
NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SPECIFIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rat
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PROSITE; PSO071; HOMBOBOX_2: 1.
Transcription regulation; DMA-binding; Homeobox; Nuclear protein; Activator; Trans-acting factor; 3D-structure.
                                                                                                                                                                                                                                polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "The X-ray structure of an atypical homeodomain present in the liver transcription factor LFB1/HNF1 and implications for DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -i - FUNCTION: REQUIRED FOR THE EXPRESSION OF SEVERAL LIVER SPECGENES. BINDS TO THE INVERTED PALINDROME 5'-GTTAATNATTAAC-3'-SUBUNIT: BINDS DNA AS A DIMER.
-i - SUBCELLULAR LOCATION: Nuclear.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Suck
                                                                                                                                               MEDLINE-93259120; PubMed-8491172;
Leiting B., de Francesco R., Tomei L., Cortese R., Otting G.,
Wuethrich K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 195-286.
MEDLINE-93259121; PubMed=8491173;
Ceska T.A., Lamers M., Monaci P., Nicosia A., Cortese R.,
                                                                                                                                                                                                                                                      fragment 195-286 of the LFB1/HNF1 transcription factor comprises a nonclassical homeodomain.";
                                                                                                                                                                                                                             'The three-dimensional NMR-solution structure of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- TISSUE SPECIFICITY: LIVER.
-!- SIMILARITY: BELONGS TO THE HNF1 HOMEOBOX FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              rat liver LFB1/HNF1 transcription factor.";
J. Mol. Biol. 267:673-683(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL, J03170; AAA41524.1; -.
EMBL, X54423; CAA38295.1; -.
EMBL, X67649; CAA47891.1; -.
EMBL, X53297; CAA37387.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001356; Homeobox.
                                                                                                                                                                                                                                                                                                                                                             STRUCTURE BY NMR OF 195-286
                                                                                                                         STRUCTURE BY NMR OF 195-286
                                                                                                                                                                                                                                                                                                            EMBO J. 12:1797-1803(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBO J. 12:1805-1810(1993).
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PIR; A34590. A34590.
PIR; S11568. S11568.
PIR; S25485; S25485.
PDB; 1LFB; 31-CCT-93.
PDB; 2LFB; 12-MAR-97.
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Cortese R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FRANSFAC; T00369
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MEDLINE-97431548; PubMed-9287053;
                                                                                                               Gaps
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MEDLINE-97100943; PubMed=8945470;
Yamaqata F., Oda N., Kaisaki P.J., Menzel S., Furuta H.,
Vaxillaire M., Southam L., Cox R.D., Lathrop G.M., Boriraj V.V.,
Chen X., Cox N.J., Oda Y., Yano H., le Beau M.M., Yamada S.,
Nishigori H., Takeda J., Fajans S.S., Hattersley A.T., Iwasaki N.,
Nishigori H., Pedersen O., Polonsky K.S., Turner R.C., Velho G.,
Chevre J.-C., Froquel P., Bell G.I.;
"Mutations in the hepatocyte nuclear factor-lalpha gene in maturity-
onset diabetes of the young (MODY3).";
                                                                                                                                                                                                                                                                                              P20823; Q99861;
01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Hepatocyte nuclear factor 1-alpha (HMR-1A) (Liver specific transcription factor LF-B1) (LFB1) (Transcription factor-1) (TCF-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                More potent transcriptional activators or a transdominant inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bach I., Galcheva-Gargova Z., Mattei M.-G., Simon-Chazottes D., Guenet J.-L., Cereghini S., Yaniv M.; "Cloning of human hepatic nuclear factor I (HNFI) and chromosomal localization of its gene in man and mouse."; Genomics 8:155-164(1990).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of the HNF1 homeoprotein family are generated by alternative RNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Novel mutations and a mutational hotspot in the MODY3 gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Iwasaki N., Oda N., Ogata M., Hara M., Hinokio Y., Oda Y.,
Yamagata K., Kanematsu S., Ohgawara H., Omori Y., Bell G.I.;
                                                                      28.7%; Score 61.5; DB 1; Length 628; 39.5%; Pred. No. 8.9;
                                                                                                             Indels
                                   67213 MW; 8D28099308C86A52 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VARIANTS MODY3 ARG-107; TRP-131; MET-260 AND HIS-272.
                                                                                                                                                                      2 KRRAKALRWIRQKSVEEGEPPGQGEGPRSRPAAESTGL 39
                                                                                                                                                                                                                                                                                    631 AA.
                                                                                                             4; Mismatches
                                                                                                                                                                                                                                                                                    PRT;
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MEDLINE=94038905; PubMed=7900999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Diabetes 46:1081-1086(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBO J. 12:4229-4242(1993).
                                                                                                           15; Conservative
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                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
                                   628 AA;
                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bach I., Yaniv M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                  TCF1 OR HNF1A.
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                                 SEQUENCE
                                                                          Query Match
                                                                                                             Matches
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Takeda J.; Infortion of mutations in the hepatocyte nuclear factor (HNF)-1-alpha gene in Japanese subjects with IDDM."; Diabetes 46:1643-1647(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VARIANTS MODY3 ASN-128; TYR-143 AND LEU-447.

WEDELINE-97230241; PubMed=9075819;

Hansen T., Eiberg H., Rouard M., Vaxillaire M., Moeller A.M.,

Rasmussen S.K., Fridberg M., Urbammer S.A., Holst J.J., Almind K.,

Echwald S.M., Hansen L., Bell G.I., Pedersen O.;

Movel MODY3 mutations in the hepatocyte nuclear factor-lalpha gene:
evidence for a hyperexictability of pancreatic beta-cells to
intravenous secretagogues in a glucose-tolerant carrier of a P447L
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                                                                                                                  MEDLINE-97431550; PubMed-9287055; Yamada S., Nishigori H., Onda H., Takahashi K., Kitano N., Morikawa A., Takeuchi T., Takeda J.; Morikawa A., Takeuchi T., Takeda J.; Mutations in the hepatocyte nuclear factor-lalpha gene (MODX3) are not a major cause of late-onset NIDDM in Japanese subjects."; Diabetes 46:1512-1513(1997).
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                                                                                                                                                                                                                                                                                                              MEDLINE-97458988; Pubmed-9313763;
Yamada S., Nishigori H., Onda H., Utsugi T., Yanagawa T., Maruyama
Onigata K., Nagashima K., Nagai R., Morikawa A., Takeuchi T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Boutin P., Chevre J.-C., Hani E.H., Gomis R., Pardini V.C., Guillausseau P.-J., Vaxillaire M., Velho G., Froguel P.;
"An automated fluorescent single-strand conformation polymorphism technique for screening mutations in the hepatocyte nuclear factor-lalpha gene (maturity-onset diabetes of the young).";
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Moeller A.M., Fridberg M., Hansen L., Hansen T., Bell G.I.,
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"Mutations in the hepatocyte nuclear factor-lalpha/MODY3 gene Japanese subjects with early- and late-onset NIDDM."; Diabetes 46:1504-1508(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VARIANTS MODY3 THR-129; TRP-131; TRP-159; LEU-519 AND ILE-620.
                                                                                                 VARIANT NIDDM MET-254, AND VARIANTS LEU-27 AND ASN-487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VARIANTS MODY3, AND VARIANT ATYPICAL DIABETES SER-574.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VARIANTS MODY3 GLN-131; GLN-229; GLY-241 AND HIS-272.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VARIANTS LEU-27; VAL-98 AND ASN-487.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=98052398; PubMed=9392505;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Diabetes 46:2108-2109(1997).
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MEDLINE-98425814; PubMed-9754819;
MEDLINE-98425814; PubMed-9754819;
Whevre J.-C., Hani E.H., Boutin P., Vaxillaire M., Blanche H.,
Vionnet N., Pardini V.C., Timmit J., Larger E., Charpentier G.,
Beckers D., Maes M., Bellanne-Chantelot C., Velho G., Froguel P.;
Mutation screening in 18 Caucasian families suggest the existence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIINE-98289379; PubMed-9626139;
Elbein S.C., Teng K., Yount P., Scroggin E.;
"Linkage and molecular scanning analyses of MODY3/hepatocyte nuclear
factor-1 alpha gene in typical familial type 2 diabetes: evidence for
novel mutations in exons 8 and 10..."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Mutations in the hepatocyte nuclear factor-lalpha gene in Caucasian families originally classified as having type I diabetes.";
                     in
                                                                                                                       MEDLINE-97252393; PubMed-9097962;

Vaxillaire M., Rouard M., Yamagata K., Oda N., Kaisaki P.J.,

Beriraj V.V., Chevre J.-C., Boccio V., Cox R.D., Lathrop G.M.,

Dussoix P., Philippe J., Timsit J., Charpentier G., Velho G.,

Bell G.I., Froguel P.,

"Identification of nine novel mutations in the hepatocyte nuclear factor I alpha gene associated with maturity-onset diabetes of the young (MODY3).";
                                                                                                                                                                                                                                                                                                                                                                                                                     "Hepatocyte nuclear factor lalpha coding mutations are an uncommon contributor to early-onset type 2 diabetes in Ashkenazi Jews."; Diabetes 47:967-969(1998).
                 "Genetic variation in the hepatocyte nuclear factor-1 alpha gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Mutations in the hepatocyte nuclear factor-1 alpha gene 'MODY3' not a major cause of early-onset non-insulin-dependent 'type 2'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene in Japanese subjects with early-onset NIDDM and functional
                                                                                                                                                                                                                                                                                                                                                      MEDLINE-98265912; Pubmed-9604876;
Behn P.S., Wasson J., Chayen S., Smolovitch I., Thomas J.D.,
Glaser B., Permutt M.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28.7%; Score 61.5; DB 1; Length 631; 39.5%; Pred. No. 8.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Moeller A.M., Dalgaard L.T., Pociot F., Nerup J., Hansen T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-98284534; Pubmed-9621514;
Nishigori H., Yamada S., Kohama T., Utsugi T., Shimizu H.,
Takeuchi T., Takeda J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VARIANTS MODY3 HIS-12; ASN-158; GLN-159 AND CYS-203.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       novel mutations in exons 8 and 10.";
J. Clin. Endocrinol. Metab. 83:2059-2065(1998)
                                                                                                      VARIANTS MODY3 CYS-122; PHE-142 AND GLN-159.
                                           Danish Caucasians with late-onset NIDDM.";
                                                                                                                                                                                                                                                                                                                                    VARIANTS LEU-27; ASN-487 AND ARG-514.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VARIANTS MODY3 ARG-537 AND LYS-619.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VARIANTS MODY3 GLU-117 AND TYR-143.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=99176457; PubMed=10078571;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 proteins.";
                                                                                                                                                                                                                                                                                           Hum. Mol. Genet. 6:583-586(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VARIANTS IDDM LYS-48 AND GLY-241.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=99083111; PubMed=9867222;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                diabetes mellitus in Japanese.";
J. Hum. Genet. 43:107-110(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Diabetologia 41:1017-1023(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Diabetologia 41:1528-1531(1998).
                                                             Diabetologia 40:473-475(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VARIANTS LEU-27 AND ASN-487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               analysis of the mutant pro
Diabetes 48:645-648(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                other MODY genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pedersen O.;
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Gaps

1;

18; Indels

4; Mismatches

15; Conservative

Matches

Best Local Similarity

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between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                          Hoshino M., Matsuzaki F., Nabeshima Y.-I., Hama C.; "Hikaru genki, a CNS-specific gene identified by abnormal locomotion in Drosophila, encodes a novel type of protein."; heuron 10:395-407(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IN LOCOMOTOR ACTIVITY.
-- SUBCELLULAR LOCATION: EXLTACELLULAR.
--- ALTERNATIVE PRODUCTS: 4 ISOFORMS; 1, 2, 3 (SHOWN HERE) AND 4; ARE PRODUCED BY ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                                    Bukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
NCBL_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCOMOTION-RELATED PROTEIN HIKARU GENKI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -1- DEVELOPMENTAL STAGE: MOST ABUNDANT DURING AND/OR AFTER NEURONAL DIFFERENTIATION AND DURING CELL SPECTFICATION OR AXOGENESIS.
-1- SIMILARITY: BELONGS TO THE IMMUNGLOBULIN SUPERFAMILY.
-1- SIMILARITY: CONTAINS 1 IMMUNGLOBULIN-LIKE C2-TYPE DONAIN.
-1- SIMILARITY: CONTAINS 4 SUSHI (SCR) DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Glycoprotein; Alternative splicing; Immunoglobulin domain; Repeat; Sushi; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- TISSUE SPECIFICITY: EXPRESSED IN PCC NEURONS AND NEUROBLASTS IN THE PROCEPHALIC NEUROGENIC REGION IN THE CENTRAL NERVOUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IG-LIKE C2-TYPE DOMAIN.
                               271 RRKEEAFRHKLAMDTYSGPPGPGPGP-ALPAHSSPGL 307
39
                                                                                                                                                                                      15-JUN-2002 (Rel. 41, Last annotation update)
Locomotion-related protein Hikaru genki precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CELL ATTACHMENT SITE.
2 KRRAKALRWIRQKSVEEGEPPGQGEGPRSRPAAESTGL
                                                                                                                      958 AA
                                                                                                                                                 01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUSHI 2.
SUSHI 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUSHI 1.
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                                                                                                                                                                                                                                      Drosophila melanogaster (Fruit fly).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR003599; Ig.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR000436; Sushi_SCR_CCP.
                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=93213498; PubMed=8461133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; D13884; BAA02984.1; -. EMBL; D13885; BAA02985.1; -. EMBL; D13886; BAA02986.1; -. EMBL; D13887; BAA02987.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FlyBase; FBgn0010114; hig.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam: PF00047; ig; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMART; SM00032; CCP; 5.
SMART; SM00409; IG; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31
958
709
769
828
891
952
320
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                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SYSTEM.
                                                                                                                    HIG_DROME Q09101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIGNAL
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DOMAIN
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SYN1_HUMAN
                                                                                                                                                                                                                                              Matches
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        ΩD
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                                                                                                                                                                                                                                                                                                                                                 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
BY SIMILARITY.
N-LINKED (GLCNAC...) (POTENTIAL).
                                                                                                                                                                                                                                            2 AND ISOFORM 4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                 5
                                                                                                                                                                                                                                                                                                              28.7%; Score 61.5; DB 1; Length 958;
                                                                                                                                                                                                                                                                                                                                              8; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                   :| :: || |::| | :|:
QRDRSPRWRRRRSTEFKGDLGQLPPESGIGPEPELAD 365
                                                                                                                                                                                                                                                                                                                                                                                3 RRAKALRWTRQKSVE-EGE----PPGQGEGPRSRPAAE 35
                                                                                                                                                                                                                                            MISSING (IN ISOFORM MISSING (IN ISOFORM
                                                                                                                                                                                                                                                                              4161258E85ABC764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P57796: Q8WWY5;
16-OCT-2001 (Rel. 40, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     275 AA
                                                                                                                                                                                                                                                                                                                                Pred. No. 13;
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InterPro; IPR003299; Calflagin.
InterPro; IPR002048; EF-hand.
                                                                                                                                                                                                                                                                          107027 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-JUN-2002 (Rel. 41, Last anno Calcium-binding protein CaBP4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Haeseleer F., Palczewski K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 65-275 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AY039217; AAK83462.1;
                                                                                                                                                                                                                                                                                                                                36.88;
                                                                                                                                                                                                                                                                                                                                              14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                     939
939
376
376
620
620
789
553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSSP; P02593; 1CDM.
                                                                                                                                                                                                                                                                          958 AA;
                                                                                                                                                                                                                                                                                                                              Similarity
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 7114
7714
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAB4_HUMAN
                                 DISULFID
                                                                   DISULFID
                                                                                                                                                       CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                         VARSPLIC
VARSPLIC
                                                                                                                     DISULFID
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                                                                                                       DISULFID
                                                                                                                                       CARBOHYD
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                                                                                                                                                                                                          CARBOHYD
                                                                                                                                                                                                                          CARBOHYD
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 DISULFID
                   DISULFID
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Matches 1
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"The 5'-flanking region of the synapsin I gene. A G+C-rich, TATA- and
AAT-less, phylogenetically conserved sequence with cell
type-specific promoter function."
J. Biol. Chem. 265:14932-14937(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SYNAPSIN IB; ARE PRODUCED BY ALTERNATIVE SPLICING.
-1- PTM. SUBSTRATE OF AT LEAST FOUR DIFFERENT PROTEIN KINASES. IT IS PROBABLE THAT PHOSPHORYLATION PLAYS A ROLE IN THE REGULATION OF SYNAPSIN I IN THE NEXUE TERMINAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    !- FUNCTION: NEURONAL PHOSPHOPROTEIN THAT COATS SYNAPTIC VESICLES, BINDS TO THE CYTOSKELETON, AND IS BELIEVED TO FUNCTION IN THE REGULATION OF NEUROTRANSMITTER RELEASE.
                                                                                                                                                                                            EF-HAND 1 (POTENTIAL).
ANCESTRAL CALCIUM SITE 2 (POTENTIAL).
EF-HAND 3 (POTENTIAL).
EF-RAND 4 (POTENTIAL).
IAEB49C93AD67DB7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SUBCELLULAR LOCATION: SYNAPSE.
-!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; SYNAPSIN IA (SHOWN HERE) AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                         12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein.";
                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 275;
                                                                                                                                                                                                                                                                                                                                                                                                                         7; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 RRAKALRWTRQKSVEEGE------PPGQGEGPRSRPAA 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Suedhof T.C.; "The structure of the human synapsin I gene and J. Biol. Chem. 265:7849-7852(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SIMILARITY: BELONGS TO THE SYNAPSIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SYN1_HUMAN STANDARD; PRT; 705 AA. P17600; 075825; 01-4001-990 (Rel. 15, Created) 01-007-1996 (Rel. 34, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                            7.5;
                                                                                                                                                                                                                                                                                                                                                                  Score 59;
                                                                                                                                                                                                                                                                                                                                                                                               Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 1-125 FROM N.A. MEDLINE=90368667; PubMed=2118519;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=90243651; PubMed=2110562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synapsin I (Brain protein 4.1).
                                                                              SMART; SM00054; EFP; 3.
PROSITE; PS00018; EFP, 3.
Calcium-binding; Repeat.
CALBIND.
Pfam; PF00036; efhand; 3.
PRINTS; PR01362; CALFLAGIN.
ProDom; PD000012; EF-hand; 2.
SMART; SM00054; EFh.
                                                                                                                                                                                                                                                                                                          30433 MW;
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                                                                                                                                                                                                                                                                                                                                                                  27.6%;
                                                                                                                                                                                                                                                                                                                                                                                            29.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 1-258 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                         13; Conservative
                                                                                                                                                                                                                   189
230
267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
                                                                                                                                                                                                                   178 1
219 2
256 2
275 AA;
                                                                                                                                                                                                                                                                                                                                                                                            Sest Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-Brain,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Grafham D.;
                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                   CA_BIND
                                                                                                                                                                                                                                                                                                                                                                  Query Match
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EMBL; EMBL;

EMBL; EMBL;

EMBL; EMBL; EMBL;

EMBL;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                              MEDLINE-90040717; PubMed=2530355,
Auer J., Spicker G., Boeck A.;
"Organization and structure of the Methanococcus transcriptional unit
homologous to the Escherichia coli 'spectinomyoin operon'.
Implications for the evolutionary relationship of 70 S and 80 S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-96121379; Pubmed-8575760; Vyas P., Vickers M.A., Picketts D.J., Higgs D.; "Conservation of position and sequence of a novel, widely expressed gene containing the major human alpha-globin regulatory element."; Genomics 29:679-689(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Domo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                          -!- SIMILARITY: BELONGS TO THE L19E FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26.6%; Score 57; DB 1; Length 149; 35.3%; Pred. No. 6.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (FEB-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Ribosomal protein.
SEQUENCE 149 AA; 17286 MW; B8868F4FD5670E0B CRC64;
 Archaea; Euryarchaeota; Methanococci; Methanococcales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 KRRAKALRWIRQKSVEEGEPPGQGEGPRSRPAAE 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               U171_HUMAN STANDARD; PRT; 569 AA. Q12980; 092469; 16-0CT-2001 (Rel. 40, Created) 16-0CT-2001 (Rel. 40, Last sequence update) 16-0CT-2001 (Rel. 40, Last annotation update) CGTHBA protein (-14 gene protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- TISSUE SPECIFICITY: Widely expressed.
-!- SIMILARITY: BELONGS TO THE UPF0171 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR000196; Ribosomal_L19e. Pfam: PF01280; Ribosomal_L19e; 1. PROSITE; PS00526; RIBOSOMAL_L19E; 1.
                  Methanococcaceae; Methanococcus
                                                                                                                                                                             J. Mol. Biol. 209:21-36(1989)
                                                                                                                                                                                                                                                                                                                                                               EMBL; X16720; CAA34698.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 35.3%;
ses 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          [2]
SEQUENCE OF 1-62 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                PIR; S05622; R5MXE.
                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                NCBI_TaxID=2187;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Thomas K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CGTHBA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               U171_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NKSQSLTNA -> KASPAQAQP (IN SYNAPSIN IB)
MISSING (IN SYNAPSIN IB).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         B (LINKER).
C (ACTIN-BINDING AND SYNAPTIC-VESICLE
BINDING).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PHOSPHORYLATION (BY PKA AND CAMKI).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PR01368; SYNAPSIN.
PR051TE; PS00415; SYNAPSIN.1; 1.
PR051TE; PS00416; SYNAPSIN.2; 1.
Synapse; Phosphorylation; Neurone; Repeat; Actin-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAMK2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         G -> E (IN REF. 3).
487831123FF6882F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            D (PRO-RICH LINKER).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PHOSPHORYLATION (BY PHOSPHORYLATION (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
50S ribosomal protein L19E (ORF E).
RPL19E.
Methanococcus vannielii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT; 149 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 59;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       516 QQPASQAAPPTQGQGRQSRPVAGGPG 541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13 QKSVEEGEPPGQGEGPRSRPAAESTG 38
                                                                                                                      JOINED.
JOINED.
JOINED.
ALT.SEQ.
JOINED.
                                                                                                                                                                                                                         AAC41931.1; JOINED.
AAC41931.1; JOINED.
AAC41931.1; JOINED.
AAC41931.1; JOINED.
AAC41931.1; JOINED.
AAC41931.1; JOINED.
AAC41931.1; JOINED.
                                            JOINED.
JOINED.
JOINED.
                                                                                           AAC41930.1; JOINED.
AAC41930.1; JOINED.
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AAC41931.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                           M58376; AAC41931.1; JOINED.
M58377; AAC41931.1; JOINED.
M55301; AAA60608.1; -.
                                                                                                                                                                                                                                                                       InterPro; IPR001359, Synapsin.
Pfam; PF02078; Synapsin; 1.
Pfam; PF02750; Synapsin_C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      73954 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27.6%;
                                                         AAC41930.1;
AAC41930.1;
                            AAC41930.1;
                                             AAC41930.1;
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AAC41930.1;
                                                                                                                                                                                            AAC41931.1;
                                                                                                                                                                                                           AAC41931.1;
                                                                                                                                                              AAC41930.1;
                                                                                                                                                                           AAC41930.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       669
705
138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alternative splicing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      705 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29
113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        421
656
9
568
661
670
138
                                                           M58359; A
                           M58351;
M58353;
                                                                                                                                                                                                                                            M58351;
M58353;
                                                                                             M58372;
                                                                                                                                                                                                        M58321;
                                                                                                                                             M58375;
                                                                                                                                                                             M58377;
                                                                                                                                                                                              M58378;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MIM; 313440;
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P14024;
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VARSPLIC CONFLICT VARSPLIC

MOD_RES MOD_RES MOD_RES

DOMAIN DOMAIN DOMAIN

DOMAIN DOMAIN SEQUENCE

Matches

RL19_METVA

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RESULT 9

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FINGER PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                           461
490
518
574
574
630
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HBP OR SLBP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SLBP_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOD_RES
VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                             ZN_FING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOD_RES
MOD_RES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 12
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ALTERNATIVE PRODUCTS: 2 ISOFORMS: PLFZA AND PLZFB (SHOWN HERE);
ARE PRODUCED BY ALTERNATIVE SPLICING.
TISSUE SPECIFICITY: WITHIN THE HEMPINOPOLETIC SYSTEM, PLZF IS
EXPRESSED IN BONE MARROW, EARLY MYELOID CELL LINES AND PERIPHERAL
BLOOD MONONUCLEAR CELLS. ALSO EXPRESSED IN THE OVARY, AND AT LOWER INDUCTION: BY RETINOIC ACID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chen S.-J., Zelent A., Tong J.-H., Yu H.-Q., Wang Z.-Y., Derre J., Berger R., Waxman S., Chen Z.; Rearrangements of the retinoic acid receptor alpha and promyelocytic leukemia zinc finger genes resulting from t(IL:17)(q23;q21) in a patient with acute promyelocytic leukemia.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Structure-function studies of the BTB/POZ transcriptional repression
                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION: PROBABLE TRANSCRIPTION FACTOR. MAY PLAY A ROLE IN MYELOID MATURATION AND IN THE DEVELOPMENT AND/OR MAINTENANCE OF OTHER DIFFERENTIATED TISSUES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DISEASE: A FORM OF ACUTE PROMYELOCYTIC LEUKEMIA (APL) IS
CHARACTERIZED BY A CHROMOSOMAL TRANSLOCATION T(11.17) (032.021)
WHICH INVOLVES SHE145 AND RETINOIC ACID RECEPTOR ALPHA (RARA).
SIMILARITY: BELONGS TO THE KRUEPPEL FAMILY OF C2H2-TYPE ZINC-
                                                                                                                                                                                                                                                                                                                                                                                                                                         Chen Z., Brand N.J., Chen A., Chen S.-J., Tong J.-H., Wang Z.-Y., Waxman S., Zelent A.; "Fusion between a novel Kruppel-like zinc finger gene and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE~20005701; PubMed=10537309;
Li X., Peng H., Schultz D.C., Lopez-Guisa J.M., Rauscher F.J. III.
Marmorstein R.;
                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           domain from the promyelocytic leukemia zinc finger oncoprotein."
Cancer Res. 59:5275-5282(1999).
                                                                                                                           ٠.
س
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               retinoic acid receptor-alpha locus due to a variant t(11:17) translocation associated with acute promyelocytic leukaemia.";
                                                                                                                                                                                                                                                              01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Zinc finger protein PLZF (Promyelocytic leukemia zinc finger
                                                                                                  DB 1; Length 569;
                                                                                                                        15; Indels
                                            InterPro; IPR005365; UPF0171.
Pfam; PF03666; UPF0171; 1.
SEQUENCE 569 AA; 63604 MW; 44BEF42AA7F2841D CRC64;
                                                                                                                                                   38
                                                                                                                                                                GSRGNKLLFRYPFQRSQE--HPASQTSKPRSRYAASNTG 52
                                                                                                                                                 1 GKRRAKAL-RWIRQKSVEEGEPPGQGEGPRSRPAAESTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 7-122.
                                                                                                                                                                                                                                        673 AA
                                                                                                                           Mismatches
                                                                                                 Score 55.5;
Pred. No. 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clin. Invest. 91:2260-2267(1993).
                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                           protein) (Zinc finger protein 145) ZNF145 OR PLZF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 424-455 FROM N.A.
MEDLINE=93253074; PubMed~8387545;
                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Heart ventricle;
MEDLINE=93209216; PubMed=8384553;
                                                                                                                        3;
         EMBL; X90857; CAA62368.1; -. EMBL; Z69666; CAA93521.1; -.
                                                                                                 25.9%;
46.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBO J. 12:1161-1167(1993).
                                                                                                             Best Local Similarity 46.2
Matches 18; Conservative
                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                         (Human).
                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                    MIM; 600928;
                                                                                                                                                                                                                                     Z145_HUMAN
                                                                                                                                                                          16
                                                                                                 Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transcription regulation: DNN-binding; Zinc-finger; Metal-binding; Nuclear protein; Repeat; Chromosomal translocation; Proto-oncogene; Phosphorylation; Alternative splicing; 3D-structure.

34 96 BTB.

DOMAIN 34 96 BTB.

ZN_FING 404 426 CZH2-TYPE.

ZN_FING 432 454 CZH2-TYPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PHOSPHORYLATION (BY PDPK) (POTENTIAL).
PHOSPHORYLATION (BY PDPK) (POTENTIAL).
PHOSPHORYLATION (BY PDPK) (POTENTIAL).
PHOSPHORYLATION (BY PDPK) (POTENTIAL).
MISSING (IN ISOSOBM PLZEA).
7CD7319E2A32109D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PHOSPHORYLATION (BY PDPK) (POTENTIAL).
PHOSPHORYLATION (BY PDPK) (POTENTIAL).
PHOSPHORYLATION (BY PDPK) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BREAKPOINT FOR TRANSLOCATION TO FORM PLZF-RAR-ALPHA ONCOGENE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Histone RNA hairpin-binding protein (Histone stem-loop binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 673;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            270 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          292 ARELHYGREESAEQVPPPAEAGQAPTGRP 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 55.5;
Pred. No. 45;
-!- SIMILARITY: CONTAINS 1 BTB/POZ DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 AKALRWIRQKSVEEGEPPGQ-GEGPRSRP 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE: PS50097; BTB; 1.
PROSITE: PS00028; ZINC_FINGER_C2H2_1; 8.
PROSITE; PS50157; ZINC_FINGER_C2H2_2; 9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C2H2-TYPE.
C2H2-TYPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C2H2-TYPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C2H2-TYPE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR000210; BTB_PO2.
InterPro; IPR000822; Znf_C2H2.
Pfam; PF000096; Zf-C2H2; 9.
Pfam; PF000051; BTB: 1.
PRINTS; PR00048; ZINCHINGER.
ProDom; PD000003; Znf_C2H2: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  74332 MW;
                                                                                                                                                                                                                                    EMBL; Z19002; CAA79489.1; -. EMBL; S60093; AAC60590.2; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SMART; SM00225; BTB; 1.
SMART; SM00355; ZnF_C2H2; 9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25.9%;
                                                                                                                                                                                                                                                                                                                                  Genew; HGNC:12930; ZNF145.
MIM; 176797; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 25.9
Best Local Similarity 37.9
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          652
426
454
483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 76
1197
1256
256
282
628
377
                                                                                                                                                                                                                                                                                   PDB; 1CS3; 09-AUG-00.
TRANSFAC; T02336; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 76
184
197
197
256
282
282
628
628
673 AA;
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32 KRRADGRRW-RPEDAEEAEHRGAERRPESFTIPEGPKPRSRCSDWASAVE 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       secretory granules.
                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        421
                                                                                                                                                                                                                                                           SYN1 OR SYN-1.
                                                                                                                    SYN1_MOUSE
                                                                                                                                                                                                                                     Synapsin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                           SYN1_MOUSE
                                                                      RESULT 13
  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the SWISS institute of Bioinformatics and the EMBL outstation. the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                      Expressed genes, Alu repeats and polymorphisms in cosmids sequenced
                                                                                  SEQUENCE FROM N.A.

MEDLINE-93251024; PubMed=1338771;

MCCombie W.R., Martin-Gallardo A., Gocayne J.D., FitzGerald M.,

Dubnick M., Kelley J.M., Castilla L., Liu L.I., Wallace S., Trapp
Tagle D., Whaley W.L., Cheng S., Gusella J., Frischauf A.-M.,

Poustka A., Lehrach H., Collins F.S., Kerlavage A.R., Fields C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGULATED DURING THE CELL CYCLE; PROTEIN
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                            "The protein that binds the 3' end of histone mRNA: a novel RNA-binding protein required for histone pre-mRNA processing."; Genes Dev. 10:3028-3040(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBUNIT: MONOMER. SUBCELLULAR LOCATION: NUCLEAR AND CYTOPLASMIC (POLYRIBOSOME-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LEVELS INCREASE 10 TO 20 FOLD IN THE LATE G1 AND DECREASE AT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RNA-binding; mRNA processing; Nuclear protein; Phosphorylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12;
                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
TISSUE-Cervical adenocarcinoma;
MEDLINE-97115884; PubMed-8957003;
Wang Z.-F., Whitfield M.L., Ingledue T.C. III, Dominski Z.,
Marzluff W.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PHOSPHORYLATION (BY CDC2) (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 270;
                     ia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4E84E502393D1BF7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 55; DB 1;
Pred. No. 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: BELONGS TO THE SLBP FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE SPECIFICITY: WIDELY EXPRESSED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RNA-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; M63544; -; NOT_ANNOTATED_CDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31285 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25.7%;
34.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; U75679; AAB97091.1; -. EMBL; Z71188; CAA94918.1; -.
                                                                                                                                                                                                                                                                              from chromosome 4p16.3.";
Nat. Genet. 1:348-353(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DEVELOPMENTAL STAGE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity 34.0
17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genew; HGNC:10904; SLBP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BORDER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           270 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-Lymphocytes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                             NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EXPRESSION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ASSOCIATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       S/G2
                                                                                                                                                                                                                                Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MIM; 602422;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local
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2 KRRAKALRWTRQKSVEEGEPPG ------QGEGPRSRPAAESTGLE 40

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                                                                                                                                                                                                                                                                                                                                                                                       Chin L.S., Li L., Greengard P.;

Chin L.S., Li L., Greengard P.;

Recific core promoter and upstream regulatory elements.";

Specific core promoter and upstream regulatory elements.";

J. Biol. Chem. 269:18507-18513(1994).

-! FUNCTION: NEBRONAL PHOSPHOROTEIN THAT COATS SYMAPIC VESICLES,
BINDS TO THE CYTOSRELETON, AND IS BELIEVED TO FUNCTION IN THE
REGULATION OF NEUROTRANSMITTER RELEASE (BY SIMILARITY).

-! SUBCELLUIAR LOCATION: SYMAPSE.

-! ALTERNATIVE PRODUCTS: 2 ISOFORMS; SYNAPSIN IA AND SYNAPSIN IB
(SHOWN HRRE); ARE PRODUCED BY ALTERNATIVE SPLICING.

-! PTM: SUBSTRATE OF AT LEAST FOUR DIFFERENT PROTEIN KINASES. IT IS
FROM THAT THAT PHOSPHORILATION PLAYS A ROLE IN THE REGULATION OF
SYNAPSIN IN THE NEWE TERMINAL (BY SIMILARITY).
                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-CSTBL,6; TISSUE-Pancreatic islets;
Matsumcto K., Ebihara K., Yamamoto H., Tabuchi H., Fukunaga K.,
Xasunami M., Ohkubo H., Shichiri M., Miyamoto E.;
"Cloning from insulinoma cells of synapsin I associated with insulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AND CAMK1) (BY
                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (ACTIN-BINDING AND SYNAPTIC-VESICLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PHOSPHORYLATION (BY CAMK2) (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PHOSPHORYLATION (BY CAMK2) (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PS00416; SYNAPSIN_2; 1.
Phosphorylation; Neurone; Repeat; Actin-binding;
                                                                                                                                                                                                                                                                                                                        Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PHOSPHORYLATION (BY PKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (PRO-RICH LINKER).
              088935; 062279;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
 670 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BINDING)
PRT;
                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=94308086; PubMed=8034599;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PR01368; SYNAPSIN.
PROSITE; PS00415; SYNAPSIN_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MGD; MGI:98460; Syn1.
InterPro; IPR001359; Synapsin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AF085809; AAD09833.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF02078; Synapsin; 1.
Pfam; PF02750; Synapsin_C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; L32025; AAA79963.1; -.
HSSP; P17599; 1AUX.
                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 1-125 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSTIE: K-C. Synapse; Phosphol, -Alternative splicing.
Alternative splicing.
28 112 28 120
STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             605
                                                                                                                          Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             605
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                                                                            ö
                                                                                                                                                                                                                                                                          Rattus norvegicus (Rat).
Sukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION: SYNAPSE.
ALTERNATIVE PRODUCTS: 2 ISOFORMS; SYNAPSIN IA (SHOWN HERE) AND SYNAPSIN IS, ARE PRODUCTS: 2 ISOFORMS; SYNAPSIN IS (SHOWN HERE) AND PUM: SUBSTRATE OF AT LEAST FOUR DIFFERENT PROTEIN KINASES. IT IS PROBABLE THAT PHOSPHORYLATION PLAYS A ROLE IN THE REGULATION OF SYNAPSIN IN THE NERVE TERMINAL (BY SIMILARITY).
SIMILARITY: BELONGS TO THE SYNAPSIN FAMILY.
SEQUENCING ERRORS.
                                                                                                                                                                                                                                                                                                                                                                                                             "Synapsins: mosaics of shared and individual domains in a family of synaptic vesicle phosphoproteins."; Science 245:1474-1480(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION: NEURONAL PHOSPHOPROTEIN THAT COATS SYNAPTIC VESICLES, BINDS TO THE CYTOSKELETON, AND IS BELIEVED TO FUNCTION IN THE REGULATION OF NEUROTRANSMITTER RELEASE.
                                                                                                                                                                                                                                                                                                                                                                           Suedhof T.C., Czernik A.J., Kao H.-T., Takei K., Johnston P.A.,
Horiuchi A., Kanazir S.D., Wagner M.A., Perin M.S., de Camilli P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 McCaffery C.A., Degennaro L.J.;
"Determination and analysis of the primary structure of the nerve "terminal specific phosphoprotein, synapsin I.";
EMBO J. 5:3167-3173(1986).
                                                                            ;
0
                                              Score 55; DB 1; Length 670;
Pred. No. 51;
                                                                         11; Indels
SIMILARITY).
P -> L (IN REF. 2).
DE64BF0090A2B58E CRC64;
                                                                                                                                                                                                P09951; 09WUX7;
01-WAR-1989 (Rel. 10, Created)
30-WAY-2000 (Rel. 39, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                       704 AA.
                                                                          4; Mismatches
                                                                                                                         516 QQSASQATPVTQGQGRQSRPVAGGPG 541
                                                                                                  13 QKSVEEGEPPGQGEGPRSRPAAESTG 38
                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                  TISSUE=Brain;
MEDLINE=89388265; PubMed=2506642;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Brain;
MEDLINE=87133474; PubMed=3028773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; M27924; AAA42148.1; -.
EMBL; X04655; CAA28353.1; ALT_SEQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR; A25704; A25704.
PIR; A30411; A30411.
PIR; B30411; B30411.
PISSP, P17599; 1AUX.
InterPro; IPR001359; Synapsin.
            44 P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; M27812; AAA42145.1; -.
                                                 25.78;
                                                            42.38;
                                                            Best Local Similarity 42.3
Matches 11; Conservative
                                                                                                                                                                                       STANDARD;
                       670 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                    Greengard P.;
                                                                                                                                                                                                                                                    Synapsin I.
            CONFLICT
                                                                                                                                                                                    SYN1 RAT
                                                 Query Match
                                                                                                                                                             RESULT
 FT
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P26221; Q08167;
01-MAY-1992 (Rel. 22, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Endoglucanase E-4 precursor (EC 3.2.1.4) (Endo-1,4-beta-glucanase E-4)
(Cellulase E-4) (Cellulase E4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                    PHOSPHORILATION (BY PKA AND CAMKI).
PHOSPHORILATION (BY CAMKZ).
PHOSPHORILATION (BY CAMKZ).
PHOSPHORILATION (BY CAMKZ).
MASSGLINA -> KASPAQAQP (IN SYNAPSIN IB).
MISSING (IN SYNAPSIN IB).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Actinomycetales; Streptosporangineae; Nocardiopsaceae; Thermobifida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Thermomonospora fusca.
Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
                                                                                                                                                                                                  (ACTIN-BINDING AND SYNAPTIC-VESICLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-94028932; PubMed-8215374;
Jung E.D., Lao G., Irwin D., Barr B.K., Benjamin A., Wilson D.B.;
EnRA sequences and expression in Streptomyces lividans of an
exoglucanase gene and an endoglucanase gene from Thermomorospora
                                                                                                 Synapse; Phosphorylation; Nerve; Neurone; Repeat; Actin-binding; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 704;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-91258320; PubMed-1904434;
Lao G., Ghangas G.S., Jung B.D., Wilson D.B.;
"DNA sequences of three beta-1,4-endoglucanase genes from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wilson D.B.;
Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                65799FEF7CFE18B5 CRC64;
                                                                                                                                                                                                                                         (PRO-RICH LINKER)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 47-651.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-97475222; PubMed-9334746;
Sakon J., Irwin D., Wilson D.B., Karplus P.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Appl. Environ. Microbiol. 59:3032-3043(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    880 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 55;
Pred. No. 5
                                                                                                                                                                                (LINKER)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        514 QOSASQATPMTQGQGRQSRPVAGGPG 539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wilson D.B.; "Cellulases of Thermomonospora fusca.";
                                                                                                                                                                                                                         BINDING).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13 QKSVEEGEPPGQGEGPRSRPAAESTG 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Meth. Enzymol. 160:314-323(1988).
Pfam; PF02078; Synapsin; 1.
Pfam; PF02750; Synapsin_C; 1.
PRINTS; PR01368; SYNAPSIN.
PROSITE; PS00415; SYNAPSIN_1; 1
PROSITE; PS00416; SYNAPSIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteriol. 173:3397-3407(1991)
                                                                                                                                                                                                                                                                                                                                                                                                73988 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                           25.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  42.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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704
9
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                                                                                                                                                                                                                                                                                                                                                                                                   704 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
es 11; Conserv
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656
9
566
603
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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MOD_RES
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DOMAIN
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GUN4_THEFU
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Matches
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstationthe European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                    HYDROLASES).
-!- SIMILARITY: CONTAINS 1 FUNGAL-TYPE CELLULOSE-BINDING DOMAIN (CBD).
"Structure and mechanism of endo/exocellulase E4 from Thermomonospora
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00561; CBD_BACTERIAL; 1.
PROSITE; PS00592; GLYCOSYL_HYDROL_F9_1; 1.
PROSITE; PS00698; GLYCOSYL_HYDROL_F9_2; 1.
Cellulose degradation; Hydrolase; Glycosidase; Signal; 3D-structure.
                             Nat. Struct. Biol. 4:810-818(1997).
-!- CAPALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-glucosidic linkages in cellulose.
-!- PATHWAY: Cellulose degradation.
-!- PATHWAY: Cellulose To CELLULASE FAMILY E (FAMILY 9 OF GLYCOSYL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 55; DB 1; Length 880; 
Pred. No. 67; 
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CELLULOSE-BINDING.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
W; 5EA9A6ABF45A4U9A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ENDOGLUCANASE
                                                                                                                                                                                                                                                                                                EMBL, L20093; AAB42155.1; ---
PIR, BA2360; BA2360.
PIR, B42360; B42360.
PDB; 1J54; 17-SEP-97.
PDB; 1T74; 04-SEP-97.
PDB; 4T74; 04-SEP-97.
PDB; 4T74; 04-SEP-97.
INTERPRO; IPR001919; Bac_celose-bind.
INTERPRO; IPR001919; Bac_celose-bind.
INTERPRO; IPR001916; FNL II.
INTERPRO; IPR001956; FNL II.
INTERPRO; IPR001961; FNL III.
INTERPRO; IPR001701; GH.9.
INTERPRO; IPR001701; GH.9.
INTERPRO; IPR001701; GH.9.
Pfam; PF00541; GR.2.
Pfam; PF00559; GRML2; 1.
Pfam; PF00559; GLRL2; 1.
Pfam; PF00559; GLRL2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95202 MW;
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83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PR00014; FNTYPEIII. SMART; SM00060; FN3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 25.7
Best Local Similarity 83.3
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17 EEGEPPGQGEGP 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   880 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACT_SITE
ACT_SITE
SEQUENCE
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                   fusca."
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Search completed: June 6, 2003, 11:01:30 Job time: 3.50788 secs

QQ

Sequence:

Run on:

Searched:

Database

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091ch6 macroprodid

081j6 ralstonia s

084j6 ralstonia s

08457 ralstonia s

090we6 leucopario

09a6d3 caulobacter

09rxj7 zea mays (m

09rzj5 deinococcus

09rzj6 deinococcus

09sun oryza sativ

09awx0 oryza sativ

08s207 oryza sativ

09s207 oryza sativ

09s207 oryza sativ
                                  Q8sq03 canis famil
Q8yb61 brucella me
Q95qa7 caenorhabdi
Q95qa6 caenorhabdi
Q95qa8 caenorhabdi
Q95kc5 streptomyce
Q9sni9 oryza sativ
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                  Q9as24 oryza sativ
Q69020 human herpe
         Q941u8 oryza sativ
                                                                                                09h7j7 homo sapien
012845 homo sapien
08x0s8 neurospora
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                            Open reading frame 6.
Mus musculus (Mouse).
Eukaryota; Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Bukarmila; Eutheria: Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 65; DB 11; Length 399;
Pred. No. 3.2;
3; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Strausberg R.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC019440; AAH19440.1; -.
SEQUENCE 399 AA; 42995 MW; B5CA88342B56932B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              081782 PRELIMINARY; PRT; 493 AA.
081782;
01.NOV-1998 (TrEMBLrel. 08, Created)
01.NOV-1998 (TrEMBLrel. 08, Last sequence update)
01.CCT-2000 (TrEMBLrel. 15, Last annotation update)
Hypotherical 56.2 kDa protein.
PREMARY.160 OR AT4631650.
Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 RRAKALRWTRQKSVEEGEPPGQGEGPRSRPAAES 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALIGNMENTS
090Y66
0941U8
09AS24
069020
08S003
                                                            0950A6
0950A8
09RKC5
                                                                                                                          091CH6
08Y1J6
08XQ57
090WE6
09A6D3
                                                                                                                                                                                                                                                                                                                                                   Created)
                                                                                                                                                                       Q8VXG7
Q9RZI5
                                           Q8YB61
Q95QA7
                                                                                                                                                                                                           Q8S207
Q9CQS4
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                                                                                        6INS60
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                                                                                                         Q12845
Q8X0S8
                                                                                                                                                                                          Q9AUN1
                                                                                                  Q9H7J7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 30.4%;
Best Local Similarity 47.1%;
Matches 16; Conservative
110
110
112
116
116
116
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20,
20,
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01-MAR-2002 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=LIVER;
58
57.53
57.53
57.53
57.55
57.55
                                                                                                08VCQ7;
                                                                                                                                                                                                                                                                                                                                Q8VCQ7
                                                                                                                                                                                                                                                                                                              RESULT 1
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ID 08
AC 08
DT 01
DT 01
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GN F2
Q8VCQ7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2917e3 drosophila
2917e4 drosophila
29560 drosophila
242174 arabidopsis
288835 oryza sativ
29917 arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q855d8 oryza sativ
Q9nks7 leishmania
Q961a3 drosophila
Q9vrv3 drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q8us87 human immun
Q910d4 streptomyce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q8vcq7 mus musculu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     081782 arabidopsis
                                                                       (without alignments)
1589.904 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Description
                                                            June 6, 2003, 10:58:04 ; Search time 5.31349 Seconds
                                                                                                                  1 GKRRAKALRWIRQKSVEEGE......PGQGEGPRSRPAAESIGLEA
       GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                              671580 seqs, 206047115 residues
                                                                                                                                                                                                                           Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                            OM protein - protein search, using sw model
                                                                                                 US-09-826-581-6_COPY_51_91
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Q81783

Q91783

Q91784

Q91784

Q42174

Q85835

Q9H522

Q8S5D8
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09VRV3
08US87
09L0D4
09BGW6
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                         sp_archea:*
sp_bacteria:*
sp_tungi:*
sp_human:*
sp_human:*
sp_mammal:*
sp_mhc:*
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sp_unclassified:*
                                                                                                                                                                                                                                                                                                                                                                                                                 sp_bacteriap:*
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sp_phage:*
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Maximum DB seq length: 200000000
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229.0
228.7
228.7
228.7
228.7
228.0
228.0
228.0
27.8
27.8
27.6
27.6
27.7
27.1
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611.55
611.55
611.55
60
60
60
60
60
60
59.55
59.55
59.55
58.58
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                                                                                                          Perfect score:
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Q910d4 streptomyce Q98gw6 rhizobium 1

Result Š.

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Hig protein.
HIG OR CG2040.
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Q917E4
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Addams M.D., Celniker S.E., Holt R.A., Evans C.A., Galle R.E.,
RA Addams M.D., Celniker S.E., Richards S.A. Ashburner M., Henderson S.N.,
S. Sutton G.G., Wortnan J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Mar K. H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendelle J., Bayraktaroglu L., Beasley E.M.,
RA Beson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P.,
RA Berson K.C., Busam D.A., Butler H., Cadleu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
Acherry J.M., Cawley S., Dahlke C., Davenport L.B., Dunkov B.C., Dunn P.,
RA Cherry J.M., Svangelista C.C., Perraz C., Ferriera S., Fleischmann W.,
RA Fosler C., Gabriellan A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibegwam C.,
RA Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibegwam C.,
RA Harris N.L., Kodira C.D., Kraft C., Kraniscon J.A., Ketchum K.A.,
RA Harris N.L., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster (Fruit fly).
Eukaryota: Metazoa; Arthropoda; Tracheata: Hexapoda; Insecta;
Errygota: Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophilidae; Drosophila.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14;
                                                                                                                                                                             Rieger M., Mueller-Auer S., Zipp M., Schaefer M., Hoheisel J., Mewes H.W., Mayer K.F.X., Schueller C., Bevan M.;
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                      Rieger M., Mueller-Auer S., Zipp M., Schaefer M., Mewes H.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 10; Length 493;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          238 KRARVQRWSQESRSKHDVREKIAEEGEP----SRRNRTSNKSTG 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 RRAKALRWT-----RQKSVEEGEPPGQGEGPRSRPAAESTG 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8; Indels
                                                                                                                                                                                                                                                                                                                                             Lencke K., Mayer K.F.X.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           EU Arabidopsis sequencing project;
Submitted (MAF-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; ALJ01044; CAA19788.1; -.
EMBL; ALJ61579; CAB79883.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein.
SEQUENCE 493 AA; 56230 MW; 0F13F7890EFEA920 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29.0%; Score 62; DB 1
35.6%; Pred. No. 9.6;
iive 7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  866 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 29.0
Best Local Similarity 35.6
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hig protein (GH23986p).
HIG OR CG2040.
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SEQUENCE FROM N.A.
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Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
Monts A.M., Moy M., Murphy B., Murphy L., Murphy D.M., Nelson D.L.,
Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
Relazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Recee M.G.,
Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
Shler B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
Spier E., Spradling A.C., Istapleton M., Skupski M.P., Smith T.,
Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Mang X.,
Williams S.M., Woodage T., Worley K.C., Mu D., Yang S., Yao Q.A.,
Williams S.M., Woodage T., Worley K.C., Mu D., Yang S., Yao Q.A.,
Xe J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zhao Q., Xhore S.M., Myers E.M., Rubin G.M., Venter J.C.;
The genome sequence of Drosophila melanogaster.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDILNE-2018006; PubMed=10731132;
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.H.C., Blacel R.G., Champe M., Pfeisffer B.D.,
Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R., Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M., Celniker S., Submitted (DEC.2011) to the EMBL/GenBank/DDBJ databases.
EMBL; AR003844; AAL39333.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5;
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 5; Length 866;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            866 AA; 96747 MW; FOFFE6BC206088ED CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        328 QRDRSPRWRRRRSTEFKGDLGQLPPESGIGPEPEDLAD 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 RRAKALRWTRQKSVE-EGE----PPGQGEGPRSRPAAE 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        933 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28.7%; Score 61.5; 36.8%; Pred. No. 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR002396; Selectin.
InterPro; IPR000436; Sushi_SCR_CCP.
                                                                                                                                                                                                                                                                                                                                                                                                       Science 287:2185-2195(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSSP; P10998; IVVD.
Flybase; FBgn0010114; hig.
InterPro; IPR003599; Ig.
InterPro; IPR003006; Ig_MHC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00047; ig; 1.
Pfam; PF00084; sushi; 4.
PRINTS; PR00343; SELECTIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART; SM00032; CCP;
SMART; SM00409; IG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sest Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-BERKELEY;
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SEQUENCE
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RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Borkova D., Boltchan M.R., Bouck J., Brokstein P., Bortkera P., Chandra I., RA Burtis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I., RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., Chandra I., RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., RA Durbin K.J., Evangelista C.C., Ferraz C., Ferraz C., Ferraz C., Ferras C., Ferra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bukaryota; Metazoā; Arthropoda; Tracheata; Hexapoda; Insecta;
Bersyota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_faxID=7227;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 61.5; DR 5; Length 933;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9C0B696854C6C9FA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update) HIG protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              328 QRDRSPRWRRRSTEFKGDLGQLPPESGIGPEPELAD 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 RRAKALRWTRQKSVE-EGE----PPGQGEGPKSRPAAE 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 22;
8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             958 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-2000 (TrEMBLrel. 13, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster (Fruit fly).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR003006; Ig_MHC.
InterPro; IPR002396; Selectin.
InterPro; IPR000436; Sushi_SCR_CCP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDI.INE-20196006; PubMed=10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       104178 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AE003834; AAG22296.1; -. HSSP; P10998; 1VVD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      36.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FlyBase; FBgn0010114; hig.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PR00343; SELECTIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 36.88
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR003599; Iq.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00047; ig; 1.
Pfam; PF00084; sushi; 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART; SM00409; IG; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SMART; SM00032; CCP;
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Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,
Baradon R.C., Rogers Y.-H.C., Blazel R.G., Change M., Pfelifer B.D.,
Nan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
Abrill J.F., Agbayani A., An H.-J., Andrews-Fannkoch C., Baldwin D.,
Ballew R.M., Basus M., Baxendale J., Bardaraoglu L., Beaaley E.M.,
Bencson K.Y., Bencs P.V., Berman B.P., Bhandari D., Bolshakov S.,
Borkova D., Botchan M.R., Butler H., Cadieu E., Center A., Chandra I.,
R. Berson K.Y., Deuge S., Dahlke C., Davenport L.B., Davless P.,
R. Dutpin R.J., Evangelista C.C., Ferrac C., Ferriers P.,
Dutpin R.J., Evangelista C.C., Ferrac C., Ferriers S., Pleischman W.,
R.A. Bouth R.J., Evangelista C.C., Ferrac C., Ferriers S., Fleischman R.
Botsen K.J., Doub L.B., Downes M., Dugan Rocha S., Dunkov B.C., Dunn P.,
R.A. Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
Allin M., Kalush F., Karpen G.H., Re Z., Kenhason J.A., Retchin K.A.,
Jasko P., Lei Y., Levitsky A.A., Li J., Li S., Moshrefi A.,
Mount S.M., Moy M., Murphy B., Morphy D., Moshrefi A.,
Mount S.M., Moy M., Murphy B., Morphy D., Woshrefi A.,
Relin Y., Mattei B., Morinosh T.C., McLeod M.P., Moshrefi A.,
Relington K.J., Spalent R., Saiter R., Saiter R., Shen H.,
Spier E., Spradling A.C., Stapleton M., Stupski M.P., Smith H.O.,
R. Shiert K., Renington K., Sameders R.D. C., Scheeler F., Shen H.,
Spier E., Spradling A.C., Stapleton M., Stupski M.P., Smith H.O.,
R. Sheng Z.H., Woster P., Weller E., Wang Z.H., Waller S., Waller S., Zaveri J.S., Zhan G., Zhao Q., 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;;
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Nagnollophyta; eudicotyledons; core eudicots; Rosldae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID+3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 5; Length 958;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              958 AA; 107027 MW; 7B2A08477672E674 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  328 QRDRSPRWRRRRSTEFKGDLGQLPPESGIGPEPEPLAD 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 RRAKALRWTROKSVE-EGE----PPGQGEGPRSRPAAE 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         136 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28.7%; Score 61.5; I 36.8%; Pred. No. 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR000436; Sushi_SCR_CCP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR002396; Selectin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AE003834; AAF58960.1;
HSSP; P10998; 1VVD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR003006; Ig_MHC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FlyBase; FBgn0010114; hig.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00047; iq; 1.
Pfam; PF00084; sushi; 5.
PRINTS; PR00343; SELECTIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR003599; Ig.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMART; SM00032; CCP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Globulin (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART; SM00409;
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01-007-2000 (TrEMBLrel. 15, Last sequence update)
01-007-2000 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota; Viridiplantee; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       McCombie W.R., Cordum H., Minx P., de la Bastide M., Spiegel L., Nascimento L., Zutavern T., Balija V., Bell M., Baker J., Santos L., Miller B., Katzenberger F., Muller S., Preston R., Kirchoff K., King L., Yang C., O'Sahughnessy A., Palmer L., Dedhia N., Wilson R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oryza sativa (Rice).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Enrhartoideae; Oryzae: Oryza.
                                       Raynal M., Grellet Laudia M., Meyer Y., Cooke R., Delseny M.; Submitted (NOV-1993) to the EMBL/GenBank/DDBJ databases.
EMBL; 227252; CAA81765.1; -.
InterPro; IFF001113; Seedstore_7s.
Pfam; PF00546; Seedstore_7s; 1.
                                                                                                                                                                                                                             5,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Genomic sequence for Oryza sativa, Nipponbare strain, clone OsJNBBOOG3003, from chromosome 10, complete sequence."; Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases. EMBL, AC021892, AAM00958.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28.0%; Score 60; DB 10; Length 314; 43.9%; Pred. No. 11; tive 6; Mismatches 15; Indels
                                                                                                                                                                                     Score 60; DB 10; Length 136;
Pred. No. 4.5;
                                                                                                                                                                                                                         6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15542 MW; EA2AFD6490BE13C1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical protein.
SEQUENCE 314 AA; 32758 MW; 0156F123C759B2C0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 KRRAKALRWTRQKSVEEGEPPGQGEG~PRSRPAAEST-GLE 40
                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                 TISSUE=DRY SEEDS OF A.THALIANA ECOTYPE COLUMBIA;
                                                                                                                                                                                                                                                                                                                                                                                 314 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          486 AA.
                                                                                                                                                                                                                         2; Mismatches
                                                                                                                                                                                                                                                         16 VEEGEPPGQG -- EGPRSRPAAES 36
                                                                                                                                                                                                                                                                             29 IDEFEPPOGEOEGPRRRPGGGS 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical 32.8 kDa protein.
OSJNBA0053D03,22.
                                                                                                                                                                                       28.0%;
56.5%;
                                                                                                                                                                                     Query Match 28.0°
Best Local Similarity 56.5
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                     SEQUENCE 136 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
nes 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=NIPPONBARE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=4530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=3702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                               088835;
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                                                                                                                                                                                                                                                                                                                                                                             088835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9LUJ7
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Matches
                                                                                                                                                                                                                                                                                                                                           RESULT 7
08S835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 8
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RR RA RR B DR DR DR DR DR DR SO SO
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1;
                                                                                                                                                                                                                                      "Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequence features of the regions of 4,504,864 bp covered by sixty Pl and TAC clones.";
                                                                                                                                                                                                                                                                                                                                                                                                                                         Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Banh J., Bawser L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y., Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M., Nayyor M., Onoders C.S., Palla C.J., Pham P.K., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K., Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T., Matsumura K.,
Nakajima Y., Mizuno T., Morinaga M., Tanigami A., Fujiwara T., Ono T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Satou M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           [4]
SEQUENCE FROM N.A.
Kim C.J., Chen H., Cheuk R., Meyers M.C., Shinn P., Banh J.,
Kim C.J., Carninci P., Chang E., Dale J.M., Goldsmith A.D.,
Bowser L., Carninci P., Chang E., Kamiya A., Karlin Neumann G.,
Rawai J., Lam B., Lee J.M., Lin J., Miranda M., Narusaka M.,
Nayyen M., Onodera C.S., Palm C.J., Quach H.L., Sakurai T., Satou M
Seki M., Southwick A., Tang C.C., Toriumi M., Nu H.C., Yamada K.,
Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2;
                          Sato S., Nakamura Y., Kaneko T., Kato T., Asamizu E., Tabata Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Foker '1. Ecker'.

I Ecker'.

I "Arabidopsis ORF clones.";

L Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.

B EMBL; AR012233: BAB01239 1;

R EMBL; AY058085; AAL24193.1;

DR EMBL; AY058087; AAL24193.1;

DR HSSP; APLSP 2PHL.

DR HSSP; DPL883: 2PHL.

DR InterPro; IPR001064; Crystallin.

PR InterPro; IPR00113; SedStore_7s.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 486;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seedstore_,,,
Seedstore_,S.;
Seedstore_,S.;
25; CRYSTALLIN_BETAGAMMA; UNKNOWN_1.
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          793 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 60;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequenty o1-Jun-2002 (TrEMBLrel. 21, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16 VEEGEPPGQG -- EGPRSRPAAES 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29 IDEFEPPOQGEQEGPRRRPGGGS 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CDNA: FLJ22757 fis, clone KAIA0803
                                                                                                                                                                                     MEDLINE=20277480; PubMed=10819329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00546; Seedstore_7s; 1
Pfam; PF02808; Seedstore_7s_C;
PROSITE; PS00225; CRYSTALLIN_E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28.0%;
56.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Arabidopsis cDNA clones.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 56.5%
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                DNA Res. 7:131-135(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
TISSUE=ILEAL MUCOSA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        486 AA;
                                                                                            [2]
SEQUENCE FROM N.A.
STRAIN=COLUMBIA;
                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN-COLUMBIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
                                                                                                                                                                                                                         Nakamura Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ecker J.R.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9H5Z2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 9
RECENT OF READ OF READ
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Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
A change M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
A Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
A Nunco J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K.,
A Nunco J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K.,
A Nunco J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K.,
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.

EMBL: AYO51740; AAK931641; -
BR Flyase; FREND032690; CG10274.

InterPro; IPR000322; Znf_CAR.

InterPro; IPR000322; Znf_CAR.

PROSITE; PS00028; ZINC_FINGER_C2H2_1; UNKNOWN_7.

PROSITE; PS00142; ZINC_FINGER_C2H2_2; 9.

PROSITE; PS00142; ZINC_FINGER_C2H2_2; 9.

PROSITE; PS00142; ZINC_FINGER_C2H2_2; 9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Perryota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBL_TaxID=7227;
                                                                                                                                                                        DB 5; Length 1400;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 514;
                                                                                                                                                                                                                                                                                                Myler P.J.;
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AC005836; AAF35994.1; -.
SEQUENCE 1400 AA; 149577 MW; OCDCF4E925BEAEF4 CRC64;
                                                                                                                                                                                                                                                              DNA-binding; Zinc-finger.
SEQUENCE 514 AA; 59029 MW; 42DC53A6A4EC5F49 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 KRRAKALRWIRQKSVEEGEPPGQGEGPRSRPAAESIGLE 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                                                        11;
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35.9%; Pred. No. 24;
Live 5; Mismatches 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                  514 AA
                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                        27.8%; Score 59.5; I
36.4%; Pred. No. 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAY 2000 (TrEMBLrel. 13, Created) 01-WAY-2000 (TrEMBLrel. 13, Last sequ 01-WAR-2002 (TrEMBLrel. 20, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila melanogaster (Fruit fly).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 2/.07
Best Local Similarity 35.99
Matches 14; Conservative
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                                                                                                                                                                                        Local Similarity
nes 16; Conserv
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            SEQUENCE FROM N.A.
                                 STRAIN-FRIEDLIN;
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                                                                                                                                                                        Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                               Q961A3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9VRV3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9VRV3;
                                                                                                                                                                                                  Best Loc
Matches
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Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y., Ota T., Suzuki Y., Obayashi M., Nishi T., Shibahara T., Tanaka T., Nakamura Y., Isogai T., Sugano S.;
"NEDO human cDNA sequencing project.";
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
BRNE, AR026410; BAB19475.1;
InterPro; IPR001194; DENN.
InterPro; IPR001194; DENN.
                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

STRAIN-NIPPONBARE;

MCCOMDLE W.R., de la Bastide M., Spiegel L., Preston R., Ferraro K.,

Kuit K., Nascimento L., Zutavern T., Balija V., Bell M., Baker J.,

Santos L., Miller B., Katzenberger F., Muller S., King L., Yang C.,

Dike S., O'Shaughnessy A., Palmer L., Dedhia N.;

Genomic sequence for Oryza sativa, Nipponbare strain, clone
OSJNBD047B19, from chromosome 10, complete sequence.";

Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Leishmania major.
Eukaryota; Buglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
NCBI_TaxID=5664;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oryza sativa (Rice).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27.8%; Score 59.5; DB 10; Length 330; 37.2%; Pred. No. 13;
                                                                                                                                                                                                                                                                                                                             28.0%; Score 60; DB 4; Length 793; 50.0%; Pred. No. 28; ive 4; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 KRRAKALRWIRQKSVEEGEPPGQGEGPRS---RPAAESIGLEA 41
                                                                                                                                                                                                                                                         Pfam; PF03456; uDENN; 1.
SEQUENCE 793 AA; 86230 WW; 3F37ACA836F24AF4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11 protein.
330 Aa; 37674 MW; 01AD287515E7DD43 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-2002 (TrEMBLrel. 21, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update) Hypothetical 37.7 kDa protein.
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                  504 GKNR--PLRPSRRQLEEGTSEPPGAGTPPLS 533
                                                                                                                                                                                                                                                                                                                                                                                                                             1 GKRRAKALRWTRQKSVEEG--EPPGQGEGPRS 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           330 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
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01-0CT-2000 (TrEMBLrel. 15,
01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                  Query Match
Sest Local Similarity 50.00,
Best Local Similarity 50.00,
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Pfam; PF02141; DENN; 1.
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Streptomyces coelicolor
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                                                        SEQUENCE FROM N.A.
                                                                                                                                                                        Western Cameroon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=1902;
                                                                            STRAIN=99CMLB33;
                                                                                                                                                                                                                                                                                                                                                    207
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Saunders D.C.,
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                                                                                                                                                                                                                                                                                                               Polyprotein.
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SEQUENCE
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                                          REDINING—20196008; Pubbmed=10731132;
RADAMENELELY:
RADAGREE RES. HOLL R.A. Evans C.A., Gocayne J.D.,
RADAGREE N.D., Celniker S.E., Holt R.A. Evans C.A., Gocayne J.D.,
RADAGREE R.A., Lewis S.E., Holt R.A. Evans C.A., Gocayne J.D.,
RADAGREE R.A., Lewis S.E., Holt R.A. Ashburner M., Henderson S.N.,
RADAGREE R.G., Worther S.E., Hichards S., Ashburner M., Pfelifer B.D.,
RADAGREE R.G., Marter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RADAGREE R.A., Dayle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RADAGREE R.W., Basan A., Baxerdale A., Bayraktaroqlu L., Beasley E.M.,
RADAGREE R.W., Bouck J., Broakstaroqlu L., Beasley E.M.,
RADAGREE R.W., Bouck J., Broakstaroglu L., Beasley E.M.,
RADAGREE R., Correll J., Brokstein P., Brottier P.,
Burtis K.C., Busam D.A., Butler H., Cadleu E., Center A., Chandra I.,
RADAGREE R., Correll J., Brokstein P., Burchies P.,
Burtis K.C., Busam D.A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RADAGREE R., Correll J., H., Cadre R.S., Dubov B.C., Dunn P.,
Burtis K.C., Gabrielian A.E., Garg N.S., Celbart W.M., Glasser K.,
RADAGREE R., Gorrell J.H., Garg N.S., Celbart W.M., Glasser K.,
RADAGREE R., Kadlar C.D., Kraft C., Kravitz S., Kulp D., Lal Z.,
Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
Alalali M., Kalush F., Karpen G.H., Kaz', Kennison J.A., Ketchum R.A.
Hostin D., Houston K.A., Howland T.J., Wein M.H., Ibagwam C.,
Jalali M., Malush F., Karpen G.H., Kaz', Kennison J.M., Ketchum R.A.
Remenlogon D.R., Nelson K.A., Mixon K., Nusskern D.R., Morbherson D.R.,
Reinert K., Remington K.J., Saunders R.D., Scheeler F., Shen H.,
Rhue B.C., Spradling A.C., Saunders R.D., Scheeler F., Shen H.,
Rhug Z.*V Massarman D.A., Wainston M., Strong R., San R.,
Rhang Z.*V Massarman D.A., Weinston M., Strong S., Yao O.A.,
Rhang Z.*V Massarman D.A., Weinston M., Strong S., Yao O.A.,
Rhang Z.*V Massarman D.A., Weinston M., Shang S., Yao O.A.,
Rhang Z.*V Massarman D.A., Weinston M., Shang S., Yao O.A.,
Rhang Z.*V Massarman D.A., Weinston M., Shang S.,
Rheng X.H., Zhong S., Zhu N., Sanith H.,

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA-binding, Metal-binding, Zinc-finger.
SEQUENCE 863 AA; 98670 MW; 6A474642498351D6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              532 KRVLRAIETYRQRQVEMGETPGEQFDNPPAPPVEGISIE 570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 KRRAKALRWTRQKSVEEGEPPGQGEGPRSRPAAESTGLE 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMART; SM00355; ZnF_C2H2; 12.

PROSITE: PS00028; ZINC_FINGER_C2H2_1; 10.
PROSITE: PS50157; ZINC_FINGER_C2H2_2; 12.
PROSITE: PS0142; ZINC_PROTESASE; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human immunodeficiency virus type 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro, IPR000822; Znf_C2H2.
InterPro, IPR000130; Zn_MTpeptdse.
Pfam; PF00096; zf-C2H2: 12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FlyBase; FBgn0035690; CG10274.
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2 (TrEMBLrel. 20, I
2 (TrEMBLrel. 21, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Science 287:2185-2195(2000).
EMBL; AE003563; AAF50679.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gag polyprotein (Fragment). GAG.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
              SEQUENCE FROM N.A.
                                      STRAIN-BERKELEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2002
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01-JUN-2002
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Genotypic and Phenotypic Analysis of HIV Type 1 Primary Isolates from
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Kanshi H., Hopwood D.A.;
A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
Mol. Microbiol. 21:77-96(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Bentley S.D., Chatter K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,
Rabbinowitsch E., Rajandaream M.A., Rutherford K., Rutter S.,
Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
                                                                                                                                                                                                                                     Tebit D.M., Zekeng L., Kaptue L., Salminen M., Krausslich H.G., Herchenroder O.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 58.5; DB 15; Length 207; Pred. No. 11;
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Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Saunders D.C., Harris D.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Firmicutes; Actinobactería; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          207 AA; 23082 MW; D99E86CA6421EE21 CRC64;
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBL_TaxID=11676;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3; Mismatches 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6 KALRWTRQKSVEEG-EPPGQGEGPRSRPAAEST 37
                                                                                                                                                                                                                                                                                                                                                                        AIDS Res. Hum. Retroviruses 18:39-48(2002).
MEBL, AFS5294, AAL68724, 1; -.
InterPro; IPR000721; Gag_p24.
InterPro; IPR000071; Retrovir_p17.
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                                                                                                                                                                                                MEDLINE=21663212; PubMed=11804555;
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MEDLINE=97000351; PubMed=8843436;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Match 27.3%;
Local Similarity 42.4%;
es 14; Conservative 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30s ribosomal protein S3. RPSC OR SCO4708 OR SCD31.33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00540; Gag_p17; 1.
Pfam; PF00607; Gag_p24; 1.
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RA Hopwood D.A.;

RT "Complete genome sequence of the model actinomycete Streptomyces
RT coelicolor A3(2)."

RL Nature 417:141-147(2002).

BR EMB: A161803: CAB82076.1; -.

DR EMB: A161803: CAB82076.1; -.

DR InterPro: IPR004044; KH_TMPE_2.

DR InterPro: IPR004044; KH_TMPE_2.

DR InterPro: IPR001351; Ribosomal_S3.

DR Pfam: PP00195; Ribosomal_S3.C. 1.

DR Pfam: PP00195; Ribosomal_S3.C. 1.

DR PGATE: PP00189; Ribosomal_S3.C. 1.

DR PR03TE; PS0023; KH_TMPE_2: 1.

DR PR03TE; PS00248; RIBOSOMAL_S3; 1.

KW Ribosomal protein.

SQ SEQUENCE 277 AA; 30273 MW; 5831536E64018135 CRC64;

Query Match
Best Local Similarity 41.5%; Pred. No. 17;

Matches 17; Conservative 5; Mismatches 15; Indels 4; Gaps 2;

Qy I GKRRAKALRWTRQKSVEGGEPROGGEPRSRPAABSTGTEA 41

Db 241 GERRG---RKDQQSAPAABAP-KABAPAABSTGTEA 277

Search completed: June 6, 2003, 11:02:51

Job time: 7.31349 secs
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6, 2003, 10:59:34 ; Search time 2.44133 Seconds
   (without alignments)
   494.132 Million cell updates/sec
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1 GKRRAKALRWTRQKSVEEGE......POQGEGPRSRPAAESTGLEA
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                        262574 seqs, 29422922 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 10%
Maximum Match 100%
Listing first 45 summaries
                                                                                              protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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length: 2000000000
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Maximum DB :
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		Appli	Appli	Appli	7, App	287, App	Appli	Appli			, Appl			, Appl	Appl ,	Appli	Appli	Appli	Appli	Appli	Appli	Appli	Appli	Appli	Appli	Appli	Appli	Appli
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	Description	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Sednence	Sequence	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
SUMMARIES	ID	US-08-927-219-8		US-08-927-219-4	-927	-199-	906-	09-129	984		US-09-055-699-40	273-	US-09-565-538-40	\prec	US-09-562-737-62	PCT-US95-02251-3	US-08-199-780-3	US-08-316-650-3	US-08-479-722B-4	US-09-206-676C-1	US-09-206-676C-2	-623	-08-933-	US-09-181-030-7	1	-09-454-854-	-09-164-67	-67
	DB	4	4	4	4	4	m	4	4	7	m	4	4	4								~	r	4	4	4	4	7
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	Score	61.5	61.5	61.5	61.5	09	59	59	52	51	51	51	51	51	51	51	51	51	51	50.5	50.5	50.5	50.5	50.5	50.5	50.5	50.5	50.5
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GENERAL NNORMATION:
APPLICANT: Bell, Graeme I.
APPLICANT: Yamaqata, Kazuya
APPLICANT: Yamaqata, Kazuya
APPLICANT: Yamaqata, Kazuya
APPLICANT: Kaisaki, Pamela J.
APPLICANT: Furuta, Hiroto
APPLICANT: Horikawa, Yukio
APPLICANT: Horikawa, Yukio
APPLICANT: MUTATIONS IN THE DIABETES SUSCEPTIBILITY
TITLE OF INVENTION: GENES HEPATOCYTE NUCLEAR FACTOR (HNF) 1 ALPHA, HNF-1BETA
NUMBER OF SEQUENCES: 147
CORRESPONDENCE ADDRESS:
                 Sequence 9, Appli
Sequence 9, Appli
Sequence 9, Appli
Sequence 4, Appli
Sequence 21, Appli
Sequence 5, Appli
Sequence 5, Appli
Sequence 5, Appli
Sequence 6, Appli
Sequence 18, Appli
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Sequence 5, Appli
Sequence 5, Appli
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SOFTWARE: PETENTIN RELEASE #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/927,219
FILING DATE: CONCURTENTLY HERWITH
CLASSIFICATION: 435
PRIOR APPLICATION ADATA:
APPLICATION NUMBER: US 60/029,679
FILING DATE: 30-0CT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/028,056
FILING DATE: 02-0CT-1996
PRIOR APPLICATION NUMBER: US 60/025,719
FILING DATE: 10-SEP-1996
APPLICATION NUMBER: US 60/025,719
FILING DATE: 10-SEP-1996
ATTORNEY,AGENT INFORMATION:
US-08-933-774-9
US-09-181-030-9
US-09-534-24-9
US-09-454-854-9
US-09-164-671-9
US-09-104-671-9
US-09-014-0758-4
US-09-014-0758-6
US-09-151-412-5
US-09-151-412-5
US-09-151-412-5
US-09-151-412-5
US-09-151-412-5
US-09-170-888-187
US-09-110-463-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Wilson, Mark B. REGISTRATION NUMBER: 37,259
REFERENCE/DOCKET NUMBER: ARCD:272
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 8, Application US/08927219 ; Patent No. 6187533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: 512/418-3000
TELEFAX: 512/474-7577
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   COMPUTER READABLE FORM:
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   RESULT 1
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APPLICANT: Kaisaki, Pamela J.

APPLICANT: Furuta, Hiroto

APPLICANT: Furuta, Hiroto

APPLICANT: Horikawa, Yukio

APPLICANT: Horikawa, Yukio

APPLICANT: Morael, Stephen

TITLE OF INVENTION: MUTATIONS IN THE DIABETES SUSCEPTIBILITY

TITLE OF INVENTION: GENES HEPATOCYTE NUCLEAR FACTOR (HNF) 1 ALPHA, HNF-1BETA

TITLE OF INVENTION: AND HNF-4ALPHA

NUMBER OF SEQUENCES: 147

CORRESPONDENCE ADDRESS:
             Gaps
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          18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18; Indels
                                                                          271 RRKEEAFRHKLAMDTYSGPPPGPGPG-ALPAHSSPGL 307
                                                2 KRRAKALRWTRQKSVEEGEPPGQGEGPRSRPAAESTGL 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 KRRAKALRWIRQKSVEEGEPPGQGEGPRSRPAAESIGL 39
        4; Mismatches
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APPLICATION NUMBER: US/08/927,219
FILING DATE: CONCURRENT! Herewith
CLASSIFFCATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/029,679
FILING DATE: 30-0CT 1996
FILING DATE: 02-0CT 1996
FILING DATE: 02-0CT 1996
FILING DATE: 02-0CT 1996
FILING DATE: 02-0CT 1996
FILING DATE: 10-SEP-1996
FILING DATE: 10-SEP-1996
APPLICATION NUMBER: US 60/025,719
FILING DATE: 10-SEP-1996
APPLICATION NUMBER: US 60/025,719
FILING DATE: 10-SEP-1996
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                                                                                                                                                                        US-08-927-219-4; Sequence 4, Application US/08927219; Patent No. 6187533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Wilson, Mark B.
REGISTRATION NUMBER: 37,259
REFERENCE/DOCKET NUMBER: AR
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                            APPLICANT: Bell, Graeme I.
APPLICANT: Yamagata, Kazuya
APPLICANT: Oda, Naohisha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : 630 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           512/418-3000
        15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 28.7%
Best Local Similarity 39.5%
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P.O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               512/474-7577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; MOLECULE TYPE: protein US-08-927-219-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Texas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           77210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET:
      Matches
                                                                                                                                                         RESULT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Odd, Nachisha
APPLICANT: Kaiski, Pamela J.
APPLICANT: Kaiski, Pamela J.
APPLICANT: Horikawa, Yukio
APPLICANT: Horikawa, Yukio
APPLICANT: Menzel, Stephen
TITLE OF INVENTION: MUTATIONS IN THE DIABETES SUSCEPTIBILITY
TITLE OF INVENTION: GENES HEPRATOCYTE NUCLEAR FACTOR (HNF) I ALPHA, HNF-1BETA
                                                                                                                                                                             ..
                                                                                                                                                                             Gaps
                                                                                                                                   DB 4; Length 415;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 61.5; DB 4; Length 630; Pred. No. 3.6;
                                                                                                                                                                      18; Indels
                                                                                                                                                                                                                                        2 KRRAKALRWIRQKSVEEGEPPGQGEGPRSRPAAESTGL 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATE: US/08/927.219
FILING DATE: CONCURRENT! HEREWITH
                                                                                                                             ; Score 61.5; DB
; Pred. No. 2.2;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: JATE: CONCULENTLY HEREWITH CLASSIFICATION DATA:
APPLICATION NUMBER: US 60/029,679
FILING DATE: 30-0CT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/028,056
FILING DATE: 02-0CT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/025,719
FILING DATE: 10-SER-1996
ATTORNEY ASENT INFORMATION:
NAME: Wilson, MATK B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Arnold, White & Durkee STREET: P.O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: ARCD:272
                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/08927219
Patent No. 6187533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Wilson, Mark B.
REGISTRATION NUMBER: 37,259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
                                                                                                                                                                                                                                                                                                                                                                                                                            Bell, Graeme I.
Yamagata, Kazuya
Oda, Naohisha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28.7%;
39.5%;
                                                                                                                          28.7%;
39.5%;
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INFORMATION FOR SEQ ID NO: 2:
LENGTH: 415 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 630 amino acids
TYPE: amino acid
                                                                                                                        Query Match
Best Local Similarity 39.58
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             147
                                     ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-927-219-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; MOLECULE TYPE: protein US-08-927-219-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS: ADDRESSEE: Arnold, W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Texas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 77210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
APPLICANT:
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APPLICANT: Forton, Barbara
APPLICANT: Ro, Hung-Teh
TITLE OF INVENTION: DNA ENCODING THE HUMAN SYNAPSIN III GENE
TITLE OF SEQUENCES: 4
CORRESPONDENCES: 4
                                                                                                                                                                                                                                                                                                                                                                                                                             28.0%; Score 60; DB 4; Length 187; 34.9%; Pred. No. 1.4; Live 6; Mismatches 16; Indels
                                                                 APPLICANT: TSONGALIS, John
TITLE OF INVENTION: VIRULENCE-ASSOCIATED NUCLEIC ACID
TITLE OF INVENTION: VIRULENCE-ASSOCIATED NUCLEIC ACID
TITLE OF INVENTION: SEQUENCES AND USES THEREOF
FILE REFERENCE: 00786/361002
CURRENT APPLICATION NUMBER: US/09/199,637A
CURRENT APPLICATION NUMBER: 05/006,517
PRIOR PILING DATE: 1997-11-25
NUMBER OF SEQ ID NOS: 437
SOFTWARE: SEQ ID NOS: 437
SEQ ID NO 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GKRRAKALRWTRQ-----KSVEEGEPPGQGEGPRSRPAAEST 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
STREET: Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OMPUTER: IPM PC COMPATIBLE
SPERAING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Jackson Esq., David A. REGISTRAILON NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-202
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: protein
DESCRIPTION: /desc = "Synapsin Ia"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/906,865
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Patent No. 6040168
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 4:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 696 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : 201-487-5800
201-343-1684
                                                 Drenkard, Eliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15; Conservative
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         Tan, Man-Wah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New Jersey
: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hackensack
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
Matches 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HYPOTHETICAL:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-906-865-4
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CITY: Ha
                                                                                                                                                                                                                                                                                                                    LENGTH: 187
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                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δ
                                                                             APPLICANT: Yamagata, Kazuya
APPLICANT: Yamagata, Kazuya
APPLICANT: Oda, Naohisha
APPLICANT: Oda, Naohisha
APPLICANT: Kaisaki, Pamela J.
APPLICANT: Furuta, Hiroto
APPLICANT: Furuta, Hiroto
APPLICANT: Horikawa, Yukio
APPLICANT: Horikawa, Yukio
APPLICANT: Morzel, Stephen
TITLE OF INVENTION: GENES HEPATOCYTE NUCLEAR FACTOR (HNF) 1 ALPHA, HNF-1BETA
TITLE OF INVENTION: AND HNF-4ALPHA
NUMBER OF SEQUENCES: 147
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CALF: //Z10
COMPUTER: READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/927,219
FILING DATE: CONCURRENT! HErewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/029,679
FILING DATE: 30-OCT-1996
PRIOR APPLICATION NUMBER: US 60/028,056
FILING DATE: 10-OCT-1996
PRIOR APPLICATION NUMBER: US 60/028,056
FILING DATE: 10-SEP-1996
PRIOR APPLICATION NUMBER: US 60/028,056
FILING DATE: 10-SEP-1996
ATTORNEY AGENT INFORMATION:
ANALY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 KRRAKALRWTRQKSVEEGEPPGQGEGPRSRPAAESTGL 39
                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Arnold, White & Durkee STREET: P.O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ARCD: 272
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Patent No. 6355411
                     Sequence 127, Application US/08927219 Patent No. 6187533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: AUSUbel, Frederick
APPLICANT: Goodman, Howard M.
APPLICANT: Rahme, Laurence G.
APPLICANT: Mahajan-Miklos, Shalina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            37,259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: AH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPAN: 512/418-3000
TELEFAX: 512/474-7577
INFORMATION FOR SEQ 1D NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 631 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 39.5%
Matches 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
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                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Houston
                                                                                                                                                                                                                                                                                                                                                                                                                               Texas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: US
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US-09-199-637A-287
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US-08-927-219-127
US-08-927-219-127
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33,779
3R: 24735-9815 (formerly 6362-9815)
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Pred. No. 2.8e+02;
3; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 51; DB 2; Length 499;
Pred. No. 66;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC Compatible
COMPUTER: IBM FC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/820,170A
FILING DATE:
CLASSIFICATION INFORMATION:
TELECHONE: (202) 293-7060
TELECHONE: (202) 293-7060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    472 KRRSLRLYARWQSRWRKKVDPSAVQGQGPGHRQRRAGRHT 511
                                                                                                                                                                                                                                                                                                                                                                                                                                           2 KRRAKAL -- RWTR -- QKSVEEGEPPGQGEGPRSRPAAEST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: Sughrue, Mion, Zinn, Macpeak & Seas 2100 Pennsylvania Avenue, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10 WTRQKSVEEGEPPGQGEGPRSRPAAESTGLE 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21 WEHSKEVSEAEPGGGSSGDSGPP--EESGQE 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 40, Application US/08820170A Patent No. 5831058 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: TSUTOMU, FUJIWARA
APPLICANT: Takeshi, WATANABE
APPLICANT: Masato, HORIE
APPLICANT: TOYOMASA, KATAGIRI
TITLE OF INVENTION: HUMAN GENE
NUMBER OF SEQUENCES: 42
                  REFERENCE/DOCKET NUMBER: 2473
TELEDAMONICATION INFORMATION:
TELEPRONE: (619) 450-8400
TELEFAX: (619) 587-5360
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 2353 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: 6491103
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23.8%;
38.7%;
                                                                                                                                                                                                                                                                                                                                                             Query Match 24.3%;
Best Local Similarity 40.0%;
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Sughrue, Mion
STREET: 2100 Pennsylvani,
CITY: Washington
STATE: D.C.
COUNTRY: United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : 499 amino acids amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12; Conservative
                                                                                                                                                                                                                                                                                  internal
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                                                                                                                                                                                  single
                                                                                                                                                                                                                        MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
    REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                       linear
                                                                                                                                                               amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20037-3202
                                                                                                                                                                                                                                                                              ; FRAGMENT TYPE: i
; ORIGINAL SOURCE:
US-08-984-709A-50
                                                                                                                                                                                                                                                               ANTI-SENSE: NO
                                                                                                                                                                                STRANDEDNESS:
                                                                                                                                                                                                                                              HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 9
US-08-820-170A-40
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APPLICANT: Greengard, Paul
APPLICANT: Porton, Barbara
APPLICANT: Kao, Hung-Teh
TITLE OF INVENTION: DNA ENCODING THE HUMAN SYNAPSIN III GENE AND USES
TITLE OF INVENTION: THERROF
FILE REFERENCE: 600-1-202 C.T.P
CURRENT FILING DATE: 1998-08-05
EARLIER APPLICATION NUMBER: 08/906,865
EARLIER FLILNG DATE: 1997-08-06
NUMBER OF SEQ ID NOS: 8
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APPLICANT: Stauderman, Kenneth A.
APPLICANT: Harpold, Michael M.
TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
TITLE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
                                                        Score 59; DB 3; Length 696;
Pred. No. 8.6;
4; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 59; DB 4; Length 696;
Pred. No. 8.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Heller Ehrman White & McAuliffe STREET: 4250 Executive Square, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4; Mismatches
                                                                                                                                                                    13 QKSVEEGEPPGQGEGPRSRPAAESTG 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13 QKSVEEGEPPGQGEGPRSRPAAESTG 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/984,709A FILING DATE: 02-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 50, Application US/08984709A Patent No. 6320032 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                              Sequence 4, Application US/09129668B Patent No. 6429010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seidman, Stephanie L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 27.6%;
Best Local Similarity 42.3%;
Matches 11; Conservative
                                                          Query Match 27.6%;
Best Local Similarity 42.3%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Ver. 2.0
  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: La Jolla
STATE: California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-984-709A-50
; ORGANISM:
US-08-906-865-4
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LENGTH: 696
                                                                                                                                                                                                                                                           US-09-129-668-4
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GENERAL INVORMATION:
APPLICANT: FUJIWARA, TSUTOMU
APPLICANT: WATANABE, TAKESHI
APPLICANT: WATANABE, TAKESHI
APPLICANT: WATANABE, TAKESHI
APPLICANT: WATANABE, TAKESHI
APPLICANT: WATANABE, TSUADE
TITLE OF INVENTION: AN ISOLATED NUCLEIC ACID MOLECULE ENCODING HUMAN
TITLE OF INVENTION: SKELETAL MUSCLE-SPECIFIC UBLQUITIN-CONJUGATING ENZYME
FILE REFERENCE: Q-5359
CURRENT PILICATION NUMBER: 09/273,565
PRIOR APPLICATION NUMBER: 09/273,565
PRIOR FILING DATE: 1999-03-22
PRIOR FILING DATE: 1999-03-22
PRIOR FILING DATE: 1997-03-19
PRIOR PELICATION NUMBER: D6820,170
PRIOR APPLICATION NUMBER: J9 69163/1997
PRIOR APPLICATION NUMBER: J9 69163/1997
PRIOR PELING DATE: 1997-03-19
PRIOR PELING DATE: 1997-03-19
SPRIOR PELING DATE: 1997-03-05
NUMBER OF SEQ ID NOS: 95
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 40
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Patent No. 6376189
Fatent No. 6376189
Fatent No. 6376189
FAMILIANI: HOROMATION:
APPLICANI: WATANABE, TSUTOMU
APPLICANI: WATANABE, TAKESHI
APPLICANI: HORIE, MASATO
TITLE OF INVENTION: AN ISOLATED NUCLEIC ACID MOLECULE ENCODING HUMAN
TITLE OF INVENTION: SKELETAL MUSCLE-SPECIFIC UBIQUITIN-CONJUGATING ENZYME
FILE REFERENCE: 0-53599
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                                                                                                                                                                                                                                                                                                                                                     10 WTROKSVEEGEPPGQGEGPRSRPAAESTGLE 40
                                                                                                                                                                                                                                                                                              1; Mismatches
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CURRENT APPLICATION NUMBER: US/09/661,468
CURRENT PILING DATE: 2000-09-13
PRIOR APPLICATION NUMBER: 09/055,699
PRIOR FILLING DATE: 1998-04-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-565-538-40; Sequence 40, Application US/09565538; Patent No. 6333404
; BARLIER FILING DATE: 1997-03-05; NUMBER OF SEQ ID NOS: 95

; SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 40; LENCTH: 499; TYPE: PRT
                                                                                                                                                                                                                                                                                                    Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                              CRGANISM: Homo sapiens US-09-273-565-40
                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 12; Conserv
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Matches 12; Conserv
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APPLICANT: FUJIMERA, TSUTOMU
APPLICANT: WATANABE, TAKESHI
APPLICANT: WATANABE, TAKESHI
APPLICANT: WATANABE, TAKESHI
APPLICANT: WATANABE, TAKESHI
TITLE OF INVENTION: SKELETAL MUSCLE-SPECIFIC UBIQUITIN-CONJUGATING ENZYME
TITLE OF INVENTION: SKELETAL MUSCLE-SPECIFIC UBIQUITIN-CONJUGATING ENZYME
FILE REFERENCE: Q-53599
CURRENT APPLICATION NUMBER: US/09/273,565A
CURRENT FILING DATE: 1999-03-22
EARLIER FILING DATE: 1998-04-07
EARLIER FILING DATE: 1998-04-07
EARLIER FILING DATE: 1998-03-19
EARLIER APPLICATION NUMBER: US/810/1996
EARLIER FILING DATE: 1996-03-19
EARLIER FILING DATE: 1996-03-19
EARLIER RILING DATE: 1996-03-19
EARLIER APPLICATION NUMBER: JP 69163/1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
GURRNY APPLICATION DATA:
APPLICATION NUMBER: US/09/055,699
                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Sughrue, Mion, Zinn, Macpeak & Seas
STREET: 2100 Pennsylvania Avenue, N.W.
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10 WTRQKSVEEGEPPGQGEGPRSRPAARSTGLE 40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
CLASSIFICATION:
PRICE APPLICATION DATA:
APPLICATION NUMBER: 08/820,170
                                                                                                          Sequence 40, Application US/09055699; Patent No. 6005088; GENERAL INFORMATION: APPLICANT: Tsutomu, FUJIWARA APPLICANT: Takeshi, WATANABE
                                                                                                                                                                                                                                             APPLICANT: Masato, HORIE
APPLICANT: Toyomasa, KATAGIRI
TITLE OF INVENTION: HUMAN GENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (202) 293-7060
TELEFAX: (202) 293-7860
TELEX: 6491103
INFORMATION FOR SEQ ID NO: 40:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 499 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; MOLECULE TYPE: protein US-09-055-699-40
                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 4. CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: United
ZIP: 20037-3202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
                                                                                    US-09-055-699-40
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NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic ; OTHER INFORMATION: Sequence US-09-562-737-62
                                                                                                                                                                                                                                                                                                                                             2;
                                                                                                                                                                                                                                                                                                 Query Match 23.8%; Score 51: DB 4; Length 499; Best Local Similarity 38.7%; Pred. No. 66; Matches 12; Conservative 1; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23.8%; Score 51; DB 4; Length 503; 23.6%; Pred. No. 67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Herz, Joachim
APPLICANT: Gotthardt, Michael
APPLICANT: Gotthardt, Michael
APPLICANTON: LDL Receptor Signaling Pathways
FILE REFERENCE: UTSW0708
CURRENT APPLICATION NUMBER: US/09/562,737
NUMBER OF SEQ ID NOS: 132
                                                                                                                                                                                                                                                                                                                                                                                     10 WTRQKSVEEGEPPGQGEGPRSRPAAESTGLE 40
                                                                                                                                                                                                                                                                                                                                                                                                                            21 WEHSKEVSEAEPGGGSSGDSGPP--EESGQE 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred, No. 67;
8; Mismatches
PRIOR APPLICATION NUMBER: 08/820,170
PRIOR FILING DATE: 1997-03-19
PRIOR APPLICATION NUMBER: JP 63410/1996
PRIOR FILING DATE: 1996-03-19
PRIOR FILING DATE: 1997-03-05
PRIOR FILING DATE: 1997-03-05
NUMBER: OF SEQ ID NOS: 95
SOFTWARE: Patentin Ver: 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: United States of America ZIP: 77210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Arnold, White & Durkee STREET: P.O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3, Application PC/TUS9502251 GENERAL INFORMATION: APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-562-737-62
; Sequence 62, Application US/09562737
; Patent No. 6428967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 23,000
The 17; Conservative
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204 STATAEETGIDA 215
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                                                                                                                                                                                                                                     ; ORGANISM: Homo sapiens
US-09-661-468-40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: Texas
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SEQ ID NO 62
LENGTH: 503
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PCT-US95-02251-3
                                                                                                                                                                     SEQ ID NO 40
LENGTH: 499
                                                                                                                                                                                                                 TYPE: PRT
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COMPUTER READBLE FORM

MEDIUM TYPE: FIOPPY disk

COMPUTER: IBM PC Compatible

SOFTWARE: PALENTIN Release #1.0, Version

SOFTWARE: PALENTIN Release #1.0, Version

SOFTWARE: PALENTIN Release #1.0, Version

CUMRENT PAPLICATION DATA:

PELLING DATE: CONCURRENTIN HERBHITH

CLASSIFICATION NUMBER: US 08/19,780

FILING DATE: 30-SEP-1994

CLASSIFICATION NUMBER: US 08/19,780

FILING DATE: 18-FEB-1994

CLASSIFICATION NUMBER: 32,165

REGISTRATION NUMBER: 32,16
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Page

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6, 2003, 11:02:59; Search time 3.37478 Seconds (without alignments) 1254.259 Million cell updates/sec
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214
1 GKRRAKALRWTRQKSVEEGE.....PGQGEGPRSRPAAESTGLEA
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1: /cgn2_6/ptodata/2/pubpaa/USOB_NEW_PUB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/VGOB_NEW_PUB.pep:*
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11: /cgn2_6/ptodata/2/pubpaa/USOB_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/USOB_PUBCOMB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/USOB_PUBCOMB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/USOB_PUBCOMB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                392085 seqs, 103240269 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                           OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. SUMMARIES

Sequence 6, Appli Sequence 132, App Sequence 132, App Sequence 44, Appli Sequence 44, Appli Sequence 6443, App Sequence 5443, Appli Sequence 2, Appli Sequence 3210, Appli Sequence 123, Appli Sequence 113, App Sequence 47489, A Sequence 38, Appl Sequence 134, Appl Sequence 57, Appl Sequence 1140, App Sequence 1131, Appl Sequence 1140, Appl Description 10 US-09-826-581-6 10 US-09-775-719-287 10 US-09-729-64-132 10 US-09-78-64-132 10 US-09-78-64-132 10 US-09-888-615-109 10 US-09-888-615-109 10 US-09-888-615-109 10 US-09-884-13-109 10 US-09-764-891-3210 10 US-09-764-891-3210 10 US-09-988-711-123 10 US-09-808-711-123 010 Query Match Length DB Score Result NO.

Sequence 108, App Sequence 571, Ap Sequence 571, Ap Sequence 184, App Sequence 158, App Sequence 158, App Sequence 22, Appli Sequence 21, App Sequence 21, App Sequence 211, App	ALIGNMENTS 81 THE HUMAN AMP-ACTIVATED PROTEIN KINASE GAMMA 3 SU 9/826,581 195,665 rsion 4.0	10; Length 489; 17; 0; Indels 0; Gaps 0; STGLEA 41 STGLEA 91 CACID
US-09-924-340-108 US-09-942-600A-108 US-09-744-783-184 US-10-0000-489-108 US-09-086-408 US-09-0864-761-41214 US-09-788-626-5773 US-09-788-626-5773 US-09-789-561-184 US-10-153-668-86 US-09-789-561-184 US-10-153-668-86 US-09-789-561-184 US-10-153-668-86 US-09-789-561-184 US-10-153-668-86 US-09-789-861-155-2 US-09-978-155-31-166 US-09-978-121-1168-697-211 US-09-978-124-211	ALIGNMENTS 26581 r OF THE HUMAN AMP-ACT -05 60/195,665 Version 4.0	Score 214, DB Pred. No. 4.1e Mismatches PGGGEGPRSRPAAE [
44444 464444	ation US/0982 14231041 N: N: Leif an, Leif an, Stefan und, Stefan 1145-07001 ON NUMBER: US TE: 2001-04-07 for Windows	larity 100.0%. Conservative RAKALRWTRQKSVEEF [
511.5 51	-6 Applic Anders Anders Luthm Markl NVENTIO ELCATIO AND DATE NOTE TO DATE LING DATE SEQ ID FastSEQ R9 HOMO S	1 1 1 51 51 51 51 51 51 51 51 51 51 51 5
011 02 02 02 02 02 02 02 02 02 02 02 02 02	RESULT 1 US-09-826-581 Sequence 6, Patent No. 6, GENERAL INF APPLICANT: APPLICANT FILE PRIOR APPLICANT FILE APPLICANT APPLICA	Query Matches Loc Matches Qy Qy Db RESULT 2 US-09-975-; Sequence; Publical; APPLICC; APPLICC; APPLICC; TITLE C;

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RESULT 6
US-09-888-615-109
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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APPLICANT: Porton, Barbara
APPLICANT: Kao, Hung-Teh
TITLE OF INVENTION: DNA ENCODING THE HÜMAN SYNAPSIN III GENE AND USES
                                                                                                                                                                                                                                                                                                   9
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                                                                                                                                                                                                                                                      Query Match 28.0%; Score 60; DB 9; Length 187; Best Local Similarity 34.9%; Pred. No. 11; Matches 15; Conservative 6; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8; Indels
                                                                                                                                                                                                                                                                                                                                                                  1 GKRRAKALRWTRQ-----KSVEEGEPPGQGEGPRSRPAAEST 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            219 RDARYQRASRKQEAQEGQPPHRGDASSALCQGPEPVRGRPA 259
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8; Mismatches
CURRENT FILING DATE: 2001-10-10
PRIOR APPLICATION NUMBER: US 09/199,637
PRIOR FILING DATE: 1980-11-25
PRIOR PELICATION NUMBER: US 60/066,517
PRIOR FILING DATE: 1997-11-25
NUMBER OF SEQ ID NOS: 437
SOFTWARE: FBELSEQ for Windows Version 4.0
SEQ ID NO 287
LENGTH: 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/729,674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Agostino, Michael J.
Steininger II, Robert J.
Spaulding, Viki
Wong, Gordon G.
Clark, Hilary
Fechtel, Kim
Genetics Institute, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT FILING DATE: 2000-12-04
PRIOR APPLICATION NUMBER: 09/539,330
PRIOR FILING DATE: 2000-03-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 132, Application US/09729674
; Patent No. US20010039335A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 4, Application US/10122805
; Publication No. US20030082645A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      McCoy, John M.
LaVallie, Edward R.
Collins-Racie, Lisa A.
                                                                                                                                                                                               ORGANISM: Pseudomonas aeruginosa
US-09-975-719-287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 28.0%;
Best Local Similarity 36.6%;
Matches 15; Conservative
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Merberg, David
Treacy, Maurice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 283
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Jacobs, Kenneth
APPLICANT: MCCOy, John M.
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ORGANISM: Homo saplens
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APPLICANT:
APPLICANT:
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APPLICANT:
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APPLICANT:
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APPLICANT:
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Sequence 44, Application US/10042417
Patent No. US20020123082A1
GENERAL INFORMATION:
APPLICANT: PAGATO, M.
TITLE OF INVENTION: PROLIFERATIVE AND DIFFERENTIATIVE DISORDERS
TITLE OF INVENTION: PROLIFERATIVE AND DIFFERENTIATIVE DISORDERS
CURRENT APPLICATION NUMBER: US/10/042,417
CURRENT APPLICATION NUMBER: 60/260,179
PRIOR APPLICATION NUMBER: 60/260,179
PRIOR FILING DATE: 2001-01-5
SOGTWARE: PAGE 10 NOS: 89
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FILE REFERENCE: 600-1-202 CIP
CURRENT APPLICATION NUMBER: 08/10/122,805
CURRENT FILING DATE: 2002-04-15
CURRENT FILING DATE: EARLIER APPLICATION NUMBER: 09/129,668
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/129,668
PRIOR FILING DATE: EARLIER APPLICATION NUMBER: 08/906,865
PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-06
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 4
TABLE CHARLES APPLICATION NUMBER: APPLICATION NUMBER: 08/906,865
NUMBER OF SEQ ID NOS: 8
SEQ ID NO 4
TABLE CHARLES APPLICATION NUMBER: DATE: 1997-08-06
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Pred. No. 55;
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Pred. No. 81;
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; Patent No. US20020064856A1
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Best Local Similarity 42.3%;
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CAENEPEEL, SEAN
CHARYDCZAK, GLEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GKRRAKALRWTRQK---
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APPLICANT: PLOWMAN, GREGORY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 26.43
Best Local Similarity 32.73
Matches 16; Conservative
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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DB 9; Length 240;

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; PRIOR APPLICATION NUMBER: US 60/261,465
; PRIOR FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 37
; SOFFWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LEWGTH: 240
; TYPE: PRT : TYPE: PRT : COMPANIEM: Lean mays
                                                                                                                                                                                            Query Match 25.7%;
Best Local Similarity 40.6%;
Matches 13; Conservative
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US-10-196-935A-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 10
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Publication No. US20030009011A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Beach, Larry
APPLICANT: Rafalski, Antoni J.
APPLICANT: Rafalski, Antoni J.
APPLICANT: GAboon, Rebecca E.
TITLE OF INVENTION: Genes and Uses Thereof
FILE REFERENCE: 1286
FILE REFERENCE: 1286
CURRENT FILING DATE: 2002-01-09
                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                  Query Match 26.2%; Score 56; DB 10; Length 447; Best Local Similarity 55.0%; Pred. No. 78; Matches 11; Conservative 1; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: ARBEAT
APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFRERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DAFE: 2000-12-18
PRIOR FILING DAFE: 1999-12-16
PRIOR FILING DAFE: 1999-12-16
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PATENTIN VET: 3.0
SOFTWARE: PATENTIN VET: 3.0
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Publication No. US20020197605Al
GENERAL INFORMATION:
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                                                                                                                                                                                                                                         19 GEPPGQGEGPRSRPAAESTG 38
                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: MIZOGOGHI, HIROSHI
APPLICANT: ANDO, SEIKO
APPLICANT: HAYASHI, MIKIRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OCHIAI, KEIKO
YOKOI, HARUHIKO
TATEISHI, NAOKO
SENOH, AKIHIRO
IKEDA, MASATO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11; Conservative
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 109
                                                                          ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best_Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                                                                                                                           US-09-738-626-6443
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                                                                                              US-09-888-615-109
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US-10-042-894A-2
                                      LENGTH: 447
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APPLICANT:
APPLICANT:
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APPLICANT: Lifton, Richard P
APPLICANT: Wilson, Frederick H
APPLICANT: Wilson, Frederick H
APPLICANT: Wilson, Frederick H
APPLICANT: Melson-Williams, Carole
APPLICANT: Nelson-Williams, Carole
TITLE OF INVENTION: HYPERTENSION
FILE REFERENCE: 044574-5113
CURRENT APPLICATION NUMBER: US/10/196,935A
CURRENT FILING DATE: 2002-10-25
PRIOR FILING DATE: 2001-07-17
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CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 10231
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-764-891-3210
Sequence 3210, Application US/09764891
Publication No. US20030077808A1
GENERAL INFORMATION:
A PAPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC006
Score 55; DB 9; Length 240
Pred. No. 54;
4; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 54; DB 9;
Pred. No. 3.8e+02;
6; Mismatches 11.
                                                                                                               1 GKRRAKALRWIRQKSVEEGEPPGQGEGPRSRP 32
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; Sequence 4, Application US/10196935A
; Publication No. US20030082720A1
; GENERAL INFORMATION:
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Best Local Similarity 39.3%;
Matches 11; Conservative 6
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SOFWARE: Patentin version 3.1
SEQ ID NO 4
LENGTH: 1243
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ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (84)
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                                                LOCATION: (125)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
                                                                                                                                                                                                                                LOCATION: (148)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                    : OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-764-891-3210
                                                                                                                                           LOCATION: (138)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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CURRENT APPLICATION NUMBER: US/09/908,711

CURRENT FILING DATE: 2001-07-20

PRIOR APPLICATION NUMBER: US/10/1360

PRIOR FILING DATE: 2001-01-17

PRIOR FILING DATE: 2001-01-17

PRIOR FILING DATE: 2001-01-17

PRIOR FILING DATE: 2001-01-17

PRIOR PLICATION NUMBER: US/10/1344

PRIOR FILING DATE: 2001-01-17

PRIOR PRIOR DATE: 2001-01-17

PRIOR FILING DATE: 2001-01-17
                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 150;
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PRIOR APPLICATION NUMBER: 05/764,888
PRIOR FILING DATE: 2001-01-17
PRIOR PLING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: 05/764,905
PRIOR PLING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: 05/764,905
PRIOR PLING DATE: 2001-01-17
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APPLICATION NUMBER: 09/764,902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                             NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                     LOCATION:
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LOCATION: (84)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids NAME/KET: SITE
LOCATION: (125)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: (138)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (148)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; LOCATION: (150); cornER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-908-711-123
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Publication No. US20030096982A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 44 Human Secreted Proteins
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                                                                   PRIOR FILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: 09/764,870
PRIOR APPLICATION NUMBER: 09/764,870
PRIOR PILING DATE: 2001-01-17
PRIOR PILING DATE: 2001-01-17
PRIOR PILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: 09/764,882
PRIOR PILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: 09/764,896
PRIOR PILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: 09/764,896
PRIOR PILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: 09/764,864
PRIOR PLING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: 09/764,864
PRIOR PILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: 09/764,866
PRIOR PILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: 09/764,866
PRIOR PILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: 06/704,866
PRIOR FILING DATE: 2001-01-17
PRIOR PILING DATE: 2000-01-17
PRIOR APPLICATION NUMBER: 06/190,628
PRIOR PILING DATE: 2000-01-17
PRIOR APPLICATION NUMBER: 60/209,467
PRIOR PILING DATE: 2000-02-04
PRIOR PILING DATE: 2000-02-04
PRIOR FILING 
FILING DATE: 2001-01-17
APPLICATION NUMBER: US01/01239
FILING DATE: 2001-01-17
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ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: SITE
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Publication No. US20030068627A1

GENERAL INFORMATION:

APPLICANT: Rosen et al.

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REPERENCE: PT2067.

CURRENT APPLICATION NUMBER: US/10/091,458

CURRENT FILING DATE: 2002-03-07

PRIOR APPLICATION NUMBER: 09/764,900

PRIOR APPLICATION NUMBER: 00/179,065

PRIOR FILING DATE: 2000-01-37

PRIOR FILING DATE: 2000-01-31

PRIOR PLING DATE: 2000-02-04

PRIOR APPLICATION NUMBER: 60/180,628

PRIOR PLING DATE: 2000-02-04

PRIOR APPLICATION NUMBER: 60/214,886

PRIOR PLING DATE: 2000-02-04

PRIOR APPLICATION NUMBER: 60/217,487

PRIOR PLING DATE: 2000-00-28
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COTHER INFORMATION: MAP TO AC008962.4
COTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 14
COTHER INFORMATION: EST_HUMAN HIT: AM602053.1, EVALUE 7.00e-25
US-09-864-761-47489
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                                                 PRIOR APPLICATION NUMBER: US 42203.0

PRIOR APPLICATION NUMBER: US 60/236,359

PRIOR FILING DATE: 2000-09-27

PRIOR FILING DATE: 2000-09-27

PRIOR FILING DATE: 2001-01-30

PRIOR PILING DATE: 2001-01-30

PRIOR PILING DATE: 2001-01-30

PRIOR FILING DATE: 2001-01-30

PRIOR PELLING DATE: 2001-01-30

PRIOR FILING DATE: 2001-01-30

PRIOR PELLING DATE: 2001-01-30

PRIOR FILING DATE: 2001-01-30

PRIOR PELLING DATE: 2001-01-30

PRIOR
                          APPLICATION NUMBER: GB 24263.6
FILING DATE: 2000-10-04
APPLICATION NUMBER: US 60/236,359
FILING DATE: 2000-09-27
APPLICATION NUMBER: PCT/US01/00666
FILING DATE: 2001-01-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-091-458-38
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APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: (131)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INPORMATION: Xaa equals any of the naturally occurring L-amino acids US-10-062-548-113
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids NAME/KEY: SITE
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CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR PILING DATE: 2000-02-04
PRIOR PILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
                              CURRENT APPLICATION NUMBER: US/10/062,548
CURRENT FILING DATE: 2002-02-05
PRIOR APPLICATION NUMBER: 09/369,247
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                                                                                                                             PRIOR FILLING DATE: 1999-08-05
PRIOR PLICATION NUMBER: 60/074,118
PRIOR FILING DATE: 1998-02-09
PRIOR FILING DATE: 1998-02-09
PRIOR FILING DATE: 1998-02-09
PRIOR FILING DATE: 1998-02-09
PRIOR PLICATION NUMBER: 60/074,137
PRIOR FILING DATE: 1998-02-09
PRIOR APPLICATION NUMBER: 60/074,141
PRIOR FILING DATE: 1998-02-09
PRIOR FILING DATE: 1998-02-09
PRIOR FILING DATE: 1998-02-09
NUMBER OF SEQ ID NOS: 172
SOFTWARE: PATENTIN VO. 2.0
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Patent No. US20020048763A1
GENERAL INFORMATION:
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ORGANISM: Homo sapiens
FILE REFERENCE: P2024P1
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LENGTH: 217
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BER: 60/225, 00-08-14 00-08-14 00-07-20, 00-07-11 00-08-14 00-08-14 BER: 60/218, 00-08-14 BER: 60/218, 00-08-14 BER: 60/225, 00-08-14	28.7. 60.20.20.20.20.20.20.20.20.20.20.20.20.20	11-17 10-20 10-20 110-20 110-20 110-20 110-20 110-20 110-20 12-06 12-06 13-
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PRIOR PILING DATE: 2000-09-05
PRIOR APPLICATION WINBER: 60/237,039
PRIOR APPLICATION WINBER: 60/237,039
PRIOR PILING DATE: 2000-10-02
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-11-08
PRIOR PILING DATE: 2000-11-08
PRIOR PILING DATE: 2000-11-03
PRIOR PILING DATE: 2000-10-05
PRIOR PILING DATE: 2000-11-03
PRIOR PILING DATE: 2000-10-05
PRIOR PILING DATE: 2000-06-14
PRIOR PILING DATE: 2000-08-14
PRIOR PILING DATE: 2000-11-17
PRIOR PILING DATE: 200

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Sequence 114. Application US/09870759
PREATURE NO. US20202177551A1
GENERAL INFORMATION:
APPLICANT: TERMAN, David S
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
TILE REFERENCE: 870759
CURRENT APPLICATION NUMBER: US/09/870,759
CURRENT FILING DATE: 2002-01-14
PRIOR APPLICATION NUMBER: US 60/208,128
PRIOR PLILNG DATE: 2000-05-30
NUMBER OF SEQ ID NOS: 166
SOFTWARE: Patentin version 3.1
SOFTWARE: Patentin version 3.1
SEQ ID NO 134
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44.0%; Pred. No. 3.3e+02;
tive 2; Mismatches 12; Indels
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PRIOR APPLICATION NUMBER: 60/249,297
PRIOR FILING DATE: 2000-11-17
PRIOR PILING DATE: 2000-11-17
PRIOR PILING DATE: 2000-09-14
PRIOR PILING DATE: 2000-09-18
PRIOR PLING DATE: 2000-09-08
PRIOR PLING DATE: 2000-09-08
PRIOR PLING DATE: 2000-09-08
PRIOR PELING DATE: 2000-09-08
PRIOR PELING DATE: 2000-09-08
PRIOR PLICATION NUMBER: 60/231,081
PRIOR PLICATION NUMBER: 60/231,414
PRIOR PLICATION NUMBER: 60/231,414
PRIOR PLICATION NUMBER: 60/231,44
PRIOR PLILING DATE: 2000-09-18
PRIOR PLILING DATE: 2000-09-14
PRIOR PRIOR APPLICATION NUMBER: 60/233,064
PRIOR FILING DATE: 2000-09-14
PRIOR PLICATION NUMBER: 60/232,397
PRIOR PLICATION NUMBER: 60/232,397
PRIOR PLICATION NUMBER: 60/232,401
PRIOR PLING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: 60/231,309
PRIOR PLING DATE: 2000-09-14
PRIOR PLING DATE: 2000-10-20
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Best Local Similarity 44.09
Matches 11; Conservative
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CORGANISM: Homo sapiens
US-09-870-759-134
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Search completed: June 6, 2003, 11:16:42 Job time : 4.37478 secs

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(without alignments)
827.023 Million cell updates/sec
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/SIDS2/gogdata/geneseq/geneseqp-emb1/AA2001_DAT:*
/SIDS2/gogdata/geneseq/geneseqp-emb1/AA2002_DAT:*
                                                                                      6, 2003, 10:55:08; Search time 6.60595 Seconds
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213
1 HILTHKRLLKFLHIFGSLLP.....PSFLYRIQDLGIGTFRDLA
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                          OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Human AMP-activate	Human AMPK gamma s	Human Prkad3 R410	Human Prkad3 V40I	Human AMPK gamma s	PRKAG3, Homo sapi	Pig AMPK gamma sub	Sus scrofa AMPK da	Sus scrofa AMPK da	Pig AMPK gamma sub
SUMMARIES	ABB11241	AAE00221	AAE00328	AAE00329	AAE00223	AAB47679	AAE00220	AAE00225	AAE00226	AAE00222
DB	22	22	22	22	22	22	22	22	22	22
% Query Match Length D	181	305	305	305	464	489	305	305	305	464
% Query Match	100.0	100.0	100.0	100.0	100.0	100.0	98.6	98.6	98.6	98.6
Score	213	213	213	213	213	213	210	210	210	210
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AAE22984 AAE22986 AAE22987 AAE22987 AAE22987 AAM88438 AAM8438 AAM8438 AAM8438 AAM86101 AAM29078 AAM290101 AAM3751 AAM33751 AAN33751 AAN33751 AAN33751 AAN33751 AAN33751 AAN33751 AAN33751 AAN33751 AAN33751 AAN33751	AAR04252 AAR13860 AAR13860 AAR13860 AAR90466 AAP90466 AAR91756 AAR97756 AAR97756 AAR97756 AAR97744 ABG22403 AAU87274 ABG22406	181 AA. Kinase subu	Human; cytokine; cell proliferation; cell di di mematopolesis regulation; tissue growth; in inhibin; chemotaxis; chemokinesis; thromboly proliferation; metastasis; cancer; tumour; hymplide cell disorder; tymphoid cell disorder chemotary condition; proliferation; atherosclerosis; coronary heart disease; art bene disorder; osteoprosis; vascular growth tissue regeneration; wound haling; infectiocell culture; drug screening; gene therapy; cell culture; drug screening; gene therapy; contastic; osteopathic; vasctropic; cardian antifungal; vulnerary; antiulcer. WO200157188-A2. 09-AUG-2001. 05-FEB-2000; 2000US-046914.
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                                                                                                                                                                                                                                       Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and sequences ABA08225-ABA09574 represent nucleic acids encoding them. The invention also relates to vectors and recombinant host cells comprising a nucleotide of the invention, methods of producing the novel polypeptides.

Or polypeptides in a sample, and methods of detecting the nucleotides of the invention although novel, many of the bind to polypeptides of the invention. Although novel, many of the polypeptides of the invention have homology to known proteins, thereby giving an insight into their probable biological activities, and hence to potential therapeutic applications. The polypeptides of the invention may have various activities; sem cell growth factor activities, and hence to prential therapeutic applications. The polypeptides of the invention may have various activities; sem cell growth factor activity; hemologisis regulatory activity; tissue growth activity; inferentiation activities; themologic or chemokinetic activities; polypeptides and mucleotides of involved in oncogenesis, cancer cell proliferation or metastasis.

Chemologic or themokinetic activities, polypeptides and nucleotides of the invention are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. Such conditions include cancers, hemaenloopietic disorders (e.g., myeloid or lymphoid cell cancers, hemaenloopietic disorders (e.g., myeloid or lymphoid cell disorders), chronic inflammatory conditions (e.g., asthma or arthritis), proliferative retinopathy, atherosclerosis, coronary heart disease, arterial issemania, bone disorders (e.g., asthma or arthritis), proliferative retinopathy, atherosclerosis, coronary heart disease, arterial issemania, bone disorders (e.g., asthma or arthritis) crepair (or nucleic acids encoding them) may be used to promote wound communomoculatory activities may be used in the treatment of viral, promote cell growth For avamila such be used in the treatment of viral, promote cell growth For avamila
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  that can be used to augment or replace cells damaged by illness, autoimmune disease or accidental damage. The polypeptides and nucleotides may also be used in the diagnosis of the above conditions, and in drug
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  manipulate stem cells in culture to give rise to neuroepithelial cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                screening techniques. The present sequence represents a novel human polypeptide of the invention.
                                                                                                                                               Human proteins and DNA encoding sequences useful for preventing, treating or ameliorating a medical condition in a mammalian subject
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    promote cell growth. For example, such polypeptides may be used to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human AMPK gamma subunit muscle-specific isoform, PRKAG3.
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                                                                                                                                                                                                               Claim 20; Page 159-160; 1963pp; English.
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                                                               Tang YT, Liu C, Drmanac RT;
27-APR-2000; 2000US-0560875.
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nes 41; Conservative
                                                                                              WPI; 2001-457740/49.
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                               (HYSE-) HYSEQ INC.
                                                                                                                 N-PSDB; ABA08485
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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                                PRKAG3; diabetes; obesity; myopathy; cardiovascular disease; anorectic; genetic testing; carbohydrate metabolism disorder; skeletal muscle; cystathione beta synthase; CBS; cardiant; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      a genetic polymorphic marker linked to a sequence encoding PRKAG3, are useful for detecting a dysfunction of carbohydrate metabolism resulting from the expression of a functionally altered allele of PRKAG3. Transgenic animal and host cell transformed with PRKAG3 or a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  evaluation, genetic testing and prognosis of a metabolic disorder, preferably a carbohydrate metabolism disorder. Primers that can detect
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rogel-Gaillard C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           monophosphate-activated kinase for diagnosis or treatment of disorders associated with energy metabolism such as diabetes, obesity, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (AMP)-activated Kinase (AMFK) gamma subunit muscle-specific isoform, PRKAG3. Mutation in Prkag3 results in an altered regulation of carbohydrate metabolism, particularly in skeletal muscle. PRKAG3 is useful as therapeutic for treating carbohydrate metabolism disorders s as diabetes, obesity, and disorders associated with muscle metabolism activity, and for restoring a normal AMFK function. PRKAG3 sequence and its functionally altered mutants are useful for the diagnostic
gamma subunit; adenosine monophosphate-activated kinase; AMPK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New variants of the gamma subunit of vertebrate adenosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      present sequence is human adenosine monophosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 HILTHKRLLKFLHIFGSLLPRPSFLYRTIQDLGIGTFRDLA 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Robic A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 213; DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kalm E, Milan D, κυμις
J, Le Roy P, Chardon P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (INRG ) INRA INST NAT RECH AGRONOMIQUE. (ANDE/) ANDERSSON L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 4; Page 55-57; 71pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAE00328 standard; Protein; 305 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        10-SEP-1999; 99EP-0402236.
18-MAY-2000; 2000EP-0401388.
                                                                                                                                                                                                                                                                                                                                                                                    11-SEP-2000; 2000WO-EP09896
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Looft C,
Gellin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2001-244810/25.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAD03296.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Iannuccelli N,
                                                                                                                                                                                                                                          WO200120003-A2.
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                                                                                                                                                                             Homo sapiens.
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                                                                                                                                                                                                                                                                                                               22-MAR-2001
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AAE00329
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      such as myopathy and cardiovascular diseases, to modulate AMPK activity, and for restoring a normal AMPK function. PRKAG3 sequence and its functionally allered mutants are useful for the diagnostic evaluation, genetic testing and prognosis of a metabolic disorder. Preferably a carbohydrate metabolism disorder. Primers that can detect a genetic polymorphic marker linked to a sequence encoding PRKAG3, are useful for detecting a dysfunction of carbohydrate metabolism resulting from the expression of a functionally altered allele of PRKAG3. Transgenic animal and host cell transformed with PRKAG3 or a heterotrimeric AMPK consisting of PKKAG3 or its mutant, are useful for eccening compounds able to modulate AMPK activity. Nucleic acid encoding PKKAG3 is useful for detecting mutations in a PFKAG3 gene, or
                                                                                                                                        Human; gamma subunit; adenosine monophosphate-activated kinase; AMFK; PRKAG3; diabetes; obesity; myopathy; cardiovascular disease; anorectic; genetic testing; carbohydrate metabolism disorder; skeletal muscle; cystathione beta synthase; CBS; cardiant; gene therapy; mutant; mutein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         a sequence encoding the first cystathione beta synthase (CBS) domain PRKAG3 and is useful in gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New variants of the gamma subunit of vertebrate adenosine monophosphate-activated kinase for diagnosis or treatment of disorders associated with energy metabolism such as diabetes, obesity, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence is a R41Q mutant of human muscle-specific isoform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rogel-Gaillard C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mutation in Prkag3 results in an altered regulation of carbohydrate metabolism, particularly in skeletal muscle. PRKAG3 is useful as therapeutic for treating carbohydrate metabolism disorders such as diabetes, obesity, and disorders associated with muscle metabolism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of gamma subunit of adenosine monophosphate (AMP)-activated kinase (AMPK) Prkag3. This mutant sequence results in increased glycogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Note: The present sequence is not shown in the specification, but
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "Wild-type Arg substituted with Gln"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Robic A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Looft C, Kalm E, Milan D, Robic Gellin J, Le Roy P, Chardon P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (INRG ) INRA INST NAT RECH AGRONOMIQUE.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page -; 71pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               content in human skeletal muscle.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11-SEP-2000; 2000WO-EP09896.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10-SEP-1999; 99EP-0402236.
18-MAY-2000; 2000EP-0401388.
(first entry)
                                                                        Human Prkag3 R41Q mutant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-244810/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Misc-difference 41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200120003-A2
                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
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13-JUN-2001
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Gaps

0;

Indels

Length 305;

100.0%; Score 213; DB 22; 100.0%; Pred. No. 2.8e-23; ive 0; Mismatches 0;

41; Conservative

Query Match Best Local Similarity Matches 41; Conserv

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metabolism, particularly in Skeletal muscle. PRRAG3 is useful as therapeutic for treating carbohydrate metabolism disorders such as diabetes, obesity, and disorders associated with muscle metabolism such as myopachy and cardiovascular diseases, to modulate AMPK such as myopachy and cardiovascular diseases, to modulate AMPK cartvity, and for restoring a normal AMPK function. PRRAG3 sequence and its functionally altered mutants are useful for the diagnostic evaluation, genetic testing and prognosis of a metabolic disorder, preferably a carbohydrate metabolism disorder. Primers that can detect a genetic polymorphic marker linked to a sequence encoding PRRAG3, are useful for detecting a dysfunction of carbohydrate metabolism resulting from the expression of a functionally altered allele of PRRAG3.

Transgenic animal and host cell transformed with PRRAG3 or a cheterotrimeric AMPK consisting of PRRAG3 or its mutant, are useful for screening compounds able to modulate AMPK activity. Nucleic acid
                                                                                                                                                                                                                                                                                               Human; gamma subunit; adenosine monophosphate-activated kinase; AMPK; RRKA3; diabetes; obesity; myopathy; cardiovascular disease; anorectic; genetic testing; carbohydrate metabolism disorder; skeletal muscle; cystathione beta synthase; CBS; cardiant; gene therapy; mutant; mutein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New variants of the gamma subunit of vertebrate adenosine monophosphate-activated kinase for diagnosis or treatment of disorders associated with energy metabolism such as diabetes, obesity, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rogel-Gaillard C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence is a V401 mutant of human muscle-specific isoform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      content in human skeletal muscle.
Mutation in Prkag3 results in an altered regulation of carbohydrate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of gamma subunit of adenosine monophosphate (AMP)-activated kinase (AMPK) Prkag3. This mutant sequence results in decreased glycogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "Wild-type Val substituted with Ile"
Robic A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ooft C, Kalm E, Milan D, Robic Gellin J, Le Roy P, Chardon P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (INRG ) INRA INST NAT RECH AGRONOMIQUE. (ANDE/) ANDERSSON L.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers Misc-difference 40
                                                                                                                                       AAE00329 standard; Protein; 305 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page -; 71pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99EP-0402236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18-MAY-2000; 2000EP-0401388
                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                            Human Prkag3 V401 mutant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Andersson L, Looft C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-244810/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOOFT C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KALM E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200120003-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tannuccelli N,
                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
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                                                                                                                                                                              AAE00329;
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                                                                                                                                                                                                                                                                                                                                                                               variant.
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Local Similarity
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                                                                                                                                                                                                                                                      464 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAH43685
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens,
                                                                                                                                                                                                                                                                                                                                                                                                                     21-JAN-2002
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                                                                                                                                                                                                                                                                                            41;
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                                                                                                                                                                                                                                                                                                                                 295
                                                                                                                                                                                                                                                                                                                                                                                                    AAB47679;
                                                                                                                                                                                                                                                                         Query Match
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Matches
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encoding PRKAG3 is useful for detecting mutations in a Prkag3 gene, or in a sequence encoding the first cystathione beta synthase (CBS) domain of PRKAG3 and is useful in gene therapy.

Note: The present sequence is not shown in the specification, but is derived from the human Prkag3 sequence SEQ.ID.NO.4 shown in page 57-58 of sequence listing (AAE00221).
                                                                                                                                                                                                                                                                        Human; gamma subunit; adenosine monophosphate-activated kinase; AMPK; FRKG3; diabetes; obesity; myopathy; cardiovascular disease; anorectic; genetic testing; carbohydrate metabolism disorder; skeletal muscle; cystathione beta synthase; CBS; cardiant; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New variants of the gamma subunit of vertebrate adenosine monophosphate-activated kinase for diagnosis or treatment of disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rogel-Gaillard C;
                                                                                                           Gaps
                                                                                                                                                                                                                                                      Human AMPK gamma subunit muscle-specific isoform, complete PRKAG3.
                                                                                                          0;
                                                                                      Length 305;
                                                                                                                                                                                                                                                                                                                                                                                                            /label= CBS
/note= "Cystathione beta synthase domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "Cystathione beta synthase domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label= CBS
/note= "Cystathione beta synthase domain"
                                                                                                                                                                                                                                                                                                                                                                        /note= "Cystathione beta synthase domain"
                                                                                                          Indels
                                                                                                                                       136 HILTHKKLLKFLHIFGSLLPRPSFLYRTIQDLGIGTFRDLA 176
                                                                                                                             1 HILTHKRLLKFLHIFGSLLPRPSFLYRTIQDLGIGTFRDLA 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kalm E, Milan D, Robic A,
I, Le Roy P, Chardon P;
                                                                                       Score 213; DB 22;
Pred. No. 2.8e-23;
                                                                                                          ;
0
                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                          /note= "RN- mutation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (INRG ) INRA INST NAT RECH AGRONOMIQUE.
(ANDE), ANDERSSON L.
(LOOF/) LOOFT C.
(RALM/) KALM E.
                                                                                                                                                                                                                                                                                                                                            Cocation/Qualifiers
172..225
                                                                                                                                                                                              AAE00223 standard; Protein; 464 AA
                                                                                      100.0%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11-SEP-2000; 2000WO-EP09896.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10-SEP-1999; 99EP-0402236.
18-MAY-2000; 2000EP-0401388.
                                                                                                                                                                                                                                                                                                                                                              /label= CBS
                                                                                                                                                                                                                                                                                                                                                                                                                                           /label- CBS
                                                                                                                                                                                                                                   13-JUN-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gellin J,
                                                                                                          41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                             .453
                                                                                                                                                                                                                                                                                                                                                                                                                                  382
                                                                                                                                                                                                                                                                                                                                                                                                    307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Looft C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                              400.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2001-244810/25.
                                                                                                 Local Similarity
                                                                   305 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAD03320.
                                                                                                                                                                                                                                                                                                                                                                                  Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Andersson L, Lo
Iannuccelli N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200120003-A2
                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22-MAR-2001
                                                                    Sequence
                                                                                                                                                                                                                 AAE00223;
                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                     Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                  Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Domain
                                                                                                                                                                                                                                                                                                                                                     Domain
                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                             Key
                                                                                                                                                                                     AAE0022
                                                                                                                                                                            RESULT
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Camplete PRRAG3. Mutation in Prkag3 results in an altered regulation of carbohydrate metabolism. Particularly in skeletal muscle- PRRAG3. Mutation in Prkag3 results in an altered regulation of carbohydrate metabolism. Particularly in skeletal muscle- PRRAG3 is carbohydrate metabolism disorders such as myopathy and cardiovascular diseases, to modulate AMPK such as myopathy and cardiovascular diseases, to modulate AMPK and its functionally altered mutants are useful for the diagnostic valuation, genetic testing an opromal AMPK function. PRRAG3 sequence and its functionally altered mutants are useful for the diagnostic preferably a carbohydrate metabolism disorder. Primers that can detect a genetic polymorphic marker linked to a sequence encoding PRRAG3, are useful for detecting a dysfunction of carbohydrate metabolism resulting from the expression of a functionally altered allele of PRRAG3. Transgenic animal and host cell transformed with PRRAG3 or a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 heterotrimeric AMPK consisting of PRKAG3 or its mutant, are useful for screening compounds able to medulate AMPK activity. Nucleic acid encoding PRKAG3 is useful for detecting mutations in a Prkag3 gene, or in a sequence encoding the first cystathione beta synthase (CBS) domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human, AMP-activated protein kinase gamma 3 subunit; PRKAG3; variant; metabolic disease; diabetes; obesity; substitution; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
associated with energy metabolism such as diabetes, obesity, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 464;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "Possible variation point R340W"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HILTHKRLLKFLHIFGSLLPRPSFLYRTIQDLGIGTFRDLA 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "Possible variation point P71A"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41
                                                                                                                                                                                                       The present sequence is human adenosine monophosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 HILTHKRLLKFLHIFGSLLPRPSFLYRTIQDLGIGTFRDLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4.5e-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 213; ilarity 100.0%; Pred. No. 4. Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRKAG3 and is useful in gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Marklund S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB47679 standard; Protein; 489 AA
                                                                                                                      Claim 5; Fig 3; 71pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-APR-2001; 2001WO-SE00765.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-APR-2000; 2000US-195665P.
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Key
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRKAG3; diabetes; obesity; myopathy; cardiovascular disease; anorectic; genetic testing; carbohydrate metabolism disorder; skeletal muscle; cystathione beta synthase; CBS; cardiant; gene therapy; RN locus;
            associated with a metabolic disease e.g. diabetes or obesity and method for determining a risk estimate of diseases in subject by detecting the
                                                                                    AMP-activated protein kinase gamma 3 subunit (PRKAG3). Detecting the presence of the PRKAG3 DNA, or a variant, is useful in determining a risk estimate of a metabolic disease, such as diabetes or obesity, in a subject. The variation may occur in exons 3, 4 or 10. In exon 3 variation may be a substitution of a G for a C at nucleotide 320, resulting in the amino acid substitution P71A; in exon 4 variation may be a substitution of a T for a C at nucleotide 103, variation may be a substitution of a T for a C at nucleotide 103, resulting in the amino acid substitution 874W. There may also be nucleotide variation in intron 6. The numbering of these position 1 of the open reading frame.
                                                                                                                                                                                                                                                                                            Gaps
                                                                              This sequence is encoded by the full length cDNA encoding the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pig; gamma subunit; adenosine monophosphate-activated kinase; AMPK;
 New variants of human AMP-activated protein kinase gamma3 subunit
                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                   Length 489;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Cystathione beta synthase domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "Cystathione beta synthase domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label = Cystathione beta synthase domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "Cystathione beta synthase domain"
                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                              320 HILTHKELKFLHIFGSLLPRPSFLYRTIODLGIGTFRDLA 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pig AMPK gamma subunit muscle-specific isoform, PRKAG3.
                                                                                                                                                                                                                                                                                                                 1 HILTHKRILKFLHIFGSLLPRPSFLYRTIQDLGIGTFRDLA 41
                                                                                                                                                                                                                                                                  Score 213; DB 22;
Pred. No. 4.8e-23;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                 AA.
                                                        Disclosure; Fig 5; 25pp; English.
                                                                                                                                                                                                                                                                                                                                                                                               AAE00220 standard; Protein; 305
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0
                                                                                                                                                                                                                                                                     100.0%;
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18-MAY-2000; 2000EP-0401388.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94..148
/label= CBS
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                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    170..223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note=
                                                                                                                                                                                                                                                                            Local Similarity
nes 41; Conserv
                                                                                                                                                                                                                                              489 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200120003-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       chromosome 15
                                                                                                                                                                                                                                                                                                                                                                                                                                            13-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sus scrofa.
                                                                                                                                                                                                                                                Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                       AAE00220;
                                                                                                                                                                                                                                                                     Query Match
                                   variant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Doma in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Domain
                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Key
                                                                                                                                                                                                                                                                                                                                                                          RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                      AAE00220
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The present amino acid sequence is pig adenosine monophosphate

(AMP) activated kinase (AMPK) gamma subunit muscle-specific isoform,

PRKAG3: Prkag3 gene is located in the RN locus of Chromosome 15.

Whatation in Prkag3 results in an altered regulation of carbohydrate
metabolism, particularly in skeletal muscle. PRKAG3 is useful as

the mappethic for treating arbohydrate metabolism disorders such as

conclusive, and for restoring a rabohydrate metabolism disorders such as myopathy and cardiovascular diseases, to modulate AMPK

conclusive, and for restoring a normal AMPK function. PRKAG3 sequence

and its functionally altered mutants are useful for the diagnostic

corlustive, and for restoring a normal AMPK function. PRKAG3 sequence

and its functionally altered mutants are useful for the diagnostic

corlustive activity and cardohydrate metabolism disorder. Primers that can detect

a genetic polymorphic marker linked to a sequence encoding PRKAG3. are

useful for detecting a dysfunction of carbohydrate metabolism resulting

from the expression of a functionally altered allele of PRKAG3. are

useful for detecting a dysfunction of PRKAG3 or its mutant, are useful for

creening compounds able to modulate AMPK activity. Nucleic acid

encoding PRKAG3 is useful for detecting mutations in a Prkag3 gene, or

n a sequence encoding the first cystathione beta synthase (CBS) domain

corporations.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRRAGÍ; diabetes, obesity, myopathy; cardiovascular disease; anorectic; genetic testing; carbohydrate metabolism disorder; skeletal muscle; cystathione beta synthase; CBS; cardiant; gene therapy; mutant; mutein;
                                                                                                                                                                                                                                                                                                                                 monophosphate-activated kinase for diagnosis or treatment of disorders associated with energy metabolism such as diabetes, obesity, and
                                                                                                                                      Rogel-Gaillard C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gamma subunit; adenosine monophosphate-activated kinase; AMPK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 210; DB 22; Length 305; Pred. No. 7.8e-23;
                                                                                                                                                                                                                                                                                                          New variants of the gamma subunit of vertebrate adenosine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sus scrofa AMPK gamma chain isoform Prkag3 mutant (R41Q).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              136 HILTHKRLLKFLHIFGTLLPRPSFLYRTIQDLGIGTFRDLA 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 HILTHKRLLKFLHIFGSLLPRPSFLYRTIQDLGIGTFRDLA 41
                                                                                                                                         Kalm E, Milan D, Robic A,
J, Le Roy P, Chardon P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Mismatches
(INRG ) INRA INST NAT RECH AGRONOMIQUE. (ANDE/) ANDERSSON L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 4; Fig 2; 71pp; English.
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97.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                         Looft C,
Gellin
                                                                                                                                                                                                                          2001-244810/25.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 305 AA;
                                                                                                                                                                                                                                                         N-PSDB; AAD03295
                                                            LOOFT C.
                                                                                                                                         Andersson L, L
Iannuccelli N,
                                                                                   KALM E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 40;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAE00225;
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                                                                                                                                                                                                                                                                                                                                                                                                myopathy
                                                                                      (KALM/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Domain
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Matches
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Sus scrofa AMPK gamma chain isoform Prkag3 mutant (R41Q).

(first entry)

13-JUN-2001

AAE00226;

AAE00226 standard; Protein; 305 AA.

AAE00226

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a genetic polymorphic marker linked to a sequence encoding PRRAG3, are useful for detecting a dysfunction of carbohydrate metabolism resulting from the expression of a functionally altered allele of PRRAG3.
Transgenic animal and host cell transformed with PRRAG3 or a heterotriment AMPK consisting of PRRAG3 or its mutant, are useful for screening compounds able to modulate AMPK activity. Nucleic acid encoding PRRAG3 is useful for detecting metations in a Prkag3 gene, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            in a sequence encoding the first cystathione beta synthase (CBS) domain of PRKAG3 and is useful in gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         metabolism, particularly in skeletal muscle. PRKAG3 is useful as therapeutic for treating carbohydrate metabolism disorders such as diabetes, obesity, and disorders associated with muscle metabolism such as myopathy and cardiovascular diseases, to modulate AMPK activity, and for restoring a normal AMPK function. PRKAG3 sequence and its functionally altered mulants are useful for the diagnostic evaluation, genetic testing and proquests of a metabolic disorder, preferably a carbohydrate metabolism disorder. Primers that can detect
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       monophosphate-activated kinase for diagnosis or treatment of disorders associated with energy metabolism such as diabetes, obesity, and myopathy -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kalm E, Milan D, Robic A, Rogel-Gaillard C;
J, Le Roy P, Chardon P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               e: The present sequence is not shown in the specification, but derived from the porcine Prkay3 sequence shown in Fig 2 (AAE00220).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence is a R41Q mutant of muscle-specific isoform of gamma subunit of adenosine monophosphate (AMP) -activated kinase (AMPK) Prkay3 from Sus scrofa. This mutant sequence results in increased glycogen content in pig skeletal muscle. Mutation in Prkay3 results in an altered requiation of carbohydrate
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                                 "Wild-type Arg substituted with Gln"
                                                                                                                                                                                                                                                                                 241..294
/label= CBS
/note= "Cystathione beta synthase domain"
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                                                                                                                                                                                                                 /label= CBS
/note= "Cystathione beta synthase domain"
                                                                                                        /label= CBS
/note= "Cystathione beta synthase domain"
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(ANDE/) ANDERSSON L.
(LOOF/) LOOFT C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 9; Page -; 71pp; English.
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18-MAY-2000; 2000EP-0401388.
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Gellin J,
                                                                   .148
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Best Local Similarity
Fra 40; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-244810/25.
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Misc-difference 41
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Iannuccelli N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (KALM/) KALM E.
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Pig; gamma subunit; adenosine monophosphate-activated kinase; AMPK; PRKAG3; diabetes; obesity; myopathy; cardiovascular disease; anorectic; genetic testing; carbohydrate metabolism disorder; skeletal muscle; cystathione beta synthase; CBS; cardiant; gene therapy; mutant; mutein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New variants of the gamma subunit of vertebrate adenosine monophosphate-activated kinase for diagnosis or treatment of disorders associated with energy metabolism such as diabetes, obesity, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rogel-Gaillard C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence is a V401 mutant of muscle-specific isoform of gamma subunit of adenosine monophosphate (AMP)-activated kinase (AMEK) Prkag3 from Sus scrofa. This mutant sequence results in decreased glycogen content in pig skeletal muscle. Mutation in Prkag3 results in an altered regulation of carbohydrate metabolism, particularly in skeletal muscle. PRKAG3 is useful as therapeutic for treating carbohydrate metabolism disorders such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               diabetes, obesity, and disorders associated with muscle metabolism such as myopathy and cardiovascular diseases, to modulate AMPK activity, and for restoring a normal AMPK function. PRKAG3 sequence and its functionally altered mutants are useful for the diagnostic evaluation, genetic testing and prognosis of a metabolic disorder,
                                                                                                                                                                                                                                                                                                          'note= "Wild-type Val substituted with Ile"
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/note= "Cystathione beta synthase domain"
                                                                                                                                                                                                                                                                       'note= "Cystathione beta synthase domain"
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/note= "Cystathione beta synthase domain"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (INRG ) INRA INST NAT RECH AGRONOMIQUE. (ANDE/) ANDERSSON L.
                                                                                                                                                                                                                               Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                      223
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                                                                                                                                                                                                                                                                                                                         .148
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                                                                                                                                                                                                                                                                                            Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200120003-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10-SEP-1999;
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                                                                                                                                                                                                    Sus scrofa.
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                                                                                                                                                                       variant.
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Gaps

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1 HILTHKRILKFLHIFGSLLPRPSFLYKTIQDLGIGTFRDLA 41

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Gellin J,
                   WPI; 2001-244810/25.
N-PSDB; AAD03319.
                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
nes 40; Conserv
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Iannuccelli N,
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                                                                                    myopathy
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                                     Prediction of the property of the prediction of the present sequence of the present sequence is not set to the present sequence is not set to the present sequence is not shown in the specification, but note: The present sequence is not shown in the specification, but is derived from the present sequence is not shown in the specification, but is derived from the present sequence is not shown in the specification, but is derived from the porcine Prkag3 sequence shown in Fig 2 (AAE00220).
                                                                                                                                                                                                                                                                                                                                                              Pig; gamma subunit; adenosine monophosphate-activated kinase; AMPK; PKKAG3; diabetes; obesity; myopathy; cardiovascular disease; anorectic; genetic testing; carbohydrate metabolism disorder; skeletal muscle;
         a genetic polymorphic marker linked to a sequence encoding PRKAG3, are useful for detecting a dysfunction of carbohydrate metabolism resulting from the expression of a functionally altered allele of PRKAG3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Robic A, Rogel-Gaillard C;
 preferably a carbohydrate metabolism disorder. Primers that can detect
                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                              cystathione beta synthase; CBS; cardiant; gene therapy; RN locus; chromosome 15.
                                                                                                                                                                                                                                                                                                                                          Pig AMPK gamma subunit muscle-specific isoform, complete PRKAG3.
                                                                                                                                                                                6
                                                                                                                                                          Length 305;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           172..225
/label- CBS
/note= "Cystathione beta synthase domain"
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/note= "Cystathione beta synthase domain"
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/note= "Cystathione beta synthase domain"
400..453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "Cystathione beta synthase domain"
                                                                                                                                                                                0; Indels
                                                                                                                                                                                                               136 HILTHKRLLKFLHIFGTLLPRPSFLYRTIQDLGIGTFRDLA 176
                                                                                                                                                                                                    1 HILTHKRLLKFLHIFGSLLPRPSFLYRTIQDLGIGTFRDLA 41
                                                                                                                                                          Score 210; DB 22;
Pred. No. 7.8e-23;
1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Milan D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "RN- mutation site"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                            AAE00222 standard; Protein; 464 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kalm E,
                                                                                                                                                          Match 98.6%;
Local Similarity 97.6%;
les 40; Conservative
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18-MAY-2000; 2000EP-0401388.
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                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .307
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                                                                                                                                      305 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Misc-difference
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                                                                                                                                                                                                                                                                                                                      13-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                               Sus scrofa
                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                 AAE00222:
                                                                                                                                                          Query Match
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                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                        RESULT 10
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The present sequence is pig adenosine monophosphate (AMP)-activated kinase (AMPK) gamma subunit muscle-specific isoform, complete PRKAG3. Prkag3 gene is located in the RN locus of chromosome 15. Mutation in Prkag3 gene is located in the RN locus of carbohydrate metabolism, particularly in skeletal muscle. PRKAG3 is useful as therapeutic for treating carbohydrate metabolism disorders such as diabetes, obesity, and disorders associated with muscle metabolism such as myopathy and cardiovascular diseases, to modulate AMPK activity, and for restoring a normal AMPK function. PRKAG3 sequence and its functionally altered mutants are useful for the diagnostic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                useful for defecting a dysfunction of carbohydrate metabolism resulting from the expression of a functionally altered allele of PRKAG3.

Transgenic animal and host cell transformed with PRKAG3 or a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     heterotrimeric AMPK consisting of PRKAG3 or its mutant, are useful for screening compounds able to modulate AMPK activity. Nucleic acid encoding PRKAG3 is useful for detecting mutations in a Prkag3 gene, or in a sequence encoding the first cystathione beta synthase (CBS) domain of PRKAG3 and is useful in gene therapy.
                                                                                                                                                                              New variants of the gamma subunit of vertebrate adenosine monophosphate-activated kinase for diagnosis or treatment of disorders associated with energy metabolism such as diabetes, obesity, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                evaluation, genetic testing and prognosis of a metabolic disorder, preferably a carbohydrate metabolism disorder. Primers that can detect a genetic polymorphic marker linked to a sequence encoding PRRAG3, are
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single nucleotide polymorphism (SNP)"
200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 210; DB 22;
Pred. No. 1.3e-22;
1; Mismatches 0;
Le Roy P, Chardon P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                         Claim 5; Fig 3; 71pp; English.
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Screening animals to determine those likely to produce larger litters and improved meat quality traits involves assaying for the presence of polymorphisms in the AMP activated protein kinase regulatory gamma
                                                                                                                                                                                                                                                                                                                                                          The invention relates to a method for screening animals to determine those more likely to produce large litters and improved meat quality traits. The method involves assaying for the presence of a genotype in the sample of genetic material obtained from animal. The genotype is characterised by polymorphism(s) in the AMP activated protein kinase regulatory gamma subunit (PRRAG3) gene. The method is used for screening animals e.g., pigs to determine those most likely to exhibit improved meat quality traits and to produce larger litters. The present sequence is pig PRRAG3 polymorphic variant (PRRAG3-30).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AMP activated protein kinase reguiatory gamma subunit; PRKAG3 gene; screening; meat quality; single nucleotide polymorphism; SNP; pig;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "Wild type Gly is substituted with Ser due to single nucleotide polymorphism (SNP)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 HILTHKRLLKFLHIFGSLLPRPSFLYRTIQDLGIGTFRDLA 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rothschild MF, Ciobanu DC, Malek M, Plastow G;
                                                                                                                      Malek M, Plastow G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 210; DB 23;
Pred. No. 1.3e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pig PRKAG3 polymorphic variant (PRKAG3-52).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                      Disclosure; Page 91-93; 109pp; English.
                                                                                (IOWA ) UNIV IOWA STATE RES FOUND INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1;
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                                                                                                                      Ciobanu DC,
08-SEP-2000, 2000US-231045P.
08-JAN-2001, 2001US-260239P.
18-JUN-2001, 2001US-299111P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10-SEP-2001; 2001WO-US28283.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-SEP-2000; 2000US-231045P.
08-JAN-2001; 2001US-260239P.
18-JUN-2001; 2001US-299111P.
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                                                                                                                                                               WPI; 2002-393850/42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Misc-difference 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 464 AA;
                                                                                                                                                                                  N-PSDB; AAD36457
                                                                                                                      Rothschild MF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200220850-A2
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08-JAN-2001;
                                                                                                                                                                                                                                                                                 subunit gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sus scrofa.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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                                                                                                                                                                                                                                                                                                                                                            Screening animals to determine those likely to produce larger litters and improved meat quality traits involves assaying for the presence of polymorphisms in the AMP activated protein kinase regulatory gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       those more likely to produce large litters and improved meat quality traits. The method involves assaying for the presence of a genotype in the sample of genetic material obtained from animal. The genotype is characterised by polymorphism(s) in the AMP activated protein kinase regulatory gamma subunit (PRRAG3) gene. The method is used conscreening animals e.g., pigs to determine those most likely to exhibit improved meat quality traits and to produce larger litters. The present sequence is pig wild-type PRRAG3 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a method for screening animals to determine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AMP activated protein kinase regulatory gamma subunit, PRKAG3 gene, screening; meat quality, single nucleotide polymorphism; SNP; pig,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "Wild type Asn is substituted with Thr due to single nucleotide polymorphism (SNP)"
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 HILTHKRLLKFLHIFGSLLPRPSFLYRTIQDLGIGTFRDLA 41
                                                                                                                                                                                                                                                            Malek M, Plastow G;
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 210; DB 23;
Pred. No. 1.3e-22;
1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pig PRKAG3 polymorphic variant (PRKAG3-30).
                                                                                                                                                                                                                         (IOWA ) UNIV IOWA STATE RES FOUND INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAE22985 standard; Protein; 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 2; Fig 1; 109pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98.6%;
                                                                                                                                        08-SEP-2000; 2000US-231045P.
                                                                                                                                                             08-JAN-2001; 2001US-260239P. 18-JUN-2001; 2001US-299111P.
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                                                                                                 10-SEP-2001; 2001WO-US28283
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                    WO200220850-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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Query Match

Matches

RESULT 12 AAE22985

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Gaps

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Length 464;

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Location/Qualifiers
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                                                                                                                                                                                                     98.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                      Query Match 98.6
Best Local Similarity 97.6
Matches 40; Conservative
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                                                                                                                                                                               464 AA;
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Misc-difference
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subunit gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sus scrofa.
                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                       RESULT 15
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                                                Screening animals to determine those likely to produce larger litters and improved meat quality traits involves assaying for the presence of polymorphisms in the AMP activated protein kinase regulatory gamma
                                                                                                                                                  those more likely to produce large litters and improved meat quality traits. The method involves assaying for the presence of a genotype in the sample of genetic material obtained from animal. The genotype is characterised by polymorphism(s) in the AMP activated protein kinase regulatory gamma subunit (PRRAG3) gene. The method is used for screening animals e.g., pigs to determine those most likely to exhibit improved meat quality traits and to produce larger litters. The present sequence is pig PRRAG3 polymorphic variant (PRRAG3-52).
                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                       The invention relates to a method for screening animals to determine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AMP activated protein kinase regulatory gamma subunit, PRKAG3 gene;
screening; meat quality; single nucleotide polymorphism; SNP; pig;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "Wild type Val is substituted with Ile due to single nucleotide polymorphism (SNP)"
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                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                              295 HILTHKRLLKFLHIFGTLLPRPSFLYRTIQDLGIGTFRDLA 335
                                                                                                                                                                                                                                                                                                                                                1 HILTHKRLLKFLHIFGSLLPRPSFLYRTIQDLGIGTFRDLA 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Malek M, Plastow G;
                                                                                                                                                                                                                                                                                            Score 210; DB 23;
Pred. No. 1.3e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pig PRKAG3 polymorphic variant (PRKAG3-199).
                                                                                                                                                                                                                                                                                                                     1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (IOWA ) UNIV IOWA STATE RES FOUND INC.
                                                                                                              Claim 36; Page 96-97; 109pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                        AAE22987 standard; Protein; 464 AA
                                                                                                                                                                                                                                                                                            98.68;
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2001US-299111P.
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                                                                                                                                                                                                                                                                                                                        40; Conservative
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          WPI; 2002-393850/42.
N-PSDB; AAD36458.
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Best Local Similarity
                                                                                                                                                                                                                                                                       464 AA;
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                                                                                       subunit gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sus scrofa.
                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAE22987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        variant
                                                                                                                                                                                                                                                                                                                       Matches
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Screening animals to determine those likely to produce larger litters and improved meat quality traits involves assaying for the presence of polymorphisms in the AMP activated protein kinase regulatory gamma
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                                                                     The invention relates to a method for screening animals to determine those more likely to produce large litters and improved meat quality traits. The method involves assaying for the presence of a genotype in the sample of genetic material obtained from animal. The genotype is characterised by polymorphism(s) in the AMP activated protein kinase regulatory gamma subunit (PRKAG3) gene. The method is used for screening animals e.g., pigs to determine those most likely to exhibit improved meat quality traits and to produce larger litters. The present sequence is pig PRKAG3 polymorphic variant (PRKAG3-199).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "Wild type Arg is substituted with Gln due to single nucleotide polymorphism (SNP)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pig PRKAG3 polymorphic variant (PRKAG3-200).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Mismatches
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Disclosure; Page 100-102; 109pp; English.
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OM protein - protein search, using sw model

6, 2003, 10:58:29; Search time 2.65674 Seconds
(without alignments)
1483.588 Million cell updates/sec June Run on:

213 1 HILTHKRLLKFLHIFGSLLP.....PSFLYRTIQDLGIGTFRDLA 41 US-09-826-581-6_COPY_320_360 Perfect score:

Scoring table:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283224 seqs, 96134422 residues Searched:

283224 Total number of hits satisfying chosen parameters:

length: 0 length: 2000000000 Minimum DB seq Maximum DB seq

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
1: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	crip	AMP-activated prot	othetical p		hypothetical prote	conserved hypothet	alpha-2-antiplasmi	hypothetical prote	hyri	probable membrane	alpha-2-antiplasmi	histone acetyltran	ABC transporter, p	prot		Ω	hypothetical prote	coproporphyrinogen	hypothetical prote	afub (AE006182) [i	ABC transporter, m	acetolactate synth	hypothetical prote	Ψ	hypothetical prote	ഗ		hypothetical prote		chemotaxis protein
		075	T25899	37	T26720	H82145	ITHUA2	T39029	S52924	267067	S43977	S61980	E87536	S46088	T18227	C64677	A71838	AG0368	D90032	F97601	AG2823	53	an a	0	\sim	F82302	m	a)	T36787	7593
	DB	5	7	~									7	7	7	7	7					C)	7						7	7
	ength	330	478	379	1270	516	491	269	305	619	492	557	371	527	629	205	234	309	373	564	564	583	202	295	412	470	160	160	181	1402
dР	ry	. ~	45.5	ď.	ů.	w.	ń	'n.	٠.	·	, 57	٠	<u>.</u>	₹.	₹.	'n.	23.9	m.	ς.	m.	ω.	m.	٣.	۳.	m,	ς.	e.	ε.	æ.	e,
	Score			63	S		₹.			2	52.5	52	٠	51.5		51	51	51	51	51	51	S	50.5	ö	0	0	50	20	20	20
	Result No.	1	7	3	7	S	٥	7	80	თ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

transporter [impor	hypothetical prote	hypothetical prote	one of two inverse	hypothetical prote	interleukin-1 rece	hypothetical prote	hypothetical prote	3-isopropylmalate	F9L1.2 protein - A	single-strand-DNA-					
690496	T23142	A05037	H90483	H72603	AC1527	C61213	G64175	T02620	T24334	G02512	A85096	S47285	H75373	E86284	A70485
7	7	~	7	7	7	7	7	7	7	7	7	ď	N	7	7
487	1579	2136	109	150	206	224	304	442	486	712	1039	146	177	290	538
23.2	23.2	23.2	23.0	23.0	23.0	23.0	23.0	23.0	23.0	23.0	23.0	22.8	22.8	22.8	22.8
5.5	49.5	49.5	49	49	49	49	49	49	49	49	49	48.5	48.5	48.5	48.5
4															

ALIGNMENTS

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Appropries: Rattus novegicus (Norway rat)
C;Species: Rattus novegicus (Norway rat)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 21-Jul-2000
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 21-Jul-2000
C;Accession: T1075
C;Accession: T1078
C;Arities: Characterization of AMP-activated protein kinase beta and gamma subunits: A A;Title: Characterization of AMP-activated protein kinase beta and gamma subunits: A A;Reference number: 206738; MUID:96215327; PMID:8626596
A;Accession: T10759
A;Coss-references: EMBL:X95578; NID:91185270; PIDN:CAA64831.1; PID:91185271
C;Complex: heterotrimer; alpha, beta and gamma chains
C;Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A:Description: is responsible for the regulation of fatty acid synthesis by phosphor C;Superfamily: CAT3 protein
C:Keywords: fatty acid biosynthesis; phosphotransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
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A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-478 AMIL>
A;Residues: 1-478 AMIL>
A;Cross-references: EMBL: U97550; PIDN: AAB52856.1; GSPDB: GN00028; CESP: T20F7.6
A;Experimental source: strain Bristol N2; clone T20F7
A;Genetics:
A;Genetics:
A;Map position: X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein T20F7.6 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-oct-1999 #sequence_revision 15-oct-1999 #text_change 18-Feb-2000
C;Accession: T25899
R;Miller, N.; Gattung, S.
Submitted to the EMBL Data Library, April 1997
A;Description: The sequence of C. elegans cosmid T20F7.
A;Reference number: 220107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Introns: 33/3; 112/2; 144/1; 205/3; 263/2; 300/3; 380/3; 402/2; 451/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
AMP-activated protein kinase (EC 2.7.1.-) gamma chain - rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 HILTHKRLLKFLHIFGSLLPRPSFLYRTIQDLGIGTFRDLA 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 52.6%; Score 112; DB 2; L Best Local Similarity 46.3%; Pred. No. 5.7e-08; Matches 19; Conservative 14; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 2
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A,Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic p
A,Reference number: A82950; MUID:20437337; PMID:10984043
A.Accession: F83641
A,Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Species: Pseudomonas aeruginosa
C; Date: 10-sep-1999 #sequence_revision 10-sep-1999 #text_change 31-Dec-2000
C; Accession: S53924; F985641
R; Hungerer, C.; Troup, B.; Jahn, D.
submitted to the EMBL Date Library, February 1995
A; Description: Cloning and requiation of the Pseudomonas aeruginosa hemF gene encodi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-305 HUN>
A; Residues: 1-305 HUN>
A; Cross references: EMBL:X85015; NID:9747872; PIDN:CAA59376.1; PID:9695693
A; Cross references: EMBL:X85015; NID:9747872; PIDN:CAA59376.1; PID:9695693
R; Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.;
Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            coproporphyrinogen oxidase (EC 1.3.3.3) oxygen-dependent - Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Residues: 1-269 <OEV>
A; Cross-references: EMBL: Z69731; PIDN: CAB40280.1; GSPDB: GN00066; SPDB: SPAC6C3.05
A; Experimental source: strain 972h-; cosmid c6C3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein SPAC6C3.05 - fission yeast (Schizosaccharomyces pombe) C,Species: Schizosaccharomyces pombe C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Devlin, K.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V. submitted to the EMBL Data Library, February 1996
                                                                                                   Gaps
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                                                                                              Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             216 IKTHYKTWLRIHTFLTLFPVPSVLSSNLKKOMYGWFEDL 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         40
                                                                                              15;
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                                                                                                                                                                                                                                                      128 TLQRLQQVLHA-GSGPCLPHLLSRLCQDLGPGAFR 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 ILTHKRLLKFLHIFGSLLPRPSFLYRTIQDLGIGTFRDL
                                                                                                                                                                               4 THKRLLKFLHIFGSLLPRPSFLYRTIQDLGIGTFR 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Accession: T39029
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 54; DB :
Pred. No. 6.9;
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3; Mismatches
                                                    Pred. No. 11;
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C;Superfamily: coproporphyrinogen oxidase
C;Reywords: oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A, Experimental source: strain PAO1 C, Genetics:
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36.8%;
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35.9%;
                                               48.68;
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Matches 14; Conservative
                                          Best Local Similarity 48.6
Matches 17; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Reference number: 221750
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Matches 14; Conserva
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A; Residues: 1-305 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Genetics:
A;Gene: SPDB:SPAC6C3.05
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Accession: T39029
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Map position:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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A; Molecule type: mRNA
A; Mossiques: 184-491 cSUNA
A; Mossiques: 218-491 cSUNA
A; Cross-references: DbbJ:D00116; NID:9219407; PIDN:BAA00070.1; PID:9219408
B; Koyama, T.; Kolke, Y.; Toyota, S.; Miyagl, F.; Suzuki, N.; Aoki, N.
B; Koyama, T.; Kolke, Y.; Toyota, S.; Miyagl, F.; Suzuki, N.; Aoki, N.
B; Koyama, T.; Kolke, Y.; Toyota, S.; Miyagl, F.; Suzuki, N.; Aoki, N.
B; Kochem: Dabphys, Ress. Commun. 200, 417-422, 1994
A; Title: Different NH2-terminal form with 12 additional residues of alpha2-plasmin inhite
A; Receive number: PC2129; MUID:94220119; PMID:8166714
A; Residues: 28-53 KKOV>
A; Residues: 28-53 KKOV>
A; Rosidues: 28-53 KKOV>
A; Reference number: S00068; MUID:872946; PMID:2446081
A; Reference number: S00068; MUID:872946; PMID:2446081
A; Rosidues: 40-46, 76, 56-574, 1987
A; Rosidues: 40-46, 76, 50-104, 70, 106-114, 72, 116-327, 72, 7329-340, 72xxxz, 735-407, 76, 409-4068-76, 50-104, 70, 50-104, 70, 106-114, 72, 116-327, 72, 7329-340, 72xxxz, 735-407, 76, 409-406-6068; MUID:9729496; PMID:98484741
A; Rosidues: 28-58 CBAN
A; Rosidues: 28-
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J. Biol. Chem. 261, 15591-15595, 1986
A; Filte: cross-linking site in fibrinogen for alpha-2-plasmin inhibitor.
A; Reference number: A92565; MUID:87057190; PMID:2877981
A; Reference annotation; cross-linking site for fibrin
C; Comment: After synthesis in the liver, 30-50% of alpha-2-antiplasmin circulates in pla inhibit activated coagulation factor XIII from forming an isopeptide cross-link with fi
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A;Contents: annotation; role of propeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25.6%; Score 54.5; DB 1; Length 491;
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A;Introns: 21/3; 34/3; 55/3; 123/1; 171/1; 239/1; 286/3; 355/1
C;Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A.Note: determination of cleavage and inhibitory sites R;Sumi, Y.; Ichikawa, Y.; Nakamura, Y.; Miura, O.; Aoki, N. J. Blochem. 106, 703-707, 1989
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A.Cross-references: GDB:120301; OMIM:262850
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A, Molecule type: protein
A, Residues: 28-43;64-69;405-409 <ENG>
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C; Genetics:

Query Match

us-09-826-581-6_copy_320_360.rpr

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24.4%;
37.9%;
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25.6%;
Ouery Match 24.6%;
Best Local Similarity 47.2%;
Matches 17; Conservative
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es 11; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                        C; Accession: S61980
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Best Local
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                                                                                                               δλ
                                                                                                                                                                            by Dobble membrane protein YOR175c - yeast (Saccharomyces cerevisiae)

N.Alternate names: hypothetical protein 03635
C;Species: Saccharomyces cerevisiae
C;Date: 12-uul-1996 #sequence_revision 12-Jul-1996 #text_change 19-Apr-2002
C;Accession: S67067; S67063
R;Hudjes, B.; Poll, T.M.
submitted to the Protein Sequence Database, July 1996
A;Reference number: S66685
A;Residues: 1-619 <HUG>
A;Rolecule type: DNA
A;Residues: 1-619 <HUG>
A;Reperimental source: strain S288C
A;Experimental source: strain S288C
A;Experimental source: strain S288C
A;Experimental source: Strain S288C
A;Residues: 270-619
A;Residues: 270-619
A;Residues: S7003
A;Residues: S7005
A;Cross-references: SGD:S0005701
A;Residues: Tansmembrane #status predicted <TM1>
F;461-477/Domain: transmembrane #status predicted <TM2>
F;461-477/Domain: transmembrane #status predicted <TM2>
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R.Christensen, S.; Sotrup-Jensen, L.
FEBS Lett. 312, 100-104, 1992
A.Title: Bovine alpha(2)-antiplasmin. N-terminal and reactive site sequence.
A; Reference number: S27260; MUID:93050153; PMID:1385210
A; Accession: S27260
A; Molecule type: protein
A; Residues: 23-27, 70', 29-39' P', 41-42', E', 44-45; 374-415 <CH2>
C; Superfamily: antithrombin III
C; Keywords: glycoprotein
F; 1-22/Domain: signal sequence #status predicted <SIG>F; 1-22/Domain: signal sequence #status predicted <SIG>F; 1-3442/Product: alpha-2-antiplasmin #status predicted <MAT>F; 71-144/Disulfide bonds: #status experimental
F; 71-144/Disulfide bonds: #status experimental
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C;Species: Bos primigenius taurus (cattle)
C;Date: 20-oct-1994 #sequence_revision 19-May-1995 #text_change 16-Jul-1999
C;Accession: S43977; S27260
R;Christensen, S.; Berglund, L.; Sottrup-Jensen, L.
R;Christensen, S.; Berglund, L.; Sottrup-Jensen, L.
R;Christensen, S.; Berglund, L.; Sottrup-Jensen, L.
A;Title: Primary structure of bovine alpha-2-antiplasmin.
A;Reference number: S43977; MUID:94229242; PMID:7513654
A;Accession: S43977
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A: Residues: 1-492 <CHR>
A: Cross-references: GB:X78436; NID:9498821; PIDN:CAA55200.1; PID:9498822
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5 HKRLLKFL---HIFGSLLPRPSFLYRTIQD~LGIGTFRDL 40
                                    34
        --RPSFLYRTIQDLGI
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Pred. No. 2
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42.5%;
        LTHKRLLKFLHIFGSLLP-
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Best Local Similarity 42.55
Matches 17; Conservative
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R;Wang, Y.; Ahmed, A.; Bussey, H.; Fortin, N.; Friesen, J.D.; Hall, J.; Storms, R.K.; submitted to the EMBL Data Library, December 1995
A;Description: The sequence of Saccharomyces cerevisiae chromosome XVI left arm.
A;Reference number: S61959
A;Accession: S61980
A;Accession: S61980
A;Residues: 1-557 < WAN>
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R. Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Hetdelberg, B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; K. n. J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C. Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A; Title: Complete Genome Sequence of Caulobacter crescentus.
A; Reference number: A87249; MUID:21173698; PMID:11259647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABC cransporter, permease protein, probable CC2318 [imported] - Caulobacter crescentu C:Species: Caulobacter crescentus C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Cross-references: EMBL: U43281; NID: 91151218; PIDN: AAB68213.1; PID: 91151240; GSPDB: C
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                                                                                                                                                                                                                                                                                                        histone acetyltransferase (EC 2.3.1.48), RNA polymerase II-associated [validated]
N;Alternate names: protein LPG22c; protein YPL086c
C;Species: Saccharomyces cerevisiae
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Length 492;
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                                                                                                                                              C;Superfamily: hypothetical protein YPL086c
C;Keywords: acyltransferase; coenzyme A; transcription
                                                       14;
                                                                                                              4 THKRLLKFLHI-FGSLLPRPSFLYRTIQDLGIGTFR 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2;
DB 2;
                                                       2; Mismatches
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29;
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Score 52.5; Pred. No. 22;
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Pred. No.
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A, Cross-references: SGD:S0006007
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Search completed: June 6, 2003, 11:03:38 Job time: 4.65674 secs
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Nypothetical protein YBR214w - yeast (Saccharomyces cerevisiae)
NyAlternate names: hypothetical protein YBR1501
C.Species: Saccharomyces cerevisiae
C.Species: Saccharomyces cerevisiae
C.Species: Saccharomyces cerevisiae
C.Species: Saccharomyces cerevisiae
C.Saccession: S46088; S46090
R.Rieger. M.
R.Rieger. M.
A.Reference number: S45734
A.Reference: Saccession: S46083; NID:9536599; PIDN:CAA85178.1; PID:9536600; MIPS:YBR214w
A.Reperimental source: strain S288c
A.Experimental sources: strain S286c
A.Ex
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C;Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 11-Jan-2000
C;Accession: C64677
R;Tomb J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D. Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenne Son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujli, C.; Bowman, C.; Watthey, L. Nature 388, 539-547, 1997
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A;Note: Ca41C10.01c
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(Species: Candida albicans
(Species: Candida albicans)
(Species: Candida
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Pred. No. 40;
7; Mismatches 14; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: DNA
A;Residues: 114-527 <DUB>
A;Cross-references: EMBL:236083; MIPS:YBR214w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A:Experimental source: strain S288C C;Genetics:
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38.9%;
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A;Accession: S46090
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A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser A;Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A;Reference number: A64520; MuID:97394467; PMID:9252185
A;Accession: C64677
A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA
A;Coss-references: GB:AE000631; GB:AE000511; NID:92314421; PIDN:AAD08305.1; PID:923
C;Superfamily: conserved hypothetical protein b1120
Query Match
Best Local Similarity 37.8%; Pred. No. 13;
Matches 14; Conservative 6; Mismatches 9; Indels 8; Gaps 2;
Mismatches 14; Conservative 6; Mismatches 9; Indels 8; Gaps 2;
C)
Cy 10 KFLHIFGSLL----PRESTURTIQDLGIGTFRDLA 41
FILLIBELLSVRSEXDPNLYYRNEXDLAG--DLA 108
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213
1 HILTHKRLLKFLHIFGSLLP......PSFLYRTIQDLGIGTFRDLA 41
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SUMMARIES	ID	- 14	AAKI_PIG	AAKH_HUMAN	AAKG_BOVIN	AAKG_MOUSE	AAKG_RAT	AAKG_HUMAN	AAKG_PIG	A2AP_HUMAN	YD55_SCHPO	HEM6_PSEAE	SZ6L_HUMAN	A2AP_BOVIN	YB64_YEAST	HEM6_YERPE	ITAE_MOUSE	ABD4_MOUSE	YCF2_MARPO	LST_HAEIN	IRA1_HUMAN	UVRA_CHLTR	SUIS_RAT	Y786_METJA	YD07_HAEIN	MTD1_YEAST	Y4ME_RHISN	CATA_PEA	LCRF_YERPE	VIRF_YEREN	ATTY_RAT	CDB2_HUMAN	CRAA_TRIIN	BRB1_HUMAN
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EMBL; AJ249977; CAB65117.1; ALT_INIT. EMBL; AF214519; AAF73987.1; -.

014678 homo sapien 020273 patersonia 036052 patersonia 036052 patersonia P73467 synechocyst P36597 schizosacch P38386 mycobacteri 034676 bacillus su 098qd8 mycoplasma Q921y5 helicobacte P56452 helicobacte P56580 saccharomyc P47653 mycoplasma		e, gamma-3 subunit (AMPK gamma-3 chain) Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.	i., Carling D.; ise gamma-subunit	Robic A., Thelander M., Rask L., Ronne H., ., Le Roy P., Chardon P.,	utation in PRKAG3 associated with excess glycogen content in pig etal muscle."; nce 288:1248-1251(2000). EVENTION: AMPK IS RESPONSIBLE FOR THE REGULATION OF FATTY ACID SYNTHESIS BY PHOSPHORYLATION OF ACETYL.COA CARBOXYLASE. ALSO REGULATES CHOLESTEROL SYNTHESIS VIA PHOSPHORYLATION AND INACTIVATION OF HYDROXYMETHYLGLUTARYL.COA REDUCTASE AND HORMONE- SENSITIYPE LIPPASE. THIS IS A REGULATORY SUBBULT. IT MAY PLAY A ROLE IN THE REGULATION OF ENERGY METABOLISM IN SKELETAL MUSCLE. SUBBULT: HEPEROTRIMER OF EN A ALPHA CATALYTIC SUBUNIT, A BETA AND A	ORY SUBUNITS. L MUSCLE, WITH WEAK EXPRESSION IN HEART 5'-AMP-ACTIVATED PROFEIN KINASE, GAMMA DOMAINS.
ABD4_HUMAN RR4_PATER RR4_PATES YC23_SYNY3 TH13_SCHPO SEC_MYCLE YODO_BACSU EFG_MYCPU SYA_HELPJ SYA_HELPJ SYA_HELPJ YA14_MYCGE	ALIGNMENTS PRI; 464 AA. ed; ed; anotation update) annotation update)	Ø	in.A. 049; PubMed=10698692; Salt I.P., Davies S.P., Hardie D.G., tion of AMP-activated protein kinase their role in AMP binding."; 46:659-669(2000).	318001; C., Amarger V., Iannuccelli N.,	ANGERSON D.; Ametation in PRKAG3 associated with excess glycogen content in parkelstal muscle."; Science 288:1248-1251(2000). Science 288:1248-1251(2000). STATHESIS AME IS RESPONSIBLE FOR THE REGULATION OF FATTY ACID SYNTHESIS BY PHOSPHORYLATION OF ACETYL.COA CARBOXYLASE. REGULATES CHOLESTEROL SYNTHESIS VIA PHOSPHORYLATION AND INACTIVATION OF HYDROXYMETHYLGIUTARYL.COA REDUCTASE AND HORWON SENSITYED LIPASE. THIS IS A REGULATORY SUBBUNIT. IT MAY PLAY A IN THE REGULATION OF ENERGY METABOLISM IN SKELETAL MUSCLE1. SUBBUNIT: HFTEROYRIMBR OF AN ALPHA CATALYTIC SUBBUNIT, A BETA AN	TORY SUBUNI AL MUSCLE, 5'-AMP-ACT DOMAINS.
606 1844 1966 1966 1346 1346 171 1047 1036 1038 1036 1036 1036	STANDARD; 11.40, Created) 1.40, Last seq	protein kinase, man) oa; Chordata; Cra ia; Primates; Cat	M N.A. 4049; PubMed=10698 Salt I.P., Davies ation of AMP-activ their role in AMP 346:659-669(2000).	scle; PubMed=10 T., Looft Paul S.,	AG3 assoc 251(2000) IS RESPC HOSPHORYI FE HYDROXY SE THIS ION OF EN	GAMMA NON-CATALYTIC REGULAY TISSUE SPECIFICITY: SKELETY AND PANCREAS. SIMILARITY: BELONGS TO THE SUBUNIT FAMILY. SIMILARITY: CONTAINS 4 CBS.
21.6 21.6 21.6 21.6 21.6 21.6 21.6 21.6	t STA NRL1; 11 (Rel.) 11 (Rel.)	-activated p gamma3). OR AMPKG3. apiens (Huma Ota; Metazoa ia; Eutheria	FROM N.A. 20164049; C., Salt arization and their J. 346:65	ROM N.A. sletal mu 1280150; Jeon J llard C.,	ISSON L.; utation in PRKAG3 etal muscle."; nce 288:1244-1251(PUNCTION: AMPR IS EVNTION: AMPR IS EVNTION: AMPR IS ENGILATES CHOLESTE INACTIVATION OF HY SENSITIVE LIPASE. IN THE REGULATION SUBUNIT: HETEROTRI	GAMMA NON-CATALYTIC TISSUE SPECIFICITY: AND PANCREAS. SIMILARITY: BELONGS SUBUNIT FAMILY.
0 0 4 4 4 4 4 4 9 9 9 9 9 9 9 9 9 9 9 9	LT 1 HUMAN S AAKI_HUMAN S QUGI9; Q9NRL1; 16-OCT-2001 (Rel 16-OCT-2001 (Rel 16-OCT-2001 (Rel	5'-AMP-activated protein kina (AMPK gamma3). PRKAG3 OR AMPKG3. HOMO sapiens (Human). Enkaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;	UENCE LINE=Z ung P. aracte forms chem.	[2] SEQUENCE FROM N.A. TISSUE-Skeletal muscle; MEDLINE-20280150; Pubmed-10818001; Milan D., Jeon JT., Looft C., Am Rogel-Gaillard C., Paul S., Iannuc Lundstreem K., Reinsch N., Gellin	Anderson L. Anderson L. Skeletal muo Science 288 -!- FUNCTION REGULATII INACTIVI SENSITII IN THE IN	GAMMA 1 -!- TISSUE AND PAI -!- SIMILAI SUBUNIT
80000000000000000000000000000000000000	RESULT 1 AAKI_HUMAN ID AAKI_ AC Q9UGI DT 16-OC DT 16-OC	OCC		RN RP RC TR RA RA R		

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RECULATES CHOLESTEROL SYNTHESIS VIA PHOSPHORYLATION AND
INACTIVATION OF HYDROXYMETHICHGUTARKL-COA REBUCTAGE AND HORMONE-
SENSITIVE LIPAGE. THIS IS A REGULATORY SUBBUIT. IT MAY PLAY A ROLE
IN THE REGULATION OF BERGY METABOLISM IN SKELETAL MUSCLE.
-!- SUBBUNT: HETEROTRIMER OF AN ALPHA CATALYTIC SUBUNIT, A BETA AND A
GAMMA NON-CATALYTIC REGULATORY SUBUNITS.
-!- TISSUE SPECIFICITY: MUSCLE.
-!- DISEASE: DEFECTS IN PRKAG3 (RN-) ARE ASSOCIATED WITH EXCESS
GLYCOGEN CONTENT (ABOUT 70%) IN SKELETAL MUSCLE. THIS MUTATION
ORIGINATED IN THE HAMPSHIRE BREED PIGS AND HAS BENEFICIAL EFFECTS
ON MEAT COMPTENT BUT DETRIMENTAL EFFECTS ON PROCESSING YIELD. THUS,
THIS MUTATION IS OF CONSIDERABLE ECONOMIC SIGNIFICANCE IN THE PIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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                                                                                                                                                                                                                                                                                                                                                      16-OCT-2001 (Rel. 40, Created)
Loct-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
5'-AMP-activated protein kinase, gamma-3 subunit (AMPK gamma-3 chain)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Milan D., Jeon J.-T., Looft C., Amarger V., Robic A., Thelander M., Rogel-Gaillard C., Paul S., Iannuccelli N., Rask L., Ronne H., Lundstroem K., Reinsch N., Gellin J., Kalm E., Le Roy P., Chardon P.,
                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "A mutation in PRKAG3 associated with excess glycogen content in pig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FUNCTION: AMPK IS RESPONSIBLE FOR THE REGULATION OF FATTY ACID
                                                                                                                                                                                                                                                                                                                                                                                                                      Sus scrofa (Pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
NCBI_TaxID=9823;
                                                                                                                                                                                                                    ;
                                                                                                                                                                                            Score 213; DB 1; Length 464; Pred. No. 2.1e-21; 0; Mismatches 0; Indels (
                                                                                                                      T -> A (IN REF. 1).
MQ -> IE (IN REF. 1).
Q -> K (IN REF. 1).
ALGA -> PSGPEKI (IN REF. 1).
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                                                                                                                                                                                                                                                          295 HILTHKRLLKFLHIFGSLLPRPSFLYRTIQDLGIGTFRDLA 335
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SEQUENCE FROM N.A., AND VARIANT RN(-) GLN-200.
                                                            Repeat; CBS domain.
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MEDLINE-20280150; PubMed-10818001;
                       InterPro; IPR000644; CBS_domain.
Pfam; PF00571; CBS; 4.
SWART; SM00116; CBS; 4.
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356 CE
428 CE
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398 Q
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51514 MW;
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                                                                                                                                                                                                          100.0%;
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                                                                                                                                                                                                                      41; Conservative
  HGNC:9387; PRKAG3.
                                                             Fatty acid biosynthesis;
DOMAIN 147 201
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              MIM; 604976;
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modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lang T., Yu L., Qiang T., Jiang J., Chen Z., Xin Y., Liu G., Zhao S.; "Molecular cloning, genomic organization, and mapping of PRKAG2, a heart abundant gamma-2 subunit of 5'-AMP-activated protein Kinase, to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9UGJO; Q9UDN8; Q9NUZ9; Q9ULX8; 16-OCT-2001 (Rel. 40, Created) | LoCT-2001 (Rel. 40, Last sequence update) | L5-UN-2002 (Rel. 41, Last annotation update) | S'-AMP-activated protein Kinase, gamma-2 subunit (AMPK gamma-2 chain) | AMPK gamma-2 (AMPK gamma-2 chain)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-20164049; PubMed=10698692;
Cheung P.C.F., Salt I.P., Davies S.P., Hardie D.G., Carling D.;
"Characterization of AMP-activated protein kinase gamma-subunit
Isoforms and their role in AMP binding.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                        biosynthesis; Repeat; CBS domain; Disease mutation. 172 - 226 \\
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 210; DB 1; Length 464;
Pred. No. 5.4e-21;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              295 HILTHKRLKKFLHIFGTLLPRPSFLYRTIQDLGIGTFRDLA 335
                                                                                                                                                                                                                                                                                                                                                                                                                                     17638CB12A2BA9DF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 HILTHKRLLKFLHIFGSLLPRPSFLYRTIQDLGIGTFRDLA 41
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                                                                                                                                                                                                                                                                                                                     CBS 2.
CBS 3.
CBS 4.
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MEDLINE~20564210; PubMed=11112354;
                                                                                                                                              EMBL; AF214520; AAF73988.1; -.
InterPro; IPR000644; CBS_domain.
Pfam; PF00571; CBS; 4.
SMART; SM00116; CBS; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. (ISOFORM B).
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                                                                                                                      EMBL; AF214521; AAF73989.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                           51308 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 98.65
Best Local Similarity 97.65
Matches 40; Conservative
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SIMILARITY: CONTAINS 4 CBS DOMAINS.
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P58108;
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PRKAG1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GAMMA NON-CATALYTIC REGULATORY SUBBULTS.

-!- ALTERNATIVE PRODUCIS: 2 ISOFORMS; A (SHOWN HERE) AND B; ARE PRODUCED BY ALTERNATIVE SPLICING.
-!- TISSUE SPECIFICITY: ISOFORM B IS UBLOUITOUSLY EXPRESSED EXCEPT IN LIVER AND THYMUS. THE HIGHEST LEVEL IS DETECTED IN HEART WITH ABUNDANT EXPRESSION IN PLACENTA AND TESTIS.
-!- DISEASE: Defects in PRRAG2 are the cause of Wolff-Parkinson-White
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ognono cause of paroxysmal superventricular techyoardia. WPMS can be associated with a form of hypertrophic cardiomyopathy (HCM), which is probably due to polysaccharide storage in the heart. Defects in PRRAG2 may not be a frequent cause of HCM where no features of pre-excitation are found in affected individuals. SIMILARITY: BELONGS TO THE 5'-AMP-ACTIVATED PROTEIN KINASE, GAMMA
                                                                                                                                                                                                        MEDLINE-21264334; PubMed-11371514; Medbulle-21264334; PubMed-11371514; Medbulle X. Redwood C., Ashrafian H., Oliveira M., Broxholme J., Rerr B., Salmon A., Osetman-Smith I., Watkins H.; Salmon the gamma(2) subunit of AMP-activated protein kinase cause familial hypertrophic cardiomyopathy; evidence for the central role of energy compromise in disease pathogenesis."; for the central Hum. Mol. Genet. 10:1215-1220(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      syndrome (WPWS or preexcitation syndrome). It is the second most
                                                                                         MEDLINE-21614537; PubMed-11748095; Sollob M.H., Seger J.J., Gollob T.N., Tapscott T., Gonzales O., Bachinski L., Roberts R. "Novel PRKAG2 mutation responsible for the genetic syndrome of
                                                                                                                                                                                                                                                                                                                                                                                                                                            Gollob M.H., Green M.S., Tang A.S.-L., Gollob T., Karibe A., Ala Sayegh A.H., Ahmad F., Lozado R., Shah G., Fananapazir L., Bachinski L.L., Roberts R.; New Engl. J. Med. 345:552-552(2001).
                                                                                                                                            ventricular preexcitation and conduction system disease with
                                                                                                                                                                                                                                                                                                                          MEDLINE-21279949; PubMed-11407343; GOLLOB M.H., Green M.S., Tang A.S.-L., Gollob T., Karibe A., Al Sayegh A.H., Ahmad F., Lozado R., Shah G., Fananapazir L., Bachinski L.L., Roberts R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gollob T., Karibe A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gollob M.H., Green M.S., Tang A.S.-L., Gollob T., Karibe A Al Sayegh A.H., Ahmad F., Lozado R., Shah G., Fananapazir Bachinski L.L., Roberts R., Bachinski L.L., Roberts R., New Engl. J. Med. 346:300-300(2002).
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
                                     Walker C., Scott K., Bauer C., Harkins R.;
Submitted (WAR-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                        childhood onset and absence of cardiac hypertrophy."; Circulation 104:3030-3033(2001).
                                                                                                                                                                                                                                                                                                                                                                             "Identification of a gene responsible for familial
                    SEQUENCE OF 254-569 FROM N.A.
Walker C., Scott K., Bauer C., Harkins R.;
                                                                                                                                                                                               VARIANTS HCM/WPWS LEU-350 INS AND ARG-383.
                                                                                                                                                                                                                                                                                                                                                                                          Wolff-Parkinson-White syndrome.";
New Engl. J. Med. 344:1823-1831(2001).
                                                                                                                                                                                                                                                                                                               VARIANT WPWS GLN-302
                                                                            VARIANT WPWS GLY-531
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SUBUNIT FAMILY

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16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last and the sequence of the second the second (Rel. 40, Last and the second th
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fatty acid biosynthesis; Repeat; CBS domain; Alternative splicing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ASPTHYAPSKAAALAA -> MLIAVLLLPLRRRWRR
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R -> G (IN WPWS; ABSENCE OF CARDIAC HYPERTROPHY; ONSET IN CHILDHOOD).
/FIId=VAR_013269.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -> RL (IN FAMILIAL HCM WITH WPWS;
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T -> N (IN WPWS WITH CARDIAC
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N -> I (IN WPWS WITH CARDIAC
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CBS 2.
CBS 3.
CBS 4.
MISSING (IN ISOFORM B).
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13; Mismatches
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EMBL; AF087875; AAK00413.1; -.
EMBL; AK001887; BAA91962.1; -.
EMBL; BC025640; AAH20540.1; -.
EMBL; AB025580; BAA84695.1; -.
EMBL; AC006966; AAF03528.1; -.
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Pfam; PF00571; CBS; 4.
SMART; SM00116; CBS; 4.
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   SUBUNIT: HETEROTRIMER OF AN ALPHA CATALYTIC SUBUNIT, A BETA AND A
                                GAMMA NON-CATALYTIC REGULATORY SUBUNITS.
SIMILARITY: BELONGS TO THE 5'-AMP-ACTIVATED PROTEIN KINASE, GAMMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5'-AMP-activated protein kinase, gamma-1 subunit (AMPK gamma-1 chain)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Métazoa; Chórdata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Characterization of AMP-activated protein kinase beta and gamma subunits. Assembly of the heterotrimeric complex in vitro."; J. Biol. Chem. 271:10282-10290(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 48-330 FROM N.A., AND PARTIAL SEQUENCE.
STRAIN-Spraque-Dawley; TISSUE-Liver;
MEDLINE-95050763; PubMed-7961907;
Stapleton D., Gao G., Michell B.J., Widmer J., Mitchelhill K.,
Teh T., House C.M., Witters L.A., Kemp B.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=Sprague-Dawley; TISSUE=Liver;
MEDLINE-96224074; PubMed-8621499;
MEDLINE-96224074; PubMed-8621499;
MEDLINE-96224074; PubMed-8621499;
MOO G., Fernandez C.S., Stappleton D., Auster A.S., Widner J.,
Dyck J.R.B., Kemp B.E., Witters L.A.;
"Non-catalytic beta- and gamma-subunit isoforms of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-96215327; PubMed-8626596;
Woods A., Cheung P.C.F., Smith F.C., Davison M.D., Scott J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 330;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Score 112; DB 1; Length 33; Pred. No. 7.3e-08; 12; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               D504707B83512DDC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 HILTHKRLLKFLHIFGSLLPRPSFLYRTIQDLGIGTFRDLA 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MGD; Moll. CBS; 4.

Pfam; PF00571; CBS; 4.

R SMRT; SM0116; CBS; 4.

W Fatty acid blosynthesis; Repeat; CBS domain.

FT DOMAIN 122 176 CBS 1.

CMAIN 122 176 CBS 2.

TOMAIN 122 176 CBS 2.

TOWAIN 122 176 CBS 3.

TOWAIN 124 CBS 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              330 AA.
                                                                                                                             -!- SIMILARITY: CONTAINS 4 CBS DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5'-AMP-activated protein Kinase.";
J. Biol. Chem. 271:8675-8681(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AF036535; AAB95475.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-FEB-1995 (Rel. 31, Created)
01-NOV-1997 (Rel. 35, Last sequ
16-OCT-2001 (Rel. 40, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              52.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 48.88
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Beri R.K., Carling D.;
                                                                                         SUBUNIT FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-Wistar;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAKG_RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (AMPKg).
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ID AAKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACCOCCOS OCCOS OCC
   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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0
                                                                                                                                                                                                                                      SYNTHESIS BY PHOSPHORYLATION OF ACETYL-COA CERBOXYLASE. ALSO REGULATES CHOLESTEROL SYNTHESIS VIA PHOSPHORYLATION AND INACTIVATION OF HYDROXYMETRYLGLUTARKI. COA REDUCTASE AND HORMONE-SENSITIVE LIPASE. THIS IS A REGULATORY SUBUNIT.
SUBUNIT: HETEROTRIMER OF AN ALPHA CATALYTIC SUBUNIT, A BETA AND A
                                                                                                                                                                                                                                                                                                                                                                                                        GAMMA NON-CATALYTIC REGULATORY SUBUNITS.
SIMILARITY: BELONGS TO THE 5'-AMP-ACTIVATED PROTEIN KINASE, GAMMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
5'-AMP-activated protein kinase, gamma-1 subunit (AMPK gamma-1 chain)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Cloning, organisation, chromosomal localization and expression
analysis of the mouse Prkagl gene.";
Cytogenet. Cell Genet. 92:134-138(2001).
-!- FUNCTION: AMPK IS RESPONSIBLE FOR THE REGULATION OF FATTY ACID
SYNTHESIS BY PHOSPHORYLATION OF ACETYL-COA CARROXILASE. ALSO
REGULATES CHOLESTERED. SYNTHESIS YIA PHOSPHORYLATION AND
INACTIVATION OF HYDROXYMETHYLGLUTARYL-COA REDUCTASE AND HORMONE-
                                                              SEQUENCE FROM N.A.
Benkel B., Kollers S., Fries R., Sazanov A., Yoshida E., Davoren J.,
                                                                                                                                                 "Characterization of the bovine AMPK gamma-1 gene.";
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: AMPK IS RESPONSIBLE FOR THE REGULATION OF FATTY ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 330;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7401 cm., 52.6%; Score 112; DB 1; Le 46 3%; Pred. No. 7.3e-08; 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fatty acid biosynthesis; Repeat; CBS domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               330 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SIMILARITY: CONTAINS 4 CBS DOMAINS.
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CBS 3.
CBS 4.
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MEDLINE-21203559; PubMed=11306812;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AF329081; AAK19307.1; -.
InterPror; IPR0006644; CBS_domain.
Pfam; PF00571; CBS; 4.
SMART; SM00116; CBS; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                37481 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                177
250
323
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            330 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBUNIT FAMILY
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PRKAG1 OR PRKAAC.
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NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   123
197
271
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAKG_MOUSE
054950;
                                                                                                                             Hickey D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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Biol. Chem. 271:8675-8681(1996).
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                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
            homologs of proteins that interact with yeast Snf1 protein Kinase.";
J. Biol. Chem. 269:2943-29346(1994).
-!- FUNCTION: AMPK IS RESPONSIBLE FOR THE REGULATION OF FATTY ACID
SYNTHESIS BY PHOSPHOKYLATION OF ACETYL.COA CARBOXYLASE. IT ALSO
REGULATES CHOLESTEROL SYNTHESIS VIA PHOSPHORYLATION AND
INACTIVATION OF HORMONE-SENSITIVE LIPASE AND
HYDROXYMETHYLGJUTARYL.COA REDUCTASE. APPEARS O ACT AS A METABOLIC
STRESS-SENSING PROTEIN KINASE SWITCHING OFF BIOSYNTHETIC PATHWAYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-96224074; PubMed-8621499; Gao G., Fernandez C.S., Stapleton D., Auster A.S., Widmer J., Gycy J.R.B., Kemp B.E., Witters L.A.; "Non-catalytic beta-and gamma-subunit isoforms of the 5'-AMP-activated protein kinase.";
                                                                                                                                                                                                                                     -1- SUBUNIT: HETEROTRIMER OF AN ALPHA CATALYTIC SUBUNIT; A BETA AND A GAMMA NON-CATALYTIC REGULATORY SUBUNITS.
-1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN HEART AND BRAIN, ALSO FOUND IN KIDNEY, WHITE ADIPOSE TISSUE, LUNG AND SPLEEN.
-1- SIMILARITY: BELONGS TO THE 5'-AMP-ACTIVATED PROTEIN KINASE, GAMMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-1996 (Rel. 34, Created)
UOCT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
5'-AMP-activated protein kinase, gamma-1 subunit (AMPK gamma-1 chain)
"Mammalian 5'-AMP-activated protein kinase non-catalytic subunits are
                                                                                                                                                                                WHEN CELLULAR ATP LEVELS ARE DEPLETED AND WHEN 5'-AMP RISES IN RESPONSE TO FUEL LIMITATION AND/OR HYPOXIA. THIS IS A REGULATORY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               52.6%; Score 112; DB 1; Length 330; 46.3%; Pred. No. 7.3e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    36031E526C1F1E97 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     164 YILTHKRILKFLKLETTEFPKPEFMSKSLEELQIGTYANIA 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 HILTHKRLLKFLHIFGSLLPRPSFLYRTIQDLGIGTFRDLA 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8;

    Patty acid biosynthesis; Repeat; CBS domain.

    DOMAIN
    47
    95
    RCBS 1.

    DOMAIN
    122
    176
    CBS 2.

    DOMAIN
    196
    249
    CBS 3.

    DOMAIN
    270
    322
    CBS 4.

    CONFLICT
    114
    E -> Q (IN REF. 3).

    CONFLICT
    201
    A -> P (IN REF. 3).

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                   -! - SIMILARITY: CONTAINS 4 CBS DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR000644; CBS_domain.
Pfam; PF00571; CBS; 4.
SMART; SM00116; CBS; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      37386 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X95578; CAA64831.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U42413; AAC52580.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Fetal liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      330 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                           SUBUNIT FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAKG HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-95050763; PubMed-7961907;
Stapleton D., Gao G., Michell B.J., Widmer J., Mitchelhill K.,
Stapleton D., Gao G., Michell B.J., Kemp B.E.;
Teh T., House C.M., Witters L.A., Kemp B.E.;
"Mammalian 5'-Amy-activated protein kinase non-catalytic subunits are homologs of proteins that interact with yeast Snfl protein kinase.";
J. Biol. Chem. 269:23943-2394(1994).
-1. FUNCTION: AMPK IS RESPONSIBLE FOR THE REGULATION OF FAUTY ACID SYNTHESIS BY PHOSPHORYLATION OF ACETYL. COA CARBOXXLASE. ALSO
                                                                                                                                                                                                                         INACTIVATION OF HYDROXYMETHYLGLUTARYL-COA REDUCTASE AND HORMONE-SENSITIVE LIPASE. THIS IS A REGILATORY SUBUNIT.
SUBUNIT: HETENOTRIMER OF AN ALPHA CATALYTIC SUBUNIT, A BETA AND A GAMMA NON-CATALYTIC REGILATORY SUBUNITS.
SIMILARITY: BELONGS TO THE 5'-AMP-ACTIVATED PROTEIN KINASE, GAMMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-FEB-1995 (Rel. 31, Last sequence update)
LoCT-2001 (Rel. 40, Last annotation update)
5'-AMP-activated protein Kinase, gamma-1 subunit (AMPK gamma-1 chain)
(AMPK9) (38 kDa subunit) (Fragments).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                           Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: AMPK IS RESPONSIBLE FOR THE REGULATION OF FATTY ACID
SYNTHESIS BY PHOSPHORYLATION OF ACETYL-COA CARBOXYLASE. ALSO
REGULATES CHOLESTEROL SYNTHESIS VIA PHOSPHORYLATION AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sus scrofa (Pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 331;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OF22B9CAlDBD87AE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 165 YILTHKRILKFLKLFITEFPKPEFMSKSLEELQIGTYANIA 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 HILTHKRLLKFLHIFGSLLPRPSFLYRTIQDLGIGTFRDLA 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                52.6%; Score 112; DB 1; Le 46.3%; Pred. No. 7.3e-08; 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fatty acid biosynthesis; Repeat; CBS domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          133 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SIMILARITY: CONTAINS 4 CBS DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CBS 1.
CBS 2.
CBS 3.
CBS 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000644; CBS_domain.
Pfam; PF00571; CBS; 4.
SMART; SM00116; CBS; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; BC000358; AAH00358.1; -. Genew; HGNN:9385; PRKAGI.
MIM; 602742; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-FEB-1995 (Rel. 31, Created)
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Best Local Similarity 46.3%
Matches 19; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                 SUBUNIT FAMILY
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9823;
                                                                  Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rissue=Liver;
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UNOV-1990 (Rel. 16, Last sequence update)
15.JUN-2002 (Rel. 41, Last annotation update)
Alpha-2-antiplasmin precursor (Alpha-2-plasmin inhibitor) (Alpha-2-PI)
REGULATES CHOLESTEROL SYNTHESIS VIA PHOSPHORYLATION AND INACTIVATION OF HYDROXYMETHYLGIUTARYL-COA REDUCTASE AND HORMONE-SENSITIVE LIPASE. THIS IS A REGULATORY SUBUNIT.
SUBUNIT: HETEROTRIMER OF AN ALPHA CAPALYTIC SUBUNIT, A BETA AND A GAMMA NON-CATALYTIC REGULATORY SUBUNITS.
SIMILARITY: BELONGS TO THE 5'-AMP-ACTIVATED PROTEIN KINASE, GAMMA
                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tone M., Kikuno R., Kume-Iwaki A., Hashimoto-Gotoh T.; "Structure of human alpha 2-plasmin inhibitor deduced from the CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 4-491 FROM N.A.
MEDLINE-87109313; PubMede-2431286;
Holmes W.E., Welles L., Lijnen H.R., Collen D.;
"Primary structure of human alpha 2-antiplasmin, a serine protease inhibitor (serpin).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                   7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDINE-88320531; Pubmed=3166140;
Hirosawa S., Nakamura Y., Miura O., Sumi Y., Aoki N.;
"Organization of the human alpha 2-plasmin inhibitor gene.";
Proc. Natl. Acad. Sci. U.S.A. 85:6836-6840(1988).
                                                                                                                                                                                                                                                             30.3%; Score 64.5; DB 1; Length 133; 31.7%; Pred. No. 0.076; ive 13; Mismatches 8; Indels 7
                                                                                                                                                                                                                                            14763 MW; 84C0C3D41E845CEF CRC64;
                                                                                                                                                                                                                                                                                                               YILTXK-----LFITEFPKPEFMSKSLEELQIGTYANIA 70
                                                                                                                                                                                                                                                                                                    1 HILTHKRLLKFLHIFGSLLPRPSFLYRTIQDLGIGTFRDLA 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hirosawa S., Nakamura Y., Miura O., Sumi Y., Aoki N.;
Proc. Natl. Acad. Sci. U.S.A. 86:1612-1613(1989).
                                                                              Pfam: PF00571; CBS; 1.
SMART; SM00116; CBS; 1.
Fatty acid biosynthesis; Repeat; CBS domain.
NON_TER | 1 CRS 1
                                                                                                                                                                                                                                                                                                                                                                      491 AA.
                                                        SUBUNIT FAMILY.
-!- SIMILARITY: CONTAINS 4 CBS DOMAINS.
InterPro; IPR000644; CBS_domain.
                                                                                                                            4. c. ω. <del>4</del>.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=88139254; PubMed=2830248;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Biochem. 102:1033-1041(1987).
                                                                                                                                                                                                                                                                       Best Local Similarity 31.7
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                        SERPINE OR PLI OR AAP.
                                                                                                                                    >42
91
127
127
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74
81
95
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                                                                                                                                                                                                                                            133 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                              (Alpha-2-AP)
                                                                                                                                                                                                                                                                                                                                                                     A2AP_HUMAN
P08697;
                                                                                                                                                                NON_CONS
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NON_CONS
NON_CONS
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Christensen S., Sottrup-Jensen L.; "Bovine alpha 2-antiplasmin. N-terminal and reactive site sequence."; FEBS Lett. 312:100-104(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Miura O., Sugahara Y., Aoki N.;
Hereditary alpha 2-plasmin inhibitor deficiency caused by a
transport-deficient mutation (alpha 2-PI-Okinawa). Deletion of Glu137
by a trinucleotide deletion blocks intracellular transport.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TRYPSIN, BUT IT ALSO INACTIVATES CHYMOTRYPSIN.
-1- DISEASE: Defects in SERPINF2 are the cause of alpha-2-plasmin inhibitor deficiency, a disease resulting in severe hemorrhagic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lind B., Thorsen S.;
"A novel missense mutation in the human plasmin inhibitor (alpha2-antiplasmin) gene associated with a bleeding tendency.";
Br. J. Haematol. 107:317-322(1999).
-i- FUNCTION: THE MAJOR TARGETS OF THIS INHIBITOR ARE PLASMIN AND
                                                                                                                                                   Sumi Y., Nakamura Y., Aoki N., Sakai M., Muramatsu M.; "Structure of the carboxyl-terminal half of human alpha 2-plasmin inhibitor deduced from that of CDNA."; "J. Biochem. 100:1399-1402(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of
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Potempa J., Shieh B.-H., Travis J.;
"Alpha-2-antiplasmin: a serpin with two separate but overlapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 481-491, AND SULFATION.
MEDLINE-87137577; PubMed=2434496;
Hortin G., Fok K.F., Toren P.C., Strauss A.W.;
"Sulfation of a tyrosine residue in the plasmin-binding domain
                                                                                                                                                                                                                                                                                                                                                                                                                                     Lijnen H.R., Holmes W.E., van Hoef B., Wiman B., Rodriguez H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDINE-78023887; PubMed-21075; Wiman B., Collen D.; "Purification and characterization of human antiplasmin, the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Amino-acid sequence of human alpha 2-antiplasmin,";
Eur. J. Biochem. 166:565-574(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -! - SIMILARITY: BELONGS TO THE SERPIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         fast-acting plasmin inhibitor in plasma.";
Eur. J. Biochem. 78:19-26(1977).
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Biol. Chem. 262:1659-1664(1987).
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MEDLINE=20051147; PubMed=10583218;
                                                                     SEQUENCE OF 218-491 FROM N.A.
MEDLINE=87137400; PubMed=3818581;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=90036902; PubMed=2572590;
                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=87275946; PubMed=2440681;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=93050153; PubMed=1385210;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Science 241:699-700(1988).
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                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 40-491.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Plasma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     reactive sites
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EMBL; EMBL; EMBL;

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EMBL;

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REC MEDLINE-21848401; PubMed-11859360;
RA MEDLINE-21848401; PubMed-11859360;
RA WOOD V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA GOOLOS J., Peat N., Hayles J., Bakher S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Gonles S., Goble A., Hamilu N., Harris D., Hiddled J., Jagels K.,
Admes K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
Admes K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Joner K., O'Neil S., Pearson D., Quail M.A., Rabbinowitsch E.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Skelton J., Simmonds M., Squares R., Schaefer M., Mullerhead S.,
Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Gobel C., Fuchs M., Fritzc C., Holzer E., Mosell D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Lucas M., Rochet M., Gaillardin C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Lucas M., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Lucas M., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
Rhakosvoki G.V., Ussery D., Barrell B.G., Nurse P.,
Rhakosvoki G.V., Ussery D., Barrell B.G., Nurse P.,
Rhakos R., Revuelte J. Barrell B.G., Nurse P.,
Rhakos R., Revuelte J. Barrell B.G., Nurse P.,
Rhakosvoki G.V., Ussery D., Barrell B.G., Nurse P.,
Rhakosvoki G.V., Stepper R., Revuelte B., Revuelte B., Revuelte R., Revuelte R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pseudomonas aeruginosa.
Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25.4%; Score 54; DB 1; Length 269;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             l protein.
269 Aa; 31234 MW; 0C3DF87A138CA5BE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Coproporphyrinogen III oxidase, aerobic (EC 1.3.3.3)
(Coproporphyrinogenase) (Coprogen oxidase).
HEMF OR PA0024.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | | | : : | | : | | | | | | IKTHYKTWLRIHTFLTLFPVPSVLSSNLKKQMYGWFGDL 254
                    Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 ILTHKRLLKFLHIFGSLLPRPSFLYRTIQDLGIGTFRDL 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     305 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; Z69731; CAB40280.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     35.9%;
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Best Local Similarity 35.9
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                           Schizosaccharomyces
                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                        NCBI_TaxID=4896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pseudomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PSEAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P43898
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MISSING (VARIANT OKINAWA; IN ALPHA-2-
PLASMIN INHIBITOR DEFICIENCY; PROBABLY
BLOCKS INTRACELLULAR TRANSPORT OF ALPHA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Serpin; Serine protease inhibitor; Glycoprotein; Plasma; Signal; Sulfation; Polymorphism; Disease mutation.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -> G (IN REF. 6).
-> N (IN REF. 6).
385AlC90E91A63CB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2-PLASMIN INHIBITOR). /FTId=VAR_013254.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /FTId=vAR_013256.

L -> G (IN REF. 6).

N -> D (IN REF. 6).

H -> D (IN REF. 4).

S -> G (IN REF. 6).

D -> N (IN REF. 6).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 THKRLLKFLHIFGSLLPRPSFLYRTIQDLGIGTFR 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /FTId-VAR_013255.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /FTId=VAR_013252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /FTId=VAR_013253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical protein C6C3.05 in chromosome I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                269 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 54.5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ş.
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                                                    49 L
105 N
289 H
408 S
455 D
54565 MW;
                                                                                                                                                                                                                                                PIR; A24708; A24708.
PIR; A26684, A26684.
PIR; A31402, A31402.
PIR; A41504, A3163.
PIR; A41504, A41504.
PIR; S00068; S00068.
HSSP; O35684; JJJO.
SWISS-2DPAGE; P08697; HUMAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR000215; Serpin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00079; serpin; 1.
SMART; SM00093; SERPIN; 1.
PROSITE; PS00284; SERPIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genew; HGNC:9075; SERPINF2.
MIM; 262850; -
                          BAA00070.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 25.6
Best Local Similarity 48.6
Matches 17; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              176
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105
289
408
455
491 AA;
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                                                                                                                                                                  M20784;
M20785;
                                                                                                                                           M20783;
                                                                                                                                                                                                                         J02654;
                                                                                                        M20782;
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Q10308;
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Gaps ö

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CONFLICT

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Identification of a 428-kb homozygously deleted region disrupting the
                                                                                                                                                                                                Gaps
                                                                               SEQUENCE FROM N.A.

STRAIN=ATCZ 15692 / PAO1;

MEDLINE-ZO437337; Pubmed=10984043;

Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M. Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y., Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G. K.-S., Wu Z., Paulsen I.T., Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;

"Complete genome sequence of Pseudomonas aeruginosa PAO1, an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nishioka M., Kohno T., Takahashi M., Niki T., Yamada T., Sone S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Porphyrin biosynthesis; Oxidoreductase; Iron; Complete proteome.
SEQUENCE 305 AA; 34806 MW; 240BD06FEA37EAE3 CRC64;
SEQUENCE FROM N.A.
STRAIN-ATCC 15692 / PAO1;
Hungerer C., Troup B., Jahn D.;
"Cloning and regulation of the Pseudomonas aeruginosa hemF gene encoding oxygen-dependent coproporphyrinogen III oxidase.";
Submitted (FEB-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24.9%; Score 53; DB 1; Length 305; 36.8%; Pred. No. 6.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SZ6L_HUMAN STANDARD; PRT; 1024 AA.
Q9BYRH; Q9YZEI; Q9WIJ3; Q9WUI5; O95917; Q9Y3J6;
L15-UNN-2002 (Rel. 41, Created)
L15-UNN-2002 (Rel. 41, Last sequence update)
L15-UNN-2002 (Rel. 41, Last annotation update)
Seizure 6-like protein precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 LTHKRLLKFLHIFGSLLP-----RPSFLYRTIQDLGI 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF01218; Coprogen_oxidas; 1.
PRINTS; PR00073; COPRGNOXDASE.
PROSITE; PS01021; COPROGEN_OXIDASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X85015; CAA59376.1; -.
EMBL; AE004442; AAG03414.1; -.
InterPro; IPR001260; Coprogen_oxidas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. (ISOFORM 4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                36.88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PubMed=11175339;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Brain;
                                                                                                                                                                                                                                                                                            FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           70kota J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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RAY MUDLIANE-1091/105, Thomsde-1091/105, Bruskiewich R., Beare D.M.,

RA Dunham I., Hunt A.R., Collins J.E., Bruskiewich R., Beare D.M.,

RA Glamp W., Smink L.J., Ainscough R., Almeida J.P., Babbage A.K.,

Bagguley C., Baliey J., Bridgeman A.M., Buck D., Burgess J.,

RA Burrill W.D., Burtron J., Carder C., Callier R.E., Connor R.,

Conroy D., Corby W. R., Cole C.G., Collier R.E., Connor R.,

RA Glegg S.M., Cobley V.E., Cole C.G., Collier R.E., Connor R.,

RA Glegg S.M., Cobley W.E., Cole C.G., Collier R.E., Davson E.,

RA Glery J.C., R. Goward M.E., Grafham D.V., Griffiths M.N.D., Hall C.,

RA Glbert J.G.R., Goward M.E., Grafham D.V., Griffiths M.N.D., Hall C.,

RA Hult S.E., Jones M.C., Kershaw J., Kimberley A.M., King A.,

Rantyn I.D., Mashreqhi-Wohammadi M., Matthews L.H., Mccann O.T.,

RA Martyn I.D., Mashredhi-Wohammadi M., Matthews L.H., Mccann O.T.,

RA Martyn I.D., Mashredhi-Wohammadi M., Matthews L.H., Mccann O.T.,

RA Martyn I.D., Mashredhi-Wohammadi M., Matthews L.H., Mccann O.T.,

RA Martyn I.D., Mashredhi-Wohammadi M., Matthews L.H., Mccann O.T.,

RA Martyn I.D., Mashredhi-Wohammadi M., Matthews L.H., Mccann O.T.,

RA Martyn I.D., Mashredhi-Wohammadi M., Matthews L.H., Mccann O.T.,

RA Martyn I.D., Mashredhi-Wohammadi M., Matthews L.H., Mccann O.T.,

RA Martyn I.D., Mashredhi-Wohammadi M., Matthews L.H., Mccann O.T.,

RA Scott C.E., Sehra H.K., Skuce C.D., Smalley S., Smith M.L.,

RA Scott C.E., Sehra H.K., Skuce C.D., Smalley S., Smith M.L.,

RA Milliams J., Walliams S.A., Williamson H., Wilmer T.E., Wilming L.,

Williams J., Walliams S.A., Williamson H., Wilmer T.E., Wilming L.,

Ray Milliams J., Rawasaki K., Sasaki T., Asakwa S., Kudoh J.,

RA Mnoshima S., Kawasaki K., Sasaki T., Asakwa S., Kudoh J.,

RA Mnoshima S., Kawasaki K., Sasaki T., Asakwa S., Kudoh J.,

RA Mnoshima S., Kawasaki K., Sasaki T., Asakwa S., Kudoh J.,

RA Mnoshima S., Kawasaki K., Sasaki T., Asakwa S., Kudoh J.,

RA Wang C., Hubbard T., Benis S., Muray J., Milliandha D.,

Rannel B.S., Olis, Wang Y., Hu P., Hu B., Wallian M.,
                                                                                                                                                                                                                                                                       Nagase T., Ishikawa R.-I., Suyama M., Kikuno R., Hirosawa M., Miyajima N., Tanaka A., Kotahi H., Nomura N., Ohara O.; Prediction of the coding sequences of unidentified human genes. XIII. The complete sequences of 100 new cDNA clones from brain which code
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"A genomic screen for genes upregulated by demethylation and histone deacetylase inhibition in human colorectal cancer.";
Nat. Genet. 31:141-149(2002).
-!- FUNCTION: Candidate tumor suppressor gene.
-!- ALTERNATIVE PRODUCTS: 4 isoforms; 1, 2, 3 and 4 (shown here);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Collins J.E., Huckle E.J.;
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
SEZ6L gene at 22q12.1 in a lung cancer cell line."; Oncogene 19:6251-6260(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "The DNA sequence of human chromosome 22.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
                                                                                                                                                                                                                             MEDLINE=99246063; PubMed=10231032;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. MEDLINE=20057165; Pubmed=10591208;
                                                                                                                                               SEQUENCE FROM N.A. (ISOFORM 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                           large proteins in vitro.";
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GENE EXPRESSION REGULATION.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA Res. 6:63-70(1999).
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Tilahun Y., Wright H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Fetal brain;
Collins J.E., Huckle
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NCBI_TaxID=9913;
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A2AP_BOVIN
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                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
ED (GLCNAC...) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                Repeat; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                          EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                            CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                 SEIZURE 6-LIKE PROTEIN.
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N-LINKED (GLCNAC...
                                                                                                                                                           EMBL; AB0031736; BAB40970.1; -.
EMBL; AL03544; BAA76771.2; ALT INIT.
EMBL; AL035545; CAB37431.1; ALT_INIT.
EMBL; AL03513; CAB43355.1; ALT_INIT.
EMBL; AL023513; CAB72345.1; -.
EMBL; AL023513; CAB72345.1; -.
EMBL; AL023513; CAB72347.1; ALT_SEQ.
Genew; HGNC:10763; SEZ6L.
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SUSHI 3.
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MISSING
                                                                                                                                                                                                                                 MIM; 607021; -...
HISSP: P28392; 1SFP.
InterPro; IPR000059; CUB_domain.
InterPro; IPR000436; Sushi_SCR_CCP.
Pfam; PF000431; CUB; 2.
SMART; SM00032, CCP; 5.
SWART; SM00042; CUB; 3.
FROSITE; PS01180; CUB; 3.
SIGNAL; Transmenbrane; Sushi; Repeat; SIGNAL; Transmenbrane; Sushi; Repeat; SIGNAL
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SUSHI 5.
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                                                                                                                                                                                                                                                                                             5
                                                         ISOFORM 2)
IMYCTDPGEVDHSTRLISDPVLLVGTTIQYTCNPGFVLEGS
SLLTCYSRETGTPIWTSRLPHCVS -> T (IN ISOFORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-DEC-1992 (Rel. 24, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-JUN-2002 (Rel. 41, Last and the sequence update)
Alpha-2-antiplasmin precursor (Alpha-2-plasmin inhibitor) (Alpha-2-PI)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Christensen S., Sottrup-Jensen L.; "Bovine alpha 2-antiplasmin. N-terminal and reactive site sequence."; "Bovine alpha 2-antiplasmin. N-terminal and reactive site sequence."; FEBS Lett. 312:100-104(1992).
- FUNCTION: THE MAJOR TRRGETS OF THIS INHIBITOR ARE PLASMIN AND TRYPSIN, BUT IT ALSO INACTIVATES CHYMOTRYPSIN.
-:- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
                                                                                                                                                                                                                                                                                                Gaps
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SERPINF2 OR PLI.
BOS tautus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
MISSING (IN ISOFORM 2).
ETREYEVSI -> GTQKV (IN ISOFORM 1 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ALPHA-2-ANTIPLASMIN.

REACTIVE BOND (FOR PLASMIN).

REACTIVE BOND (FOR CHYMOTRYPSIN).

SULFATION (BY SIMILARITY.

N-LINKED (GLONAC. . .) (POTENTIAL).

N-LINKED (GLONAC. . .) (POTENTIAL).
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                                                                                                                                                                                                                                                                                                ..
8
                                                                                                                                                                                                                                Score 53; DB 1; Length 1024;
Pred. No. 24;
9; Mismatches 10; Indels
                                                                                                                                                                             1024 AA; 111781 MW; CBC0679E22C23B6E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                        347 VLANQTLL----VEGQVIRSPINTISVYFRIFQDDGLGTFQ 383
                                                                                                                                                                                                                                                                                                                                                       2 ILTHKRLLKFLHIFGSLLPRP----SFLYRTIQDLGIGTFR 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Christensen S., Berglund L., Sottrup-Jensen L.; "Primary structure of bovine alpha 2-antiplasmin."; FEBS Lett. 343:223-228(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. MEDLINE=94229242; PubMed=7513654;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Plasma;
MEDLINE=93050153; PubMed=1385210;
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SEQUENCE OF 23-45 AND 374-410.
                                                                                                                                                                                                                                      24.9%;
34.1%;
                                                                                                                                                                                                                                      Query Match 24.9
Best Local Similarity 34.1
Matches 14; Conservative
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                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dubois E., el Bakkoury M., Glansdorff N., Messenguy F., Pierard A., Scherens B., Vierendeels F.; Submitted (AuG-1994) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: TO YEAST YGLOSGC AND S.POMBE SDS23.
   N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
T -> Q (IN REF. 2).
Q -> P (IN REF. 2).
Q -> E (IN REF. 2).
Q -> E (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
NCBI_TaxID=4932;
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                                                                                                                                                            3;
                                                                                                                                                                                                                                                                                               YB64_YEAST STANDARD; PRT; 527 AA.
93314,
01-0CT-1994 (Rel. 30, Created)
01-0CT-1994 (Rel. 30, Last sequence update)
Hypothetical 57.2 kba protein in MET8-HFC2 intergenic region.
YBR214M OR YBR1501.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 24.2%; Score 51.5; DB 1; Length 527; Best Local Similarity 42.1%; Pred. No. 19; Matches 16; Conservative 6; Mismatches 9; Indels
                                                                                                                              Score 52.5; DB 1; Length 492; Pred. No. 13; 2; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rieger M.;
Submitted (AUG-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         527 AA; 57187 MW; DC2741550A69C154 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 ILTHKRLLKFL----HIFGSLLPRPSFLYRTIQDLGIG 35
                                                                                                                                                                                                             129 TLQRLKEVLHADSGPCLPH--LLSRLCQDLGPGAFR 162
                                                                                                                                                                                           4 THKRLLKFLHI-FGSLLPRPSFLYRTIQDLGIGTFR 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein; Repeat; CBS domain. DOMAIN 196 251 CBS 1. DOMAIN 283 335 CBS 2.
                                                                                                                                                                                                                                                                                                                                                                                                          Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; 236083; CAA85178.1; -.
PIR; S46088; S46088.
SGD; S0000418; SDS24.
InterPro: IPR000644; CBS_domain.
Pfam; PF00571; CBS; 4.
296 N
310 N
317 28
40 Q
43 Q
43 Q
54710 MW;
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                                                                                                                                            Local Similarity 47.2 les 17; Conservative
                                                                                                 492 AA;
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                                                                                CONFLICT
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CARBOHYD
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                                     CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-21470413; PubMed=11586560; Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G., Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G., Prentice M.B., Sebaihia M., James K.D., Churcher C., Mungall K.L., Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M., Chillingworth T., Cronin A., Davies R.M., Davis P., Douqan G., Feltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.; Genome sequence of Yersinia pestis, the causative agent of plague."; Nature 413:523-527(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -i- CATALYTIC ACTIVITY: Coproporphyrinogen-III + O(2) = protoporphyrinogen-IX + 2 CO(2).
-i- COFACTOR: Iron (By similarity).
-i- PATHWAY: POTPHYRIN blosynthesis.
-i- SUBCELLUIAR LOCATION: Cytoplasmic (By similarity).
-i- SUMILARITY: BELONGS TO THE AEROBIC COPROPORPHYRINOGEN III OXIDASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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PROSITE; PS01021; COPROGEN.OXIDASE; 1.
POTPHYIN blosynthesis: Oxidorductase; Iron; Complete proteome.
SEQUENCE. 309 AA, 3504 MW; A3DEZ59C4C3714D9 CRC64;
                                                                                                                                                                                                                                                                                         Versinia pestis.
Bacteria; Proteobacteria; gamma subdivísion; Enterobacteriaceae;
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                                                                                                                                            15-JUN-2002 (Rel. 41, Last annotation update)
Coproporphyrinogen III oxidase, aerobic (EC 1.3.3.3)
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                                                                                                              15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23.9%; Score 51; DB 34.4%; Pred. No. 13; tive 6; Mismatches
                                                                                                                                                                                                                 (Coproporphyrinogenase) (Coprogen oxidase)
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                                                                        5-JUN-2002 (Rel. 41, Created)
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HEM6_YERPE
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(without alignments)
1589.904 Million cell updates/sec
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213
1 HILTHKRLLKFLHIFGSLLP......PSFLYRTIQDLGIGTFRDLA 41
                                                                                                                         June 6, 2003, 10:58:04; Search time 5.31349 Seconds
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Gapop 10.0 , Gapext 0.5
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1: sp_archea:*
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3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp_vertebrate:*
sp_unclassified:*

sp_plant:*
sp_rodent:*
sp_virus:*

sp_rvirus:*
sp_bacteriap:*

sp_archeap:*

sp_mammal:*
sp_mhc:*
sp_organelle:*
sp_phage:*

SUMMARIES

	Description	Q91wg5 mus musculu	Q9bhl6 caenorhabdi	Q9vdd2 drosophila	096613 drosophila	Q8sxt8 drosophila	Q8szs7 drosophila	002168 caenorhabdi	Q9n501 caenorhabdi	Q91tp2 tupaia herp	Q8ssv7 dictyosteli	Q41108 phaseolus v	Q95nr8 caenorhabdi	062462 caenorhabdi	Q9kqx3 vibrio chol	008329 bacillus st	Q9bv31 homo sapien
	a	Q91WG5	овнт6	Q9VDD2	096613	Q8SXT8	088287	002168	-		-				Q9KQX3		Q9BV31
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	Query Match Length DB	266	372	634	647	906	1400	423	448	1055	577	379	1268	1270	516	798	71
æ	Query	58.2	51.6	49.3	49.3	49.3	49.3	45.5	39.4	31.0	30.8	29.6	26.3	26.3	26.1	25.8	25.4
	Score	124	110	105	105	105	105	97	84	99	65.5	63	99	26	55.5	55	54
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0993d1 homo sapien 090tt2 homo sapien 0976%2 sulfolobus 984g1 streptomyce 0854g saccharomyce 085917 homo sapien 095917 homo sapien 094y3 homo sapien 094y2 homo sapien 094y2 homo sapien 094y4 homo sapien 094y4 homo sapien 096d2 homo sapien 096d3 homo sapien 099d0 homo sapien 099d1 homo sapien 099d1 homo sapien 099d1 arabidopsis 09a59 caulobacter 094035 candida alb 093v15 oryza sativ 091vv3 arabidopsis 091vv3 arabidopsis	eleost rinae; 566;	AA. : update) on update)
4 0993D1 4 098TT2 2 09AFG1 2 09AFG1 3 098548 4 095917 4 0993J6 4 09Y3J6 4 09Y3J6 4 09Y3J6 4 09Y2J6 4 09PE1 11 08R4F9 11 08R4F9 11 08R4F9 4 09PEF 4 09PEF 6 09PE 7 08PEQ1 6 09PEQ1 7 09PEQ1 8 09PEQ1 10	The same of the sa	PRT; 372 , Created) , Last sequence
255.4 257.4 25	PRELIMINARY; 2001 (TrEMBLEEL. 19, Cz 2002 (TrEMBLEEL. 21, Lz 2002 (TrEMBLEEL. 21, Lz tical 63.0 kDa protein culus (Mouse). ta; Metazoa; Chordata; ax Metazoa; Chordata; xxD=10090; E FROM N.A. KIDNEX; erg R.: 2001) to the Ex C015283; AAH15283.1; c0; IPRO00644; CBS_doma; co; TREMOME44; CBS_doma; by Similarity 51.28; lical protein. E 566 AA; 62997 MW; h 58.28; Similarity 51.28; lical conservative 13; lill 1 HILTHKRILKFLHIFGSLLP	PRELIMINARY; (TrEMBLrel. 17 (TrEMBLrel. 17
117 554 554 554 554 554 555 555 555 555 55	SULT 1 1905 091905 091905 01-DEC-2001 (TrEMBLre) 01-DEC-2001 (TREMBLre) 01-DEC-2001 (TREMBLre) 01-DUN-2002 (TREMBLre) Hypothetical 63.0 kDa Mus musculus (Mouse). Eukaryota; Metazoa; Cl Mammalia; Eutheria; R NCBI_TAXID=10090; [1] SEQUENCE FROM N.A. TISSUE-KIDNEY; Strausberg R.; Strausberg R.; Strausberg R.; Strausberg R.; FROUGA4; Pfam; PFOO571; CBS; 4 Hypothetical protein. SEQUENCE 56 AA; 6 Query Match Best Local Similarity Matches 21; Conservat 1 HILTHRRILKFL. 1 HILTHRRILKFL. 1 HILTHRRILKFL.	$\sigma\sigma$
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Adams M.D., Celniker S.E., Hill R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
An K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
Ballew R.M., Basu A., Barxendelle J., Bayraktaroglu L., Beasley E.M.,
Ballew R.M., Basu A., Barman B.P., Bhandari D., Bolshakov S.,
Beson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
Berkoya D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
R.B. Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
Dodson K., Doup L.E., Downes M., Digan-Rocha S., Dunkov B.C., Dunn P.,
R.A. Godoriellan A.E., Garg N.S., Gelbart W.M., Glasser K.,
Antolek A., Gong F., Gorrell J.H., We Z., Kennison J.A., Ketchum K.A.,
R. Harris N.L., Harvey D., Heinan T.J., Wei M.-H., Ibegwam C.,
Alalin M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
B. Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
Liang Y., Lin X.,
Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
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Bakaryota, Metazoa, Arthropoda; Tracheata; Hexapoda; Insecta;
Pterrygota; Neoptera; Endopterrygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                         Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
                                                                                                                                                                                                                                                                                                                                                                   ;
                                                                                                                                                                                                                                                                                                                                        Length 372;
                                                                                                                                                                                                       'Genome sequence of the nematode C.elegans: A platform for
                                                                                                                                                                                                                                                                                                                                                                   9; Indels
                                                                                                                               Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                         372 AA; 41376 MW; 81A39670877167DF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                               1 HILTHKRLLKFLHIFGSLLPRPSFLYRTIQDLGIGTFRDL 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                   Query Match 51.6%; Score 110; DB 5; Best Local Similarity 52.5%; Pred. No. 3.4e-07; Matches 21; Conservative 10; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    634 AA.
                                                         Rhabditidae; Peloderinae; Caenorhabditis.
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                                                                                                                                                                          MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                   investigating biology.", Science 282:2012-2018 (1998). EMBL; ALI32904; CAC35836.1: InterPro; IPR000644; CBS_domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                     Pfam; PF00571; CBS; 4.
SMART; SM00116; CBS; 4.
SEQUENCE 372 AA: 413
                      Caenorhabditis elegans.
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 Y111B2A.8 protein.
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                                                                                                  SEQUENCE FROM N.A.
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                                                                       NCBI_TaxID=6239;
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               Y111B2A.
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RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy D.M., Nelson D.L.,
RA Palazzolo M., Pittaman G.S., Paollard J., Pacleb J.M.,
RA Palazzolo M., Pittaman G.S., Poollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Wang Z.-Y. Wassarman D.A., Weinstcok G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q.A.,
RA Jheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhao G.S.,
R. The genome Sequence of Drosophila melanogaster.",
RMBL, AE003733; AAP55864.1;
RMBL, AE003733; AAP55864.1;
RMBL, REMBL, REMO3733; AAP55864.1;
REMBL, REMO3733; AAP55864.1;
REMBL, REMO3733; AAP55864.1;
REMBL, REMBL, REMO3733; AAP55864.1;
REMBL, REMB
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Bukaryota Metacoa, Arthropoda; Tracheata; Hexapoda; Insecta;

Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.
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; Pred; No. 3e-06;
18; Mismatches 6; Indels
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Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF094764; AAC95306.1; -.
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SWART; SM00116; CBS; 4.
SEQUENCE 634 AA; 70174 MW; 3FFD0D53E54BBE7C CRC64;
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01-UNN-2002 (TrEMBLrel. 21, Last annotation update)
SNF4/AMP-activated protein kinase gamma subunit.
SNF4-GAMMA OR CG17299.
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              49.3%; Score 105; DB 5; 40.0%; Pred. No. 2.9e-06;
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InterPro; IPR000644; CBS_domain.
Pfam; PF00571; CBS; 4.
SMART; SM00116; CBS; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR000644; CBS_domain.
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Les 16; Conserva
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hes 16; Conserva
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Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBL_TaxID=6239;
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                                                                                                                                                                                                                "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
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Pred. No. 2.6e-05;
9: Mismatches 8; Indels
                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
Miller N., Gattung S.;
"The sequence of C. elegans cosmid T20F7.";
Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.

EMBL, 197550; AAK18981.2; -.
InterPro: IPR00064; CBS_domain.
Pfam; PF00571; CBS; 4.
SWART; SW00116; CBS; 4.
Hypothetical protein.
SEQUENCE 423 AA; 47451 MW; 6997065D515E7B21 CRC64;
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Ryan E., Wohldman P., Walker C., Fielder T.;
"The sequence of C. elegans cosmid Y41G9A.";
"Ubmitted (MRR-1999) to the EMBL/GenBank/DDBJ databases.
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 51.5 KDa protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   192 ILTHKRILKFLWLFGKHLAPLEYLHKSPKELGIGTW 227
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                                                                                                                                                          STRAIN-BRISTOL N2;
MEDLINE-99069613; PubMed-9851916;
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MEDLINE-99069613; PubMed~9851916;
      Hypothetical 47.5 kDa protein.
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52.8%;
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Les 19; Conservative
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                                      Caenorhabditis elegans.
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STRAIN=BRISTOL N2;
Waterston R.;
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STRAIN-BRISTOL N2;
Waterston R.;
                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                                  None;
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                                                      Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Eplydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster (Fruit fly).

Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophilia.
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                                                                                                                                                                                                        Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E., George R., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G., Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S., Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M., Celniker S.
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Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,
Miranda A., Wungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,
Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
Celniker S.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases. EMBL: AY070541; AAL48012.1; -. SEQUENCE 1400 AA: 152380 MW; 411B93CC6B9EC7AF CRC64;
                                                                                                                                                                                                                                                                                                                              Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AY084138; AAL89876.1; -. SEQUENCE 906 AA; 99970 MW; C867D9556F42D57F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         565 YILTHKRILRFLFLYINELPKPAYMQKSLRELKIGTYNNI 604
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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Last annotation update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                             49.3%; Score 105; DB 5; 40.0%; Pred. No. 4.2e-06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   18; Mismatches
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Best Local Similarity 40.08
Matches 16; Conservative
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Best Local Similarity 40.0%
Matches 16; Conservative
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                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                     NCBI_TaxID=7227;
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                                      SNF4 AGAMMA.
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Q95NR8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bahr \overline{\mathbf{U}} , Darai \mathbf{G} , "Ahalysis and Characterization of the Complete Genome of Tupaia (Tree
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                            39.4%; Score 84; DB 5; Length 448; 40.0%; Pred. No. 0.0018; Live 13; Mismatches 11; Indels
"Direct Submission.";
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
BMBL, ACOGOFG1, ABFG0550.1; -.
InterPro; IPR000644; CBS_domain.
Pfam: PF00571; CBS; 4.
SMART: SM00116; CBS; 3.
Hypothetical protein.
SEQUENCE 448 AA; 51514 MW; B689218979299479 CRC64;
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Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF281817; AAK57095.1; -.
SEQUENCE 1055 AA; 117780 MW; CCA51E416FD38C39 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8; Mismatches 13; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Betaherpesvirinae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
SNF4/AMP-activated protein kinase gamma subunit.
Dictyostelium discoideum (Slime mold).
Eukaryota; Mycetozoa; Dictyostellium;
NCBI_TaxID=44689;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 HILTHKRLLKFLHIFGSLLPRPSFLYRTIQDLGIGTFRDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT; 1055 AA
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01-DEC-2001 (TrEMBLrel. 19, Last seq
01-JUN-2002 (TrEMBLrel. 21, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE~21211637; PubMed=11312357;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Shrew) Herpesvirus.";
J. Virol. 75:4854-4870(2001).
[2]
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32.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 40.0% tes 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tupaia herpesvirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local
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Q8SSV7
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2017P2
1D 021TP2
2017P2
1D 021TP2
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"A cDNA Clone Encoding Yeast SNF4-Like Protein (Accession No. U40713)
"Incom Phasoolus vulgaris L (PGR95-126).";
Plant Physiol. 110:336-336(1995).
EMBL; U40713; AAA91175.1;
InterPro; IPR000644; CBS_domain.
FAm; PF00571; CBS; 2.
SWART; SW00116; CBS; 2.
SWART; SW00116; CBS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Pepematophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Ph
                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                              1;
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                                                                                                                                                                                      30.8%; Score 65.5; DB 5; Length 577; 48.6%; Pred. No. 0.91; ive 2; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29.6%; Score 63; DB 10; Length 379; 48.6%; Pred. No. 1.3;
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BENEL; ALO21488; CA042378.1; -.
                                                                                                                                                                                                                                                                               16; Indels
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases. EMBL; AC115599; AAL92329.1; -. SEQUENCE 577 AA; 64209 MW; 3FBC56EA649B25A9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases
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01-NOV-1996 (TrEWBLrel. 01, Last sequence update)
01-JUN-2002 (TrEWBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                        1 HILTHKRLLKFLHIFGSLLPRPSFLYRTIQDLGIGTF 37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Phaseolus vulgaris (Kidney bean) (French bean).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT; 1268 AA
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NCBI_TaxID=6239;
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SEQUENCE FROM N.A.
MEDLINE-99069613; PubMed-9851916;
                                                                                                                                                                                                                                       48.68;
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01-DEC-2001 (TrEMBLrel. 19,
01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                      Query Match 30.89
Best Local Similarity 48.69
Matches 18; Conservative
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Best Local Similarity 48.6
Matches 17; Conservative
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TISSUE=IMMATURE SEEDS;
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SEQUENCE FROM N.A.

STRAIN=EL TOR N16961 / SERCTYPE 01;

MEDLINE=20406833; PubMed=10952301;

Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,

Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,

Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,

Emolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,

McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,

Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,

Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        J. Bacteriol. 179:4689-4698(1997).
-!- FUNCTION: PHOSPHORYLASE IS AN IMPORTANT ALLOSTERIC ENZYME IN CARBOHYDRATE METABOLISM. ENZYMES FROM DIFFERENT SOURCES DIFFER IN THEIR REGULATORY MEGRANISMS AND IN THEIR NATURAL SUBSTRATES. HOWEVER, ALL KNOWN PHOSPHORYLASES SHARE CATALYTIC AND STRUCTURAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Takata H., Takaha T., Okada S., Takaqi M., Imanaka T.; and a "Characterization of a gene cluster for glycogen biosynthesis and a heterotetrameric ADP-glucose pyrophosphorylase from Bacillus
                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-JUL-1997 (TrEMBLrel. 20, Last annotation update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
01-MAR-2002 (TremBLrel. 20, Last annotation update)
(Storch phosphorylase (EC 2.4.1.1) (Alpha-glucan phosphorylase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "DNA sequence of both chromosomes of the cholera pathogen Vibrio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales; Geobacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 516;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             305 LLSDKFMLEFLHSHTSVVAQPPYNSRYFSGINPYALGFAMFRDI 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 ILTHKRIJKFLHIFGSLLPRPSFLYRTIQD-----LGIGTFRDL 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical protein; Complete proteome.
SEQUENCE 516 AA; 60882 MW; 18F2C1365D46DFF7 CRC64;
                                                 01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein VC1874.
                          FLHIFGSLLPRP---SFLYRT----IQDLGIGTFRDLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 16;
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                                                                                                                                                                                       516 AA
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                                                                                                                                                                                       PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=1422;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TIGR; VC1874; -.
                                                                                                                                                                                                                                                                                                                                                   Vibrio cholerae
                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=666;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-TRBE14
                            11
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                                                                                                                                                                                       Q9KQX3
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                                                                                                                                         RESULT 14
                                                                                                                                                                 09KQX3
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MEDILINE-94150718; PubWed=7906398;

MEDILINE-94150718; PubWed=7906398;

A Milson R., Ainscough R., Anderson K., Baynes C., Berks M.,

A Milson R., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,

Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,

A Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,

Jones M., Kershaw J., Kirsten J., Laister M., Latrellle P.,

Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M.,

A Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.,

Raddon N., Smith A., Sonnhammer E., Staden R., Sulston J.,

Thierry Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,

Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.,

"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
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                                                                                                                                                                                                                                                            DB 5; Length 1268;
EMBL; AL021483; CAC42378.1; JOINED.
EMBL; AL021488; CAC42374.1; -
EMBL; AL021488; CAC42374.1; -
InterPro; IPR002048; EF-hand.
InterPro; IPR004182; GRAM_dom.
InterPro; IPR000195; RabGAP_TBC.
Pfam, PF02893; GRAM, 2.
Pfam; PF00565; TBC.
Pfam; PF00565; TBC.
PROSITE; PS00018; EF_HAND; UNKNOWN_1.
SEQUENCE 1268 AA; 144714 MW; 6D9FAA919E19CB16 CRC64;
                                                                                                                                                                                                                                                                               43.6%; Pred. No. 43;
tive 3; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PFUUJOO, ..... SMART; SMO0164; TBC; 1.
PROSITE; PS00018; EF_HAND; UNKNOWN_1.
PROSITE: """ AA: 144948 MW; ED95EBA90E4D8115 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MCMULTAY A.;
Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                              | :| ||| | |: | | ||| || 895 FSEVFPRLLDISDNGLLTFRDLA 933
                                                                                                                                                                                                                                                                                                                                                   11 FLHIFGSLLPRP---SFLYRT-----IQDLGIGTFRDLA 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT; 1270 AA.
                                                                                                                                                                                                                                                         26.3%; Score 56;
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EMBL, ALO21483; CAA16568.1; --
EMBL, ALO21483; CAA16349.1; --
EMBL, ALO21488; CAA16349.1; JOINED.
InterPro; IPR002048; EF-hand.
InterPro; IPR004182; GRAM_dom.
InterPro; IPR000195; RabGAP_TBC.
Pfam; PF02893; GRAM; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
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43.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-AUG-1998 (TrEMBLrel. 07, 01-NOV-1998 (TrEMBLrel. 08, 01-JUN-2002 (TrEMBLrel. 21, Y45F10A.6 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 26.3
Best Local Similarity 43.6
Matches 17; Conservative
                                                                                                                                                                                                                                                         Query Match 26.3
Best Local Similarity 43.6
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature 368:32-38(1994)
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SEQUENCE FROM N.A.
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Mcmurray A.

X45F10A.6

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Gaps

5;

Search completed: June 6, 2003, 11:02:53 Job time: 7.31349 secs

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TELEX:
INFORMATION FOR SEQ ID NO: 7:
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LENGTH: 328 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LIBRARY: PENITUT01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
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IMMEDIATE SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 497, App Sequence 8, Appli Sequence 9, Appli Sequence 9, Appli Sequence 6, Appli Sequence 5, Appli Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli Sequence 193, Appli 194 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 7, Appli
Sequence 6, Appli
Sequence 61, Appli
Sequence 64, Appl
Sequence 21, Appl
Sequence 5, Appli
Patent No. 5463025
Patent No. 5463025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 7, Appli
Sequence 7, Appli
                                                                                                                                         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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213
1 HILTHKRLLKFLHIFGSLLP......PSFLYRIQDLGIGTFRDLA 41
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Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/pcTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-330-611-8
US-09-134-001C-3105
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US-09-488-364-9
US-09-488-364-9
US-08-587-889-2
US-09-307-185-5
PCT-US96-09193-2
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US-09-576-160B-3
US-08-229-418-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-359-161-6
US-08-878-989-21
US-09-101-146-64
US-09-272-796-21
US-09-359-161-5
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US-09-576-160B-1
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-09-576-160B-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                protein search, using sw model
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                                                                                                                                                                                                                                                                                                                                        BLOSUM62
Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Match
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Sequence 4507, Appl
Sequence 10, Appl
Sequence 5, Appl 1
Sequence 5, Appl 1
Sequence 34, Appl
Sequence 34, Appl
Sequence 34, Appl
Sequence 34, Appl
Sequence 69, Appl
Sequence 108, Appl
Sequence 108, Appl
                         Sequence
                                                                                                                                                                                                                                                                                                              APPLICANT: Bandman, Olga
APPLICANT: Hillman, Jennifer L.
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl G.
APPLICANT: Guegler, Karl G.
APPLICANT: Goli, Surya K.
APPLICANT: Shah, Purvi
TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN
TITLE OF INVENTION: KINASES
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
US-08-932-761A-2
US-09-307-912-2
US-09-307-912-2
US-09-134-001C-4507
US-09-316-611-10
US-08-261-663A-6
US-09-357-206A-5
PCT-US95-07754A-6
US-08-34-55B-34
US-08-346-455B-34
US-09-483-831B-34
US-09-483-831B-69
US-08-946-455B-69
US-08-946-455B-69
US-08-946-455B-69
US-08-946-9458-69
US-08-310-912A-108
US-08-310-912A-108
US-08-310-912A-108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
ODERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/878,989
                                                                                                                                                                                                                             ALIGNMENTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Incyte Pharmaceuticals, STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PF-0321
                                                                                                                                                                                                                                                                                 Sequence 7, Application US/08878989
Patent No. 5885803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J J
REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION
TELEPHONE: 415-855-0555
   353
353
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825
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11143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Palo Alto
                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
   USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                        7-686-878-80-SC
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OPERATING SYSTEM: DOS
SOFTWARE: RastSEG for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/878,989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: Incyte Pharmaceuticals, Inc. 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 21, Application US/08878989
; Patent No. 5885803
                                                   Sequence 6, Application US/09359161A Patent No. 6342656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bandman, Olga
Hillman, Jennifer L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMpatible
OPERATING SYSTEM: DOS
                                                                                         GENERAL INFORMATION:
APPLICANT: Bradford, Kent J.
APPLICANT: Dahal, Peetambar
APPLICANT: Yang, Hong
APPLICANT: Cooley, Michael
APPLICANT: Cooley, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Corley, Neil C.
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                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 46.3%
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS ADDRESSE: Incyte P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94304
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APPLICANT:
APPLICANT:
APPLICANT:
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STATE: C.
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                   RESULT 3
US-09-359-161-6
                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 330
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                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
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                                                     58.2%; Score 124; DB 2; Length 328; 51.2%; Pred. No. 4.2e-10; Live 13; Mismatches 7; Indels
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                                                                                                                             1 HILTHKRLLKFLHIFGSLLPRPSFLYRTIQDLGIGTFRDLA 41
                                                                                                                                                                                                                                                                                                       APPLICANT: Bandman, Olga
APPLICANT: Hillman, Jennifer L.
APPLICANT: OCALEY, Neil C.
APPLICANT: GOALEY, KARI G.
APPLICANT: Lal, Preeti
APPLICANT: GOAL, SULYA K.
APPLICANT: SAL, SULYA K.
APPLICANT: Shah, Purvi
TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN
TITLE OF INVENTION: KINASES
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DAMS:
APPLICATION NUMBER: US/09/272,796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: Incyte Pharmaceuticals, Inc.
3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: PF-0321 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/878,989
                                                                                                                                                                                                                                                       Sequence 7, Application US/09272795
; Patent No. 6207148
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J J
REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 328 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                       Query Match 58.2%
Best Local Similarity 51.2%
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; LIBRARY: PENITUT01
; CLONE: 1452972
US-09-272-796-7
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Best Local Similarity
'-has 21; Conserve
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; CLONE: 1452972
US-08-878-989-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
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STREET: 31
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                                                                                                                                                                                                                                        US-09-272-796-7
                                                                                                                                                                                                                     RESULT 2
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APPLICANT: Gee, Oliver
APPLICANT: The Regents of the University of California
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Regulation of Source-Sink Relationships and Responses
TITLE OF INVENTION: LO Stress Conditions in Plants
FILE REFERENCE: 023070-095900US
CURRENT APPLICATION NUMBER: US/09/359,161A
NUMBER OF SEO ID NOS: 7
SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: gamma subunit of AMP-activated protein kinase; OTHER INFORMATION: (AMPK-gamma)
US-09-359-161-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 330;
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APPLICANT: Lal, Preeti
APPLICANT: Goli, Surya K.
TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN
TITLE OF INVENTION: KINASES
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Pred. No. 2.2e-08;
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1 HILTHKRILKFIHIFGSLLPRPSFLYRTIQDLGIGTFRDLA 41
                                                                                                                                                                                      APPLICANT: Bandman, Olga
APPLICANT: Bandman, Olga
APPLICANT: Hillman, Jennifer L.
APPLICANT: Corley, Neil C.
APPLICANT: Gooler, Karl G.
APPLICANT: Goll, Breeti
APPLICANT: Goll, Surya K.
APPLICANT: Shah, Purvi
TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN
TITLE OF INVENTION: KINASES
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: PF-0321 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-055
TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/272,796
                                                                                                                              ; Sequence 21, Application US/09272796
; Patent No. 6207148
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
CLASSIFICATION
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/878,989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-359-161-5
; Sequence 5. Application US/09359161A
; Patent No. 6345656
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J J
REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 21:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 46.34
Matches 19; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 331 amino acid
TYPE: amino acid
STRANDEDNESS: single
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CLONE: 1335856
                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 3174 Por CITY: Palo Alto
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US-09-272-796-21
                                                                                                                  US-09-272-796-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 64, Application US/09101146
Patent No. 6124125
GENERAL INFORMATION:
APPLICANT: Dartmouth College, St. Vincents Institute of APPLICANT: Medical Research, Kemp et al.
TITLE OF INVENTION: No. 6124125el AMP Activated Protein Kinase NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jane Massey Licata, Esq.
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Best Local Similarity 46.3%; Pred. No. 2.3e-08;
Matches 19; Conservative 14; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                    8; Indels
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                                                                                                                                                                                                                                                                                                                                            Query Match 52.6%; Score 112; DB 2; Best Local Similarity 46.3%; Pred. No. 2.3e-08; Matches 19; Conservative 14; Mismatches 8.
NAME: Billings, Lucy J J
RECISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0321 US
TELECOMMULICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E: Jane Massey Licata, Esq.
66 E. Main Street
                                                                                                                            INFORMATION FOR SEQ ID NO: 21: SEQUENCE CHARACTERISTICS: LENGTH: 331 amino acids TYPE: amino acid STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Jane Massey Licata
REGISTRATION NUMBER: 32,257
REFERENCE/DOCKET NUMBER: DC
TELECOMMUNICATION:
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TELEPAX: (856) 810-1454
INFORMATION FOR SEQ ID NO: 64.
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                   ; LIBRARY: GenBank
; CLONE: 1335856
US-08-878-989-21
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                                                                                                                                                                                                                                                   IMMEDIATE SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
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ZIP: 08053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Marl
STATE: NJ
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                                                                                                               Length 464;
                                                                                                                                                  Indels
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                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Edwards, Jean-Baptiste D.
APPLICANT: Duelert, Aymeric
APPLICANT: Lacroix, Bruno
ITILE OF INVENTION: 5' ESTS FOR SECRETED PROTEINS
                                                                                                                                                15;
                                                                                                             DB 6;
                                                                                                                                                                                                         4 THKRLLKFLHIFGSLLPRPSFLYRTIQDLGIGTFR 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: -26...1
IDENTIFICATION METHOD: Von Heijne matrix
OTHER INFORMATION: score 3.6
OTHER INFORMATION: seq ARSLLQFLRLVGQ/LK
                                                                                                                                                2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E: Knobbe, Martens, Olson & Bear
501 West Broadway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7; Mismatches
                                                                                                             Score 54.5;
Pred. No. 6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : ||:|| : | | :|| :|| 15 RSLLQFLRLVGQLKRVPRTGWVYRNVQ 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/905,223
                                                                                                                                                                                                                                                                                                               Sequence 497, Application US/08905223; Patent No. 6222029; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550
TELEPRAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 497:
SEQUENCE CHARACTERISTICS:
LENGTH: 92 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Israelsen, Ned A.
REGISTRATION NUMBER: 29,655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IBM PC compatible
APPLICATION NUMBER: 419,913
FILING DATE: 05-SEP-1989
                                                                                                             25.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 92101-3505
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compati
                                                                                                             Query Match 25.69
Best Local Similarity 48.69
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                  503
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Best Local Similarity 40.77
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: 5'
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
CLASSIFICATION: 536
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: San Diego
STATE: California
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                                                         LENGIH: 464
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                                      SEQ ID NO:1:
                                                                                                                                                                                                                                                                                   RESULT 10
                                                                         5463025-1
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                              APPLICANT: Cooley, Michael
APPLICANT: Downie, Bruce
APPLICANT: Bee, Oliver
APPLICANT: Gee, Oliver
APPLICANT: Gee, Oliver
APPLICANT: Gee, Oliver
TITLE OF INVENTION: Regulation of Source-Sink Relationships and Responses
TITLE OF INVENTION: to Stress Conditions in Plants
FILE REFERENCE: 023070-095900US
CURRENT APPLICATION NUMBER: 1999-07-21
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 5
LENGTH: 379
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                                                                                                                                                                                                                                                                                                                                                                                            29.6%; Score 63; DB 4; Length 379;
48.6%; Pred. No. 0.29;
tive 5; Mismatches 11; Indels
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; APPLICANT: Sumi, Yoshihiko;Ichikawa, Yataro;Aoki, Nobuo
;Muramatsu, Masami
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 THKRLLKFLHIFGSLLPRPSFLYRTIQDLGIGTFR 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 ILTHKRLLKFLHIFGSLLPRPSFLYRTIQDLGIGT
                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Phaseolus vulgaris L. Pv42 US-09-359-161-5
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Pred. No. 2.1;
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APPLICATION NUMBER: US/08/185,162
FILING DATE: 24-JAN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60,691
FILING DATE: 13-MAY-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/185,162 FILING DATE: 24-JAN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60,691
FILING DATE: 13-MAY-1993
APPLICATION NUMBER: 419,913
FILING DATE: 05-SEP-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25.6%;
48.6%;
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Best Local Similarity 48.00.
Best Local 17; Conservative
                                                                                                                                                                                                                                                                                                    ORGANISM: Phaseolus vulgaris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 25.6
Best Local Similarity 48.6
Matches 17; Conservative
     Peetambar
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   Dahal, Peet
Yang, Hong
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 179
                                                                                                                                                                                                                                                                                   TYPE: PRT
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; Sequence of Application US/09488364
; Partent No. 6307015
; GENERAL INFORMATION:
   APPLICANT: Bliedge, Stephen J.
; APPLICANT: Sanchez, Yolanda
; TITLE OF INVENTION: MAMMALIAN CHECKPOINT GENES AND PROTEINS
; FILE REFERENCE: 120541-1013
; CURRENT APPLICATION NUMBER: US/09/488,364
; CURRENT FILING DATE: 2000-01-12
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 9
                                                                                                                                                           Score 49; DB 4; Length 483;
Pred. No. 38;
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38;
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Patent No. 5654307:
REGERRAL INFORMATION:
APPLICANT: CAO, Zhaodan
APPLICANT: CROSTON, Glenn E.
APPLICANT: GOEDDEL, David V.
TITLE OF INVENTION: INTERLEUKIN-1 RECEPTOR-ASSOCIATED
TITLE OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT STREET: 4 Embarcadero Center, Suite 3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SYSTEM: PC-DOS/MS-DOS
Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                        4; Mismatches
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Pred. No.
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APPLICATION NUMBER: US/08/587,889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21 RPSFLYRTIQDLGIGTFRDL 40
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19 QPESLYRVVQTLGEGAFGEV 38
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19 QPESLYRVVQTLGEGAFGEV 38
                                                                                                   ; ORGANISM: Caenorhabditis elegans US-08-924-183-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT ORGANISM: Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23.0%;
                                                                                                                                                               23.0%;
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NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best_Local Similarity 45.0 Matches 9; Conservative
                                                                                                                                                                                                        9; Conservative
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STATE: California
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                                                                                                                                                                                       Best Local Similarity
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CLASSIFICATION:
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US-09-488-364-9
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US-08-587-889-2
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                                                            LENGTH: 483
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                                                                               TYPE: PRT
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Face No. 6800130
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: UNBRER: US/09/134,001C
CURRENT APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1998-08-13
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 3155
LENGTH: 808
TYPE: PRI
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APPLICANT: RUZICKA, Frank J.
TILLE OF INVENTION: DNA MOLECULES ENCODING BACTERIAL LYSINE 2,3-AMINOMUTASE
FILE REFERBACE: 032026/0476
CURRENT APPLICATION NUMBER: US/09/330,611
EARLIER APPLICATION NUMBER: US 09/198,942
EARLIER FILING DATE: 1998-11-24
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin Ver. 2.0
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CURRENT APPLICATION NUMBER: US/08/924,183A
CURRENT FILING DATE: 1997-09-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       270 THVMKRL---VHLLVKMRVRPYXIYVCDLSLGIGHFR 303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                           24.6%; Score 52.5; 40.5%; Pred. No. 10;
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                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Porphyromonas gingivalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-924-183-9; Sequence 9, Application US/08924183A; Sequence 9, Application US/08924183A; Patent No. 6218109; GENERAL INFORMATION:
                                                          Sequence 8, Application US/09330611 Patent No. 6248874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Elledge, Stephen J. APPLICANT: Sanchez, Yolanda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 40.59
Matches 15; Conservative
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Best Local Similarity
                                                                                                     ; GENERAL INFORMATION:
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                                  US-09-330-611-8
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(without alignments)
1254.259 Million cell updates/sec
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1 HILTHKRLLKFLHIFGSLLP......PSFLYRTIQDLGIGTFRDLA
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2. /cgn2_6/ptodata/2/pubpaa/NCS_NEW_PUB.pep:*
3. /cgn2_6/ptodata/2/pubpaa/NCSOB_NEW_PUB.pep:*
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3. /cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*
3. /cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*
3. /cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*
3. /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
3. /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
4. /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-10-038-072-200
US-10-128-072-200
US-10-139-94-200
US-10-140-470-200
US-10-175-746-200
US-10-176-746-200
US-10-176-746-200
US-10-176-746-200
US-10-176-918-200
US-10-176-918-200
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US-09-925-297-461
US-10-108-605-71
                                                                                                                                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                     392085 seqs, 103240269 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUMMARIES
                                                                                                                                                                                                                  US-09-826-581-6_COPY_320_360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Published_Applications_AA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                      protein search, using sw model
                                                                                                                                                                                                                                                                                                        BLOSUM62
Gapop 10.0 , Gapext 0.5
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Match Length DB
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Maximum DB
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US-09-826-581-6
Sequence 6, Application US/09826581
Pactent No. US20020142310A1
GENERAL INFORMATION:
APPLICANT: Andersoo, Leif
APPLICANT: Luthman, L. Holger
APPLICANT: MARKING OF THE HUMAN AMP-ACTIVATED PROTEIN KINASE GAMMA 3 SUI
TITLE OF INVENTION: VARIANTS OF THE HUMAN AMP-ACTIVATED PROTEIN KINASE GAMMA 3 SUI
CURRENT APPLICATION NUMBER: US/09/826,581
CURRENT APPLICATION NUMBER: US/09/826,581
PRIOR APPLICATION NUMBER: US 60/195,665
PRIOR FILING DATE: 2000-04-07
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Sequence 200,
Sequence 200,
Sequence 200,
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Patent No. US20020081659A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INFURITON: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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100.0%; Pred. No. 1.6e-21;
ilve 0; Mismatches 0;
US-10-121-050-200

US-10-141-755-200

US-10-143-108-200

US-10-123-236-200

US-10-123-236-200

US-10-123-236-200

US-10-123-22-200

US-10-140-922-200

US-10-123-903-200

US-10-123-903-200

US-10-123-903-200

US-10-124-819-200

US-10-124-819-200

US-10-124-822-200

US-10-124-822-200

US-10-123-903-200

US-10-123-903-200

US-10-123-902-200

US-10-123-910-200

US-10-123-910-200

US-10-123-910-200

US-10-123-910-200

US-10-123-910-200

US-10-124-813-200

US-10-124-813-200

US-10-124-813-200

US-10-124-813-200
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6
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CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41; Conservative
   TYPE: PRT
ORGANISM: Homo sapiens
US-09-826-581-6
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   US-09-925-297-461
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Best Local S:
Matches 41
   RESULT 2
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CURRENT FILING DATE: 2001-12-19
PRIOR PELICATION NUMBER: 60/049911
PRIOR FILING DATE: 1997-06-18
PRIOR FILING DATE: 1997-06-18
PRIOR FILING DATE: 1997-05-17
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-17
PRIOR PLILORION NUMBER: 60/059115
PRIOR FILING DATE: 1997-09-17
PRIOR PLILORION NUMBER: 60/059122
PRIOR FILING DATE: 1997-09-17
PRIOR PLILORION NUMBER: 60/059124
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-18
PRIOR FILING DATE: 1997-09-19
PRIOR APPLICATION NUMBER: 60/059588
PRIOR FILING DATE: 1997-09-19
PRIOR APPLICATION NUMBER: 60/059886
PRIOR FILING DATE: 1997-09-19
PRIOR FILING DATE: 1997-09-19
PRIOR FILING DATE: 1997-09-19
                                                                                                                                                                                                                                                                         LOCATION: (20)
CTHER INFORMATION: Xaa = any amino acid
US-09-510-332-47
                                                                                                                                                                                                          OTHER INFORMATION: human T2R26 (hGR26) NAME/KEY: MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 200, Application US/10028072; Publication No. US20030004311A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 HILTHKRLLKFLHIFGSL-----
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Gurney, Austin L.
Sherwood, Steven
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Goddard, Audrey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Baker, Kevin P. APPLICANT: Beresini, Maureen
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   PatentIn Ver. 2.1
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Filvaroff, Ellen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wood, William
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tumas,Daniel
                                                                                                                                          ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
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FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      133 PLGS 136
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SOFTWARE: Pai
SEQ ID NO 47
LENGTH: 264
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APPLICANT:
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                                                                                                          TYPE: PRT
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APPLICANT: Bachmann, Jane
APPLICANT: Bachmann, Jane
APPLICANT: Kain
TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FROM DROSOPHILA MELANOGASTER THAT ENCODE
TITLE OF INVENTION: PROTEINS ESSENTIAL FOR LARVAL VIABILITY AND USES THEREOF
FILE REFERENCE: 31133B
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Publication No. US2003002227841
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Adder, Charles S.
APPLICANT: Ryba Nick
APPLICANT: Mueller, Ken
APPLICANT: Hoon, Mark
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: T2R, a No. US20030022278Alel Family of Taste Receptors
FILE REFERENCE: 02307E-098010US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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CURRENT FILING DATE: 2002-03-27
PRIOR APPLICATION NUMBER: US 09/761,142
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2000-01-14
PRIOR FILING DATE: 2000-01-14
NUMBER OF SEQ ID NOS: 361
SEQ ID NO 71
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CURRENT FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 09/393,634
PRIOR FILING DATE: 1999-09-10
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION UNDRER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 928
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 461
LENGTH: 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 71, Application US/10108605 Patent No. US20020160934A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Drosophila melanogaster US-10-108-605-71
                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 46.3%
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 40.0%
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APPLICANT: Broadus, Julie
                                                                                                                                                                                                                                                                             ; ORGANISM: Homo sapiens
US-09-925-297-461
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US-10-108-605-71
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NUMBER: 60/062250 1997-10-17 NUMBER: 60/062285 1997-10-17 1997-10-17 NUMBER: 60/062814 11997-10-24 11997-10-24 NUMBER: 60/063045 11997-10-24 NUMBER: 60/063045 11997-10-24 NUMBER: 60/063045 11997-10-24 NUMBER: 60/063045 11997-10-24 NUMBER: 60/063045	1997-10 1997-10 1997-10 1997-10 1997-10 1997-10 1997-10 1997-10 1997-10 1997-10 1997-10 1997-10 1997-11 1997-11 1997-11 1997-11 1997-11 1997-11	NUMBER: 6 1997-11- NUMBER: 6 1997-11- NUMBER: 6 1997-12- NUMBER: 6 1997-12- NUMBER: 6 1997-12- NUMBER: 6 1997-12- NUMBER: 6 1998-01-
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PRIOR FILING DATE: 1996-02-27

PRIOR APPLICATION NUMBER: 60/08105

PRIOR PILING DATE: 1998-03-31

PRIOR PILING DATE: 1998-03-31

PRIOR PILING DATE: 1998-03-31

PRIOR PILING DATE: 1998-03-31

PRIOR PILING DATE: 1998-04-16

PRIOR PILING DATE: 1998-04-12

PRIOR PILING DATE: 1998-04-13

PRIOR PILING DATE: 1998-05-07

PRIOR PILING DATE: 1998-05-13

PRIOR PILING DATE: 1998-05-10

PRIOR PILING DATE: 1998-06-10

PRIOR PILING DATE: 1998-06-10

PRIOR PILING DATE: 1998-06-10

PRIOR PILING DATE: 1998-06-11

PRIOR PILING DATE: 1998-06-12

PRIOR PILING DATE: 1998-06-13

PRIOR PILING DATE: 1998-06

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APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330RIC160
                                                                                                                                                                                   APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REPERENCE: P3330R.C54
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66;
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66;
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NUMBER OF SEQ ID NOS: 550
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Pred. No. 6
                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/10/123,904 CURRENT FILING DATE: 2002-04-16
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34.1%;
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Tumas, Daniel
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Tumas, Daniel
                   Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
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Godowski, Paul J.
Gurney, Austin L.
Sherwood, Steven
Smith, Victoria
   Gerritsen, Mary E.
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Wood, William
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Filvaroff, Ellen
Gao, Wei-Qiang
                                                                        Sherwood, Steven
Smith, Victoria
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Best Local Similarity 34.11
Matches 14; Conservative
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US-10-123-904-200
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Best Local Similarity
Matches 14; Conserva
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LENGTH: 1023
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APPLICANT:
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C17
CURRENT APPLICATION NUMBER: US/10/121,049
CURRENT FILING DATE: 2002-04-12
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                                                                                                                                                                  24.9%; Score 53; DB 9; Length 1023; 34.1%; Pred. No. 66;
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SEQ ID NO 200
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PRIOR APPLICATION NUMBER: 60/090863
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/091360
PRIOR FILING DATE: 1998-07-01
PRIOR FILING DATE: 1998-07-02
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091582
PRIOR APPLICATION NUMBER: 60/091982
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Publication No. US20030022328A1
GENERAL INFORMATION:
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DeForge, Laura
Desnoyers, Luc
Filvaroff, Ellen
Gao, Wei-Qiang
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Watanabe, Colin K
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Gurney, Austin L.
Sherwood, Steven
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APPLICANT: Beresini, Maureer
APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
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Filvaroff, Ellen
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Best Local Similarity 34.1'
Matches 14; Conservative
                                                                                                                                                                                   Best_Local Similarity 34.1%
Matches 14; Conservative
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; ORGANISM: Homo Sapien
US-10-121-049-200
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US-10-121-049-200
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Gaps

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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P9330R1C2B
CURRENT APPLICATION NUMBER: US/10/176,921
CURRENT FILING DATE: 2002-06-20
PRIOR APPLICATION TEMOVED - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
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66;
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                                            Prior Application removed - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 550 SEQ ID NO 200
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Pred. No. 66;
9; Mismatches
                                                                                                                                                                                                                                                                                                                                             9; Mismatches
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Pred. No. 6
CURRENT APPLICATION NUMBER: US/10/176,918 CURRENT FILING DATE: 2002-06-20
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; Publication No. US20030032155A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     . Sequence 200, Application US/10176921
; Publication No. US20030027276A1
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Sherwood, Steven
Smith, Victoria
Stewart, Timothy A.
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34.1%;
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34.1%;
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APPLICANT: Beresini, Maureen
APPLICANT: Deforge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
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Watanabe, Colin K
Wood, William
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Goddard, Audrey
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APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
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Filvaroff, Ellen
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Best Local Similarity 34.1'
Matches 14; Conservative
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Best Local Similarity 34.15
Matches 14; Conservative
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US-10-176-921-200
                                                                                                                                                                        TYPE: PRT; ORGANISM: Homo Sapien
US-10-176-918-200
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US-10-137-865-200
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US-10-176-921-200
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LENGTH: 1023
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Watanabe, Colin K
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE OF INVENTION: ACIDS ENCODING THE SAME
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ch 24.9%; Score 53; DB 9; Length 1023; l Similarity 34.1%; Pred. No. 66; l4; Conservative 9; Mismatches 10: rada
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/175,746 CURRENT FILING DATE: 2002-06-19
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                                                                                                                                                                           Sequence 200, Application US/10175746 Publication No. US20030027270A1
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Stewart, Timothy A.
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Godowski, Paul J.
Gurney, Austin L.
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Wood, William
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Gerritsen,Mary E.
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APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
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Filvaroff, Ellen
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Filvaroff, Ellen
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ORGANISM: Homo Sapien
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Best Local Similarity
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US-10-176-918-200
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Gaps

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APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
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                 347 VLANQTLL----VEGQVIRSPTNTISVIFRIFQDDGLGTFQ 383
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2 ILTHKRLLKFLHIFGSLLPRP----SFLYRTIQDLGIGTFR 38
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CURRENT APPLICATION NUMBER: US/10/142,431
Prior anniant
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                                                                                                                             Sequence 200, Application US/10142431 Publication No. US20030036179A1 GENERAL INFORMATION:
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Godowski, Paul J.
Gurney, Austin L.
Sherwood, Steven
Smith, Victoria
Stewart, Timothy A.
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Gao, Wei-Qiang
Gerritsen, Mary E.
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Filvaroff, Ellen
Gao, Wei-Qiang
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Wood,William
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Goddard, Audrey
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Wood,William
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Gurney, Austin L.
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Smith, Victoria
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Matches 14; Conservative
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CORGANISM: Homo Sapien
US-10-142-431-200
                                                                                            RESULT 14
US-10-142-431-200
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APPLICANT: Zhang, Zemin
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFRENCE: P3330RIC162
CURRENT APPLICATION NUMBER: US/10/140,474
CURRENT FILING DATE: 2002-05-06
                                                                                                                                                                                                       APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330RIC15A
CURRENT APPLICATION NUMBER: US/10/137,865
CURRENT FILING DATE: 2002-05-03
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&
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Pred. No. 66;
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                                                                                                                                                                                                                                                                                                                   Prior Application removed - See Palm or File Wrapper NUMBER OF SEQ ID NOS: 550 SEQ ID NO 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9; Mismatches
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; Publication No. US20030032156A1
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34.1%;
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Stewart, Timothy A.
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Gerritsen,Mary E.
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Wood,William
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APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
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Gurney, Austin L.
Sherwood, Steven
                                                        Godowski, Paul J.
Gurney, Austin L.
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Filvaroff, Ellen
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Best Local Similarity 34.1

Matches 14; Conservative
                                                                                            Sherwood, Steven
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                                      Goddard, Audrey
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ORGANISM: Homo Sapien
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US-10-137-865-200
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LENGTH: 1023
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; FILE REFERENCE: P3330R1C211
; CURRENT APPLICATION NUMBER: US/10/143,114
; CURRENT FILING DATE: 2002-05-09
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 200
; LENGTH: 1023
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-143-114-200

Query Match
US-10-143-114 - 200

Query Matches 14; Conservative 9; Mismatches 10; Indels 8; Gaps

Z ILPHKRLLKFLHIFGSLLPRP----SFLYRTIQDLGIGFR 38

Qy
Z ILPHKRLLKFLHIFGSLLPRP----SFLYRTIQDLGIGFR 383

Search completed: June 6, 2003, 11:16:44
Job time: 5.37478 secs
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June 6, 2003, 10:55:08 ; Search time 78.7881 Seconds (without alignments) 827.023 Million cell updates/sec
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| S1D52/959dta/ygneseq/geneseqp-embl/AA1989_DAT:*
| S1D52/gcgdata/geneseq/geneseqp-embl/AA1990_DAT:*
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1 MEPGLEHALRRTPSWSSLGG......LSDILQALVLSPAGIDALGA 489
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 908470 seqs, 133250620 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                              OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Perfect score:
Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

			Description	PRKAG3. HOMO Sapi	Human AMPK gamma s	Sus scrofa Prkag3	Piq PRKAG3 polymor	Piq AMPK gamma sub	Pig wild-type PRKA	Piq PRKAG3 polymor	Pig PRKAG3 polymor	Pig PRKAG3 polymor	Human AMPK gamma s
COLUMNICO			ID	AAB47679	AAE00223	AAE00224	AAE22985	AAE00222	AAE22984	AAE22987	AAE22988	AAE22986	AAE00221
			DB	22	22	22	23	22	23	23	23	23	22
		Query	Length	489	464	514	464	464	464	464	464	464	305
	æ	Query	Match	100.0	94.5	82.2	79.3	79.2	79.2	79.2	79.1	79.0	61.1
			Score	2538	2398	2085	2013	2011	2011	2010	2007	2005	1551
		Result	No.		7	3	4	S	9	7	89	9	10

Human Prkag3 v401 Fuganes as Sand Sand Sus scrofa AMPK ga Sus scrofa AMPK ga Disease associated Human protein sequence associated Human protein sequence and manualian AMPK-gam Human NS protein sequence Novel human diagno Drosophila melanog Novel human diagno Drosophila melanog Novel human diagno Human AMP-activate Human AMP-activate Human polypeptide Soybean sucrose no Partial Z. mays su Rice sucrose non-famen sucrose non-Herbicidally activ Herbicidally activ Herbicidally activ Herbicidally activ Harbidopsis thalia Arabidopsis thalia Arab	GNTS camma 3 subunit; PRKAG3; variant; substitution; ss. ation point P71A" ation point R340W"
AAE00329 AAE00320 AAE00320 AAE00225 AAE00225 AAW88438 AAB88438 AAB86245 AAB6245 AAB6245 AAB6245 AAB6245 AAG7798 ABG11241 AAG77798 AAG7778 AAG7778 AAG7789 AAG7781	AA. AA. sase g sity; vari
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	RESULT AAB476 AAB476 AAB476 AAB476 AAC AAC AAC AAC AAC AAC AAC AAC AAC AA

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13-JUN-2001 (first entry)
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(ANDE/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AQIYMRFMQEHTCYDAMATSSKLVIFDTMLEIKKAFFALVANGVRAAPLWDSKKQSFVGM 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LRQRTLCLEGVLSCQPHESLGEVIDRIAREQVHRLVLVDETQHLLGVVSLSDILQALVLS 480
                                                                                                                                                                                                                                                                                                                                                                                                           1 MEPGLEHALRRTPSWSSLGGSEHQEMSFLEQENSSSWPSPAVTSSSERIRGKRRAKALRW 60
                                    New variants of human AMP-activated protein kinase gamma3 subunit associated with a metabolic disease e.g. diabetes or obesity and method for determining a risk estimate of diseases in subject by detecting the
                                                                                                                                  AMP-activated protein kinase gamma 3 subunit (PRKAG3). Detecting the presence of the PRKAG3 DNA, or a variant, is useful in determining a risk estimate of a metabolic disease, such as diabetes or obesity, an a subject. The variation may occur in exons 3, 4 or 10. In exon 3 variation may be a substitution of a G for a C at nucleotide 320, resulting in the amino acid substitution P71A; in exon 4 variation may be a substitution of a T for a C at nucleotide 320, ratiation may be a substitution of a T for a C at nucleotide 1037, resulting in the amino acid substitution R340%. There may also be nucleotide variation in intron 6. The numbering of these variation in intron 6. The numbering of these position 1 of the open reading frame.
                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                             This sequence is encoded by the full length cDNA encoding the human
                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                           Score 2538; DB 22; Length 489; Pred. No. 7.3e-254;
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                                                                                                      Disclosure; Fig 5; 25pp; English.
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100.0%;
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 WPI; 2001-657170/75.
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Best Local Similarity
Matches 489; Conserv
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             N-PSDB; AAH43685
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Human; gamma subunit; adenosine monophosphate-activated kinase; AMPK; prefectio; publetee; obesity; myopathy; cardiovascular disease; anorectio; genetic testing; carbohydrate metabolism disorder; skeletal muscle; cystathione beta synthase; CBS; cardiant; gene therapy.
Human AMPK gamma subunit muscle-specific isoform, complete PRKAG3
                                                                                                                                                                                                                                                                                                                                                                                                                                        253..307
/label= CBS
/note= "Cystathione beta synthase domain"
                                                                                                                                                                                                                                                                                                                                                     'note= "Cystathione beta synthase domain"
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/label= CBS
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                                                                                                                                                                                                          Homo sapiens.
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11-SEP-2000; 2000WO-EP09896

10-SEP-1999; 99EP-0402236. 18-MAY-2000; 2000EP-0401388.

) INRA INST

NAT RECH AGRONOMIQUE. L. LOOFT C. Rogel-Gaillard C; Robic A, Looft C, Kalm E, Milan D, Robic Gellin J, Le Roy P, Chardon P; Iannuccelli N, Andersson L,

WPI; 2001-244810/25.

OD

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New variants of the gamma subunit of vertebrate adenosine monophosphate-activated kinase for diagnosis or treatment of disorders associated with energy metabolism such as diabetes, obesity, and

Claim 5; Fig 3; 71pp; English.

The present sequence is human adenosine monophosphate (AMP) activated kinase (AMPK) gamma subunit muscle-specific isoform, complete PRKAG3. Mutation in Prkag3 results in an altered regulation of carbohydrate metabolism, particularly in skeletal muscle. PRKAG3 is useful as therapeutic for treating carbohydrate metabolism disorders such as diabetes, obesity, and disorders associated with muscle metabolism such as myopathy and cardiovascular diseases, to modulate AMPK activity, and for restoring a normal AMPK function. PRKAG3 sequence and its functionally altered mutants are useful for the diagnostic evaluation, genetic testing and prognosis of a metabolic disorder, preferably a carbohydrate metabolism disorder. Primers that can detect a genetic polymorphic marker linked to a sequence encoding PRKAG3, are useful for detecting a dysfunction of carbohydrate metabolism resulting from the expression of a functionally altered allele of PRKAG3.

Transgenic animal and host cell transformed with PRKAG3 or a heterotrimeric AMPK consisting of PRKAG3 or its mutant, are useful for screening compounds able to modulate AMPK activity. Nucleic acid encoding PRKAG3 is useful for detecting mutations in a Prkag3 gene, or in a sequence encoding the first cystathione beta synthase (CBS) domain

AAE00223 standard; Protein; 464 AA.

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AAE00223

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460 ETQHLLGVVSLSDILQALVLSPAGIDALGA 489
                                                                                                                                                                                                                                                                              514 AA;
                        N-PSDB; AAD0332]
Iannuccelli N,
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                                                                                                                                                                                                                                                                                                                                                                                                                    Pig; gamma subunit; adenosine monophosphate-activated kinase; AMPK; PRKAG3; diabetes; obesity; myopathy; cardiovascular disease; anorectic; genetic testing; carbohydrate metabolism disorder; skeletal muscle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Robic A, Rogel-Gaillard C;
                                                                MSFLEQENSSSWPSPAVTSSSERIRGKRRAKALRWTRQKSVEEGEPPGQGEGPRSRPAAE
                                                                         STGLEATFPKTTPLAQADPAGVGTPPTGWDCLPSDCTASAAGSSTDDVELATEFPATEAW
                                                                                                              STGLEATFPKTTPLAQADPAGVGTPPTGWDCLPSDCTASAAGSSTDDVELATEFPATEAW
                                                                                                                              ECELEGLIEERPALCISPQAPFPKLGWDDELRKPGAQIYMRFMQEHTCYDAMATSSKLVI
                                                                                                                                                              FDTMLEIKKAFFALVANGVRAAPLWDSKKQSFVGMLTITDFILVLHRYYRSPLVQIYEIE
                                                                                                                                                                      QHKIETWREIYLQGCFKPLVSISPNDSLFEAVYTLIKNRIHRLPVLDPVSGNVLHILTHK
                                                                                                                                                                                                                             RLLKFLHIFGSLLPRPSFLYRTIQDLGIGTFRDLAVVLETAPILTALDIFVDRRVSALPV
                                                                                                                                                                                                                                       VNECGOVYGLYSRFDVIHLAAQQTYNHLDMSVGEALRQRTLCLEGVLSCQPHESLGEVID
                                                                                                                                                                                                                                                                      VNECGQVVGLYSRFDVIHLAAQQTYNHLDMSVGFALRQRTLCLEGVLSCQPHESLGEVID
                                                 Gaps
                                                0;
                                 Length 464;
                                                                                                                                                                                                                                                                                             RIAREQVHRLVLVDETQHLLGVVSLSDILQALVLSPAGIDALGA 489
                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                           cystathione beta synthase; CBS; cardiant; gene therapy
                                DB 22;
                               Score 2398; DB 22;
Pred. No. 2.2e-239;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Milan D,
of PRKAG3 and is useful in gene therapy.
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L.
                                                                                                                                                                                                                                                                                                                                                    AAE00224 standard; Protein; 514 AA
                                                                                                                                                                                                                                                                                                                                                                                                    Sus scrofa Prkag3 splice variant.
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                               94.5%;
99.8%;
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                                                                                                                                                                                                                                                                                                                                                                                    13-JUN-2001 (first entry)
                                               463; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Looft C,
                                       Similarity
                464 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10-SEP-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sus scrofa.
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                                       Local
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such as myopathy and cardiovascular diseases, to modulate AMPK
activity, and for restoring a normal AMPK function. PRKAG3 sequence
and its functionally altered mutants are useful for the diagnostic
evaluation, genetic testing and prognosis of a metabolic disorder,
preferably a carbohydrate metabolism disorder. Primers that can detect
a genetic polymorphic marker linked to a sequence encoding PRKAG3, are
useful for detecting a dysfunction of carbohydrate metabolism resulting
from the expression of a functionally altered allele of PRKAG3.

Transgenic animal and host cell transformed with PRKAG3 or a
heterotrimeric AMPK consisting of PRKAG3 or its mutant, are useful for
screening compounds able to modulate AMPK activity. Nucleic acid
encoding PRKAG3 is useful for detecting mutations in a Prkag3 gene, or
in a sequence encoding the first cystathione beta synthase (CBS) domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               41 AVTSSSERIRGKRRAKALRWTRQKSVEBGEPPGQGEGPRSRPAAESTGLEATFPKTTPLA 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QADP-AGVGTPPTGWDCLPSDCTASAAGSSTDDVELATEFPATEAWECELEGLLEERPAL 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         245 VANGVRAAPLMDSKKQSFVGMLTITDFILVLHRYYRSPLVQIYEIEEHKIETWREIYLQG 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 65
                                                                                                                                          New variants of the gamma subunit of vertebrate adenosine monophosphate-activated kinase for diagnosis or treatment of disorders associated with energy metabolism such as diabetes, obesity, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --- TPSWSSLGGSEHQEMSFLEQENSSSWPSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLSPQAPFPKLGWDDELRKPGAQIYMRFMQEHTCYDAMATSSKLVIFDTMLEIKKAFFAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VANGVRAAPLWDSKKQSFVGMLTITDFILVLHRYYRSPLVQIYEIEQHKIETWREIYLQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            280 CFKPLVSISPNDSLFEAVYTLIKNRIHRLPVLDPVSGNVLHILTHKRLLKFLHIFGSLLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RPSFLYRTIQDLGIGTFRDLAVVLETAPILTALDIFVDRRVSALPVVNECGQVVGLYSRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DVIHLAAQQTYNHLDMSVGEALRQRTLCLEGVLSCQPHESLGEVIDRIAREQVHRLVLVD
                                                                                                                                                                                                                                                                                                                                                  The present sequence is pig adenosine monophosphate (AMP)-activated kinase (AMPK) agamma subunit muscle-specific isoform, PRRAG3 spilce variant. Prkag3 gene is located in the RN locus of chromosome 15. Mutation in Prkag3 results in an altered regulation of carbohydrate metabolism, particularly in skeletcal muscle. PRRAG3 is useful as therapeutic for treating carbohydrate metabolism disorders such as diabetes, obesity, and disorders associated with muscle metabolism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26;
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Pred. No. 7.5e-207;
0; Mismatches 46;
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Chardon
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                                                                                                                                                                                                                                                                                          Page 70-71; 71pp; English.
Roy
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82.0%;
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Gellin J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 82.0
Matches 418; Conservative
                                                    2001-244810/25.
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us-09-826-581-6.rag

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EQHKIETWREIYLQGCFKPLVSISPNDSLFEAVYTLIKNRIHRLPVLDPVSGNVLHILTH 324
                                                                                                                                                                                                       325 KRLLKFLHIFGSLLPRPSFLYRTIQDLGIGTFRDLAVVLETAPILTALDIFVDRRVSALP 384
                                                                                                                                                                                                                                                                        385 VVNECGQVVGLYSRFDVIHLAAQQTYNHLDMSVGEALRQRTLCLEGVLSCQPHESLGEVI 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pig; gamma subunit; adenosine monophosphate-activated kinase; AMPK; PRKAG3; diabetes; obesity; myopathy; cardiovascular disease; anorectic; genetic testing; carbohydrate metabolism disorder; skeletal muscle; cystathione beta synthase; CBS; cardiant; gene therapy; RN locus;
                                                                    I FDTMLEIKKAFFALVANGVRAAPLWDSKKQSFVGMLTITDFILVLHRYYRSPLVQIYEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pig AMPK gamma subunit muscle-specific isoform, complete PRKAG3.
                                                                                                                                                                                                                                                                                                                                             DRIAREQVHRLVLVDETQHLLGVVSLSDILQALVLSPAGIDALGA 489
                                                                                                                                                                                                                                                                                                                                                               /note= "Cystathione beta synthase domain"
200
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/note= "Cystathione beta synthase domain"
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(ANDE/) ANDERSSON L.
(LOOF/) LOOFT C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAE00222 standard; Protein; 464 AA.
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/label= CBS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      chromosome 15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-JUN-2001
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                                                                                                                                                                                                                                                                                                                                             445
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   85
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Screening animals to determine those likely to produce larger litters and improved meat quality traits involves assaying for the presence of polymorphisms in the AMP activated protein kinase regulatory gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26 MSFLEQENSSSWPSPAVTSSSERIRGKRRAKALRWTRQKSVEEGEPPGQGEGPRSRPAAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a method for screening animals to determine those more likely to produce large litters and improved meat quality traits. The method involves assaying for the presence of a genotype in the sample of genetic material obtained from animal. The genotype is characterised by polymorphism(s) in the AMP activated protein kinase regulatory gamma subunit (PRRAG3) gene. The method is used for screening animals e.g., pigs to determine those most likely to exhibit improved meat quality traits and to produce larger litters. The present sequence is pig PRRAG3 polymorphic variant (PRRAG3-30).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                          AMP activated protein kinase regulatory gamma subunit; PRKAG3 gene; screening; meat quality; single nucleotide polymorphism; SNP; pig;
                                                                                                                                                                                                                                                                                                                                                                             /note= "Wild type Asn is substituted with Thr due to single nucleotide polymorphism (SNP)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Malek M, Plastow G;
     Pig PRKAG3 polymorphic variant (PRKAG3-30).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 91-93; 109pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (IOWA ) UNIV IOWA STATE RES FOUND INC
                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
30
                                                                                                        AAE22985 standard; Protein; 464 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000US-231045P.
2001US-260239P.
2001US-299111P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rothschild MF, Clobanu DC,
                                                                                                                                                                       09-AUG-2002 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-393850
N-PSDB; AAD36457
                                                                                                                                                                                                                                                                                                                                                               Misc-difference
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18-JUN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            subunit gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                14-MAR-2002
                                                                                                                                                                                                                                                                                                             Sus scrofa.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KRLLKFLHIFGSLLPRPSFLYRTIQDLGIGTFRDLAVVLETAPILTALDIFVDRRVSALP 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  385 VVNECGQVVGLYSRFDVIHLAAQQTYNHLDMSVGEALRQRILCLEGVLSCQPHESLGEVI 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            265 EQHKIETWREIYLQGCFKPLVSISPNDSLFEAVYTLIKNRIHRLPVLDPVSGNVLHILTH 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09
                                                                                                                                                                                                                                                                        The present sequence is pig adenosine monophosphate (AMPY) activated Kinsase (AMPK) gamma subunit muscle-specific isoform, complete PRRAG3. Prkag3 gene is located in the RN locus of chromosome 15. Mutation in Prkag3 results in an altered regulation of carbohydrate metabolism, particularly in skeletal muscle. PRRAG3 is useful as therapeutic for treating carbohydrate metabolism disorders such as diabetes, obesity, and disorders associated with muscle metabolism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                useful for detecting a dysfunction of carbohydrate metabolism resulting from the expression of a functionally altered allele of PRRAG3. Transgenic animal and host cell transformed with PRRAG3 or a heterotrimeric AMPK consisting of PRRAG3 or its mutant, are useful for screening compounds able to modulate AMPK activity. Nucleic acid encoding PRRAG3 is useful for detecting mutations in a Prkag3 gene, or in a sequence encoding the first cystathione beta synthase (CBS) domain of PRRAG3 and is useful in gene therapy.
                                                                                                                        New variants of the gamma subunit of vertebrate adenosine monophosphate-activated kinase for diagnosis or treatment of disorders associated with energy metabolism such as diabetes, obesity, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   evaluation, genetic testing and prognosis of a metabolic disorder, preferably a carbohydrate metabolism disorder. Primers that can detect a genetic polymorphic marker linked to a sequence encoding PRRAG3, are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MSFLEQGESRSWPSRAVTISSERSHGDQGNKASRWTRQEDVEEGGPPGPREGPQSRPVAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IFDTMLEIKKAFFALVANGVRAAP1.WDSKKQSFVGMLTITDFILVLHRYYRSPLVQIYEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rogel-Gaillard C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26 MSFLEQENSSSWPSPAVTSSSERIRGKRRAKALRWTRQKSVEEGEPPGQGEGPRSRPAAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STGLEATFPKTTPLAQADP-AGVGTPPTGWDCI.PSDCTASAAGSSTDDVELATEFPATEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WECEL.EGLLEERPAJ.CI.SPQAPFPKI.GWDDHI.RKPGAQIYMRFMQEHTCYDAMATSSKLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   240 EEHKIETWREIYLQGCFKPLVSISPNDSLFEAVYALIKNRIHRLPVLDPVSGAVLHILTH
                                                                                                                                                                                                                                                                                                                                                                                                                        such as myopathy and cardiovascular diseases, to modulate AMPK activity, and for restoring a normal AMPK function. PRKAG3 sequence and its functionally altered mutants are useful for the diagnostic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 464;
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  Robic A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 79.2%; Score 2011; DB 22;
86.0%; Pred. No. 3e-199;
Live 19; Mismatches 44;
ooft C, Kalm E, Milan D, Robic Gellin J, Le Roy P, Chardon P;
                                                                                                                                                                                                                                 Claim 5; Fig 3; 71pp; English.
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Looft C,
                                                             WPI; 2001-244810/25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
ses 400; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            464 AA;
                                                                                   N-PSDB; AAD03319.
                   Iannuccelli N,
  Andersson L,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Screening animals to determine those likely to produce larger litters and improved meat quality traits involves assaying for the presence of polymorphisms in the AMP activated protein kinase regulatory gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a method for screening animals to determine those more likely to produce large litters and improved meat quality traits. The method involves assaying for the presence of a genotype in the sample of genetic material obtained from animal. The genotype is characterised by polymorphism(s) in the AMP activated protein kinase regulatory gamma subunit (PRRAG3) gene. The method is used for screening animals e.g., pigs to determine those most likely to exhibit improved meat quality traits and to produce larger litters. The present sequence is pig wild-type PRRAG3 protein.
                                                                                                                                                                                                                                                        /note= "Wild type Asn is replaced with Thr during single nucleotide polymorphism (SNP)" \,
                                                                                                                                                                                                                                                                                                        /note= "Wild type Gly is replaced with Ser during single nucleotide polymorphism (SNP)"
                                                                                                                                                                                                                                                                                                                                                /note= "Wild type Val is replaced with Ile during single nucleotide polymorphism (SNP)"
                                                                                                                                                                                                                                                                                                                                                                                                /note= "Wild type Arg is replaced with Gln during single nucleotide polymorphism (SNP)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
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                                                                                                                                                  AMP activated protein kinase regulatory gamma subunit, PRKAG3 screening; meat quality; single nucleotide polymorphism; SNP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        44; Indels
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Pred. No. 3e-199;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (IOWA ) UNIV IOWA STATE RES FOUND INC
                                                                                                                                                                                                                            Location/Qualifiers
                            AAE22984 standard; Protein; 464 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 2; Fig 1; 109pp; English.
                                                                                                                    Pig wild-type PRKAG3 protein.
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86.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08-JAN-2001; 2001US-260239P.
18-JUN-2001; 2001US-299111P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10-SEP-2001; 2001WO-US28283.
                                                                                         (first entry)
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                                                                                                                                                                                                  Sus scrofa
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                                                         AAE22984;
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Length 464;
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                                                                                                                      Score 2010; DB 23;
Pred. No. 3.8e-199;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pig PRKAG3 polymorphic variant (PRKAG3-200).
                                                                                                                                       Mismatches
Page 100-102; 109pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
200
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                                                                                                                      79.2%; Sco
85.8%; Pre
tive 20;
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                                                                                                       464 AA;
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Disclosure;
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                                                                                                              EQHKIETWREIYLQGCFKPLVSISPNDSLFEAVYTLIKNRIHRLPVLDPVSGNVLHILTH 324
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                                                                                                                                                                                 VVNECGQVVGLYSRFDVIHLAAQQTYNHLDMSVGEALRQRTLCLEGVLSCQPHESLGEVI 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Screening animals to determine those likely to produce larger litters and improved meat quality traits involves assaying for the presence of polymorphisms in the AMP activated protein kinase regulatory gamma
                                                    45 WECELEGLLEERPALCLSPQAPFPKLGWDDELRKPGAQIYMRFMQEHTCYDAMATSSKLV
                                                                            IFDTMLEIKKAFFALVANGVRAAPLWDSKKQSFVGMLTITDFILVLHRYYRSPLVQIYEI
                                                                                                                                                KRLLKFLHIFGSLLPRPSFLYRTIQDLGIGTFRDLAVVLETAPILTALDIFVDRRVSALP
        STGLEATFPKTTPLAQADP-AGVGTPPTGWDCLPSDCTASAAGSSTDDVELATEFPATEA
                                                                                                                                                                                                                                                                                                                                                  AMP activated protein kinase regulatory gamma subunit; PRKAG3 gene; screening; meat quality; single nucleotide polymorphism; SNP; pig;
                                                                                                                                                                                                                                                                                                                                                                                                                       /note- "Wild type Val is substituted with lie due
to single nucleotide polymorphism (SNP)"
                                                                                                                                                                                                                            DRIAREQVHRLVLVDETQHLLGVVSLSDILQALVLSPAGIDALGA 489
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                                                                                                                                                                                                                                                                                                                                   PRKAG3 polymorphic variant (PRKAG3-199).
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                                                                                                                                                                                                                                                                                                                 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   145 WECELEGILEERPALCLSPQAPFPKLGWDDELRKPGAQIYMRFMQEHTCYDAMATSSKLV
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The invention relates to a method for screening animals to determine those more likely to produce large litters and improved meat quality traits. The method involves assaying for the presence of a genotype in the sample of genetic material obtained from animal. The genotype is characterised by polymorphism(s) in the AMP activated protein kinase regulatory gamma subunit (PRKAG3) gene. The method is used for screening animals e.g., pigs to determine those most likely to exhibit improved meat quality traits and to produce larger litters. The present sequence is pig PRKAG3 polymorphic variant (PRKAG3-199).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5;
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STGLEATFPKTTPLAQADP-AGVGTPPTGWDCLPSDCTASAAGSSTDDVELATEFPATEA 144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               those more likely to produce large litters and improved meat quality traits. The method involves assaying for the presence of a genotype in the sample of genetic material obtained from animal. The genotype is characterised by polymorphism(s) in the AMP activated protein kinase regulatory gamma subunit (PRRAG3) gene. The method is used con screening animals e.g., pigs to determine those most likely to exhibit improved meat quality traits and to produce larger litters. The present sequence is pig PRRAG3 polymorphic variant (PRRAG3-52).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a method for screening animals to determine
                                                                                                                                                                                     AMP activated protein kinase regulatory gamma subunit, PRKAG3 gene; screening; meat quality; single nucleotide polymorphism; SNP; pig;
                                                                                                                                                                                                                                                                                                                                                   /note= "Wild type Gly is substituted with Ser due to single nucleotide polymorphism (SNP)"
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85.8%; Pred. No. 1.3e-198;
cive 19; Mismatches 45;
                                                                                                                                               Pig PRKAG3 polymorphic variant (PRKAG3-52).
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                                                                                                                                                                                                                                                                                                      Location/Qualifiers
52
                     AAE22986 standard; Protein; 464 AA.
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08-JAN-2001, 2001US-260239P.
18-JUN-2001; 2001US-299111P.
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Matches 399; Conservative
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N-PSDB; AAD36458.
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                                                                                                                                                                                                                              Malek M,
                                                                                                                                                                                     (IOWA ) UNIV IOWA STATE RES FOUND INC
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08-JAN-2001; 2001uS-260239P.
18-JUN-2001; 2001uS-299111P.
                                                         10-SEP-2001; 2001WO-US28283
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145 WECELEGILEERPALCLSPQAPFPKLGWDDELRKPGAQIYMRFMQEHTCYDAMATSSKLV
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Location/Qualifiers
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                                                                                                                                                                          Conservative
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Matches 305; Conserv
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                                                                                                                               305 AA;
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                                324
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                                                                                                                               Human; gamma subunit; adenosine monophosphate-activated kinase; AMPK; PRKAG3; diabetes; obesity; myopathy; cardiovascular disease; anorectic; genetic testing; carbohydrate metabolism disorder; skeletal muscle;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kalm E, Milan D, Robic A, Rogel-Gaillard C;
J, Le Roy P, Chardon P;
useful as therapeutic for treating carbohydrate metabolism disorders says diabetes, obesity, and disorders associated with muscle metabolism such as myopathy and cardiovascular diseases, to modulate AMPK activity, and for restoring a normal AMPK function. PRKAG3 sequence and its functionally altered mutants are useful for the diagnostic
                                EQHKIETWREIYLQGCFKPLVSISPNDSLFEAVYTLIKNRIHRLPVLDPVSGNVLHILTH
                                           325 KRLLKFLHIFGSLLPRPSFLYRTIQDLGIGTFRDLAVVLETAPILFALDIFVDRRVSALP
                                                                                                                   VVNECGQVVGLYSRFDVIHLAAQQTYNHLDMSVGEALRQRTLCLEGVLSCQPHESLGEVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (AMP)-activated kinase (AMPK) gamma subunit muscle-specific isoform, PRKAG3. Mutation in Prkag3 results in an altered regulation of carbohydrate metabolism, particularly in skeletal muscle. PRKAG3 is
                                                                                                                                                                        DRIAREQVHRLVLVDETQHLLGVVSLSDILQALVLSPAGIDALGA 489
                                                                                                                                                                                                                                                                                                          Human AMPK gamma subunit muscle-specific isoform, PRKAG3.
                                                                                                                                                                                                                                                                                                                                                                cystathione beta synthase; CBS; cardiant; gene therapy.
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                                                                                                                                                                                                                                         AAE00221 standard; Protein; 305 AA
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Gellin J,
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                              265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (KALM/)
                                                                                                                                                                                                                    RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                141 TLCLEGVLSCQPHESLGEVIDRIAREQVHRLVLVDETQHLLGCVSLSDILQALVLSPAGI 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DFILVLHRYYRSPLVQIYEIEQHKIETWREIYLQGCFKPLVSISPNDSLFEAVYTLIKNR 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IHRLPVLDPVSGNVLHILTHKRLLKFLHIFGSLLPRPSFLYRTIQDLGIGTFRDLAVVLE 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    365 TAPILIALDIFVDRRVSALPVVNECGQVVGLYSRFDVIHLAAQQTYNHLDMSVGEALRQR 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 TAPILTALDIFVDRRVSALPVVNECGQVVGLYSRFDVIHLAAQQTYNHLDMSVGEALRQR 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TLCLEGVLSCOPHESLGEVIDRIAREQVHRLVLVDETQHLLGVVSLSDILQALVLSPAGI 484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MREMOEHTCYDAMATSSKLVIFDTMLEIKKAFFALVANGVRAAPLWDSKKOSFVGMLTIT 60
evaluation, genetic testing and prognosis of a metabolic disorder, prieferably a carbohydrate metabolism disorder. Primers that can detect a genetic polymorphic marker linked to a sequence encoding PRRAG3, are useful for detecting a dysfunction of carbohydrate metabolism resulting from the expression of a functionally altered allele of PRKAG3. Transpenic animal and host cell transformed with PRKAG3 or a recening compounds able to modulate AMPK activity. Nucleic acid encoding PRKAG3 is useful for detecting mutant, are useful for screening compounds to modulate AMPK activity. Nucleic acid encoding PRKAG3 is useful for Systathione beta synthase (CBS) domain of PRKAG3 and is useful in gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; gamma subunit; adenosine monophosphate-activated kinase; AMPK; strKRG3; diabetes; obesity; myopathy; cardiovascular disease; anorectic; genetic testing; carbohydrate metabolism disorder; skeletal muscle; cystathione beta synthase; CBS; cardiant; gene therapy; mutant; mutein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   185 MRFMQEHTCYDAMATSSKLVIFDTMLEIKKAFFALVANGVRAAPLWDSKKQSFVGMLTIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 305;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "Wild-type Val substituted with Ile"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61.1%; Score 1551; DB 22; 100.0%; Pred. No. 7.7e-152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
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INRA INST NAT RECH AGRONOMIQUE.

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o;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             in a sequence encoding the first cystathione beta synthase (CBS) domain of PRKAG3 and is useful in gene therapy.

Note: The present sequence is not shown in the specification, but is derived from the human Prkag3 sequence SEQ.ID.NO.4 shown in page 57-58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MRFMQEHTCYDAMATSSKLVIFDTMLEIKKAFFALVANGVRAAPLWDSKKQSFVGMLTIT 244
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TAPILTALDIFVDRRVSALPVVNECGQVVGLYSRFDVIHLAAQQTYNHLDMSVGEALRQR 424
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   useful for detecting a dysfunction of carbohydrate metabolism resulting from the expression of a functionally altered allele of PRKAG3. Transgenic animal and host cell transformed with PRKAG3 or a
                                                                                                                                               New variants of the gamma subunit of vertebrate adenosine monophosphate-activated kinase for diagnosis or treatment of disorders associated with energy metabolism such as diabetes, obesity, and
                                                                                                                                                                                                                                                               e present sequence is a V40I mutant of human muscle-specific isoform gamma subunit of adenosine monophosphate (AMP)-activated kinase MPK) Prkag3. This mutant sequence results in decreased glycogen
                                                                                                                                                                                                                                                                                                                                                                                                                                             evaluation, genetic testing and prognosis of a metabolic disorder, preferably a carbohydrate metabolism disorder. Primers that can detect a genetic polymorphic marker linked to a sequence encoding PRRAG3, are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               heterotrimeric AMPK consisting of PRKAG3 or its mutant, are useful for screening compounds able to modulate AMPK activity. Nucleic acid encoding PRKAG3 is useful for detecting mutations in a Prkag3 gene, or
                                                                  Rogel-Gaillard C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DFILVLHRYYRSPLVQIYEIEQHKIETWREIYLQGCFKPLVSISPNDSLFEAVYTLIKNR
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                                                                                                                                                                                                                                                                                                                                   carbohydrate
                                                                                                                                                                                                                                                                                                                                Mutation in Prkag3 results in an altered regulation of carbohydrate metabolism, particularly in skebteial muscle. PRKAG3 is useful as therapeutic for treating carbohydrate metabolism disorders such as diabetes, obesity, and disorders associated with muscle metabolism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 305;
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                                                                  Robic A,
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Pred. No. 9.8e-152;
L; Mismatches 0;
                                                                  ooft C, Kalm E, Milan D, Robic Gellin J, Le Roy P, Chardon P;
                                                                                                                                                                                                                                 Disclosure; Page -; 71pp; English.
                                                                                                                                                                                                                                                                                                                  content in human skeletal muscle.
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                                                                  Looft C,
                                                                                                                WPI; 2001-244810/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DALGA 489
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ANDERSSON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                305 AA;
                  LOOFT C.
                                (KALM/) KALM E.
                                                                 Andersson L, L
Iannuccelli N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61
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                                                                                                                                                                                                    myopathy
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(ANDE/)
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Human; gamma subunit; adenosine monophosphate-activated kinase; AMPK; PRKAG3; diabetes; obesity; myopathy; cardiovascular disease; anorectic; genetic testing; carbohydrate metabolism disorder; skeletal muscle; cystathione beta synthase; CBS; cardiant; gene therapy; mutant; mutein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       evaluation, genetic testing and prognosis of a metabolic disorder, preferably a carbohydrate metabolism disorder. Primers that can detect a genetic polymorphic marker linked to a sequence encoding PRKAG3, are useful for detecting a dysfunction of carbohydrate metabolism resulting from the expression of a functionally altered allele of PRKAG3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  encoding PRKAG3 is useful for detecting mutations in a Prkag3 gene, or in a sequence encoding the first cystathione beta synthase (CBS) domain of PRKAG3 and is useful in gene therapy.

Note: The present sequence is not shown in the specification, but
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New variants of the gamma subunit of vertebrate adenosine monophosphate-activated kinase for diagnosis or treatment of disorders associated with energy metabolism such as diabetes, obesity, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence is a R41Q mutant of human muscle-specific isoform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Transgenic animal and host cell transformed with PRKAG3 or a heterotrimeric AMPK consisting of PRKAG3 or its mutant, are useful for screening compounds able to modulate AMPK activity. Nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rogel-Gaillard C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mutation in Prkag3 results in an altered regulation of carbohydrate metabolism, particularly in skeletal muscle. PRKAG3 is useful as therapeutic for treating carbohydrate metabolism disorders such as diabetes, obesity, and disorders associated with muscle metabolism
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    such as myopathy and cardiovascular diseases, to modulate AMPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "Wild-type Arg substituted with Gln"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kalm E, Milan D, Robic A, I, Le Roy P, Chardon P;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                      AAE00328 standard; Protein; 305 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page -; 71pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                content in human skeletal muscle.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11-SEP-2000; 2000WO-EP09896.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10-SEP-1999; 99EP-0402236.
18-MAY-2000; 2000EP-0401388.
                                                                                                                                                                                                   (first entry)
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                                                                                                                                                                                                                                                                                    Human Prkag3 R41Q mutant.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-244810/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Misc-difference 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOOFT C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (KALM/) KALM E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Iannuccelli N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200120003-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
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                                                                                                                                                                                                   13-JUN-2001
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                                                                                                                       AAE00328;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rariant.
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AAE00328
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18-MAY-2000; 2000EP-0401388.
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                                                                                                                                                                                                                                                                                                                                            Sequence
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                                                                                                                              myopathy
                                        (KALM/)
                        (ANDE/)
                               (LOOF/)
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                                                                                                               61 DFILVLHRYYRSPLYQIYEIEQHKIETWREIYLQGCFKPLVSISPNDSLFBAYTLIKNR 120
                                                                                                                                                      180
                                                                                                                                                                      424
                                                                                                                                                                                                    is derived from the human Prkag3 sequence {\rm SEQ.ID.NO.4} shown in page 57-58 of sequence listing (AAE00221).
                                                                                                                                      IHRLPVLDPVSGNVLHILTHKRLLKFLHIFGSLLPRPSFLYRTIQDLGIGTFRDLAVVLE 364
                                                                                                      DFILVLHRYYRSPLVQIYFIEQHKIETWREIYLQGCFKPLVSISPNDSLFEAVYTLIKNR 304
                                                                                Pig; gamma subunit; adenosine monophosphate-activated kinase; AMPK; PRKAG3; diabetes; obesity; myopathy; cardiovascular disease; anorectic; genetic testing; carbohydrate metabolism disorder; skeletal muscle; cystathione beta synthase; CBS; cardiant; gene therapy; RN locus; chromosome 15.
                                                                                                                                               185 MRFMQEHTCYDAMATSSKLVIFDTMLEIKKAFFALVANGVRAAPLWDSKKQSFVGMLTIT
                                                                                                                                                                      365 TAPILTALDIFVDRRVSALPVVNECGQVVGLYSRFDVIHLAAQQTYNHLDMSVGEALRQR
                                                                                                                                                                              Gaps
                                                        ;
                                        Length 305;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label= CBS
/note= "Cystathione beta synthase domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Cystathione beta synthase domain"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  synthase domain"
                                                        Indels
                                                                                                                                                                                                                                                                                                                                            Pig AMPK gamma subunit muscle-specific isoform, PRKAG3.
                                        DB 22;
                                                       ;
0
                                        Score 1547; DB 2:
Pred. No. 2e-151;
                                                        1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label= CBS
/note= "Cystathione beta
                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                           AAE00220 standard; Protein; 305 AA.
                                        61.0%;
99.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label= CBS
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                                                                                                                                                                                                                                                                                                                            13-JUN-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .294
                                        Query Match
Best Local Similarity 99.7
Matches 304; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .223
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                                                                                                                                                                                                                                     DALGA 489
                                                                                                                                                                                                                                                    DALGA 305
                        305 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                          Sus scrofa
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                        Sequence
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Liberton and the sequence is ply authorophognate (AMK) gamma subunit muscle-specific isoform, PRRAG3. Prkag3 gene is located in the RN locus of chromosome 15.

RRAG3. Prkag3 gene is located in the RN locus of chromosome 15.

Rutation in Prkag3 results in an altered requilation of carbohydrate metabolism, particularly in skeletal muscle. PRRAG3 is useful as therefore, obesity, and disorders associated with muscle metabolism control and proposes, obesity, and disorders associated with muscle metabolism of its functionally and cardiovascular diseases, to modulate AMFK cardity, and for restoring a normal AMFK function. PRRAG3 sequence and its functionally altered mutants are useful for the diagnostic cardity, and for restoring a normal AMFK function. PRRAG3 sequence and its functionally altered mutants are useful for the diagnostic control and carbohydrate metabolism disorder. Primers that can detect a genetic polymorphic marker linked to a sequence encoding PRRAG3. are useful for detecting a dysfunction of carbohydrate metabolism resulting from the expression of a functionally altered allele of PRRAG3 or a neterotrimeric AMPK consisting of PRRAG3 or its mutant, are useful for encoding PRRAG3 is useful for detecting mutations in a Prkag3 gene, or in a sequence encoding the first cystathione beta synthase (CBS) domain control in a sequence encoding the first cystathione beta synthase (CBS) domain control in a sequence encoding the first cystathione beta synthase (CBS) domain control in the control in a sequence and in a sequence encoding the first cystathione beta synthase (CBS) domain control in the control in a sequence encoding the first cystathione beta synthase (CBS) domain control in the control in a sequence and control in a sequence encoding the first cystathione beta synthase (CBS) domain control in the control in a sequence and control in the control in a sequence and control in a sequence and control in a sequence and control in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 DFILVLHRYYRSPLVQIYEIEEHKIETWREIYLQGCFKPLVSISPNDSLFEAVYALIKNR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                484
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IHRLPVLDPVSGNVLHILTHKRLLKFLHIFGSLLPRPSFLYRTIQDLGIGTFRDLAVVLE 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TAPILTALDIFVDRRVSALPVVNECGQVVGLYSRFDVIHLAAQQTYNHLDMSVGEALRQR 424
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New variants of the gamma subunit of vertebrate adenosine monophosphate-activated kinase for diagnosis or treatment of disorders associated with energy metabolism such as diabetes, obesity, and
                                                                                                                                                                                                                                            Rogel-Gaillard C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         185 MRFMQEHTCYDAMATSSKLVIFDTMLEIKKAFFALVANGVRAAPLWDSKKQSFVGMLTIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TLCLEGVLSCQPHESIGEVIDRIAREQVHRLVLVDETQHLLGVVSLSDILQALVLSPAGI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present amino acid sequence is pig adenosine monophosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 305;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                       ooft C, Kalm E, Milan D, Robic A,
Gellin J, Le Roy P, Chardon P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59.4%; Score 1507; DB 22; 97.0%; Pred. No. 2.8e-147;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5;
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4; Mismatches
(INRG ) INRA INST NAT RECH AGRONOMIQUE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 4; Fig 2; 71pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 97.0
Matches 296; Conservative
                                                                                                                                                                                                                                            Looft C,
                                                                                                                                                                                                                                                                                                                                                                                         2001-244810/25.
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DALGA 305
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                                                       ANDERSSON
                                                                                               LOOFT C.
KALM E.
                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAD03295
                                                                                                                                                                                                                                                                                    Tannuccelli N,
                                                                                                                                                                                                                                                 Andersson L,
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13-JUN-2001
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                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                      Query Match
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                                                                                                                                                                                 PRKAG3; diabetes; obesity; myopathy; cardiovascular disease; anorectic; genetic testing; carbohydrate metabolism disorder; skeletal muscle; cystathione beta synthase; CBS; cardiant; gene therapy; mutant; mutein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New variants of the gamma subunit of vertebrate adenosine monophosphate-activated kinase for diagnosis or treatment of disorders associated with energy metabolism such as diabetes, obesity, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Robic A, Rogel-Gaillard C;
                                                                                                                                                                     gamma subunit; adenosine monophosphate-activated kinase; AMPK;
                                                                                                                                                                                                                                                                                                                                                                                          'note= "Wild-type Val substituted with Ile"
                                                                                                                                                                                                                                                                                                                                                        'note= "Cystathione beta synthase domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "Cystathione beta synthase domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label= CBS
/note= "Cystathione beta synthase domain"
                                                                                                                                   scrofa AMPK gamma chain isoform Prkag3 mutant (R41Q).
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Le Roy P, Chardon P;
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L.
                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                               AAE00226 standard; Protein; 305 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 9; Page -; 71pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kalm
                                                                                                                                                                                                                                                                                                                                          /label= CBS
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                                                                                                                                                                                                                                                                                                                                                                                                                            /label= CBS
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                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               294
                                                                                                                                                                                                                                                                                                                                                                                                                                                             170..223
                                                                                                                                                                                                                                                                                                                                                                                                            148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-244810/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (INRG ) INRA INST
(ANDE/) ANDERSSON
(LOOF/) LOOFT C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOOFT C.
                                                                                                                                                                                                                                                                                                                                                                          Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (KALM/) KALM E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Andersson L, L
Iannuccelli N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200120003-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10-SEP-1999;
                                                                                                 13-JUN-2001
                                                                                                                                                                                                                                                                        Sus scrofa,
                                                                 AAE00226;
                                                                                                                                                                                                                                        variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 myopathy
                                                                                                                                                                                                                                                                                                        Key
Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IHRLPVLDPVSGNVLHILTHKRLLKFLHIFGSLLPRPSFLYRTIQDLGIGTFRDLAVVLE 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              365 TAPILTALDIFVDRRVSALPVVNECGQVVGLYSRFDVIHLAAQQTYNHLDMSVGEALRQR 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DFILVLHRYYRSPLVQIYEIEQHKIETWREIYLQGCFKPLVSISPNDSLFEAVYTLIKNR 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          a genetic polymorphic marker linked to a sequence encoding PRKAG3, are useful for detecting a dysfunction of carbohydrate metabolism resulting from the expression of a functionally altered allale of PRKAG3. Transgenic animal and host cell transformed with PRKAG3 or a heterotrimeric AMPK consisting of PRKAG3 or its mutant, are useful for screening compounds able to modulate AMPK activity. Nucleic acid encoding PRKAG3 is useful for detecting mutations in a Prkag3 gene, or in a sequence encoding the first cystathione beta synthase (CBS) domain of PRKAG3 and is useful for detecting mutations in a Prkag3 gene, or in a sequence encoding the first cystathione beta synthase (CBS) domain of PRKAG3 and is useful in gene therapy.

Note: The present sequence is not shown in the specification, but is derived from the porcine Prkag3 sequence shown in Fig 2 (AAE00220).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pig, gamma subunit; adenosine monophosphate-activated kinase; AMPK; PRKAG3; diabetes; obesity; myopathy; cardiovascular disease; anorectic; genetic testing; carbohydrate metabolism disorder; skeletal muscle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cystathione beta synthase; CBS; cardiant; gene therapy; mutant; mutein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         185 MRFMQEHTCYDAMATSSKLVIFDTMLEIKKAFFALVANGVRAAPLWDSKKQSFVGMLTIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 305;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sus scrofa AMPK gamma chain isoform Prkag3 mutant (R41Q).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "Cystathione beta synthase domain"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 1506; DB 22;
Pred. No. 3.6e-147;
5; Mismatches 5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAE00225 standard; Protein; 305 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          59.38;
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/label= CBS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label= CBS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
Matches 295; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                              305 AA;
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us-09-826-581-6.rag

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  a genetic polymorphic marker linked to a sequence encoding PRRAG3, are useful for detecting a dystunction of carboh/drate metabolism resulting from the expression of a functionally altered allele of PRRAG3. Transgenic animal and host cell transformed with PRKAG3 or a heterotrimente AMPK consisting of PKRAG3 or its mutant, are useful for screening compounds able to modulate AMPK artivity. Nucleic acid encoding PRKAG3 is useful for detecting mutations in a Prkag3 gene, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          in a sequence encoding the first cystathione beta synthase (CBS) domain of PRKAG3 and is useful in gene therapy.

Note: The present sequence is not shown in the specification, but
                                                                                                                                                                                                                                                                                                                                                                                                                                                 New variants of the gamma subunit of vertebrate adenosine monophosphate-activated kinase for diagnosis or treatment of disorders associated with energy metabolism such as diabetes, obesity, and
                                                                                                                                                                                                                                                                                                                                                    Robic A, Rogel-Gaillard C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     preferably a carbohydrate metabolism disorder. Primers that can detect
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       is derived from the porcine Prkag3 sequence shown in Fig 2 (AAE00220).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence is a R410 mutant of muscle-specific isoform of gamma subunit of adenosine monophosphate (AMP)-activated kinase (AMPK) Prkag3 from Sus scrofa. This mutant sequence results in increased glycogen content in pig skeletal muscle.

Mutation in Prkag3 results in an altered regulation of carbohydrate metabolism, particularly in skeletal muscle. PrkAG3 is useful as therapeutic for treating carbohydrate metabolism disorders such as such ass myopathy and carbohydrate metabolism disorders associated with muscle metabolism activity, and for restoring a normal AMPK function. PRKAG3 sequence and its functionally altered mutants are useful for the diagnostic evaluation, genetic testing and prognosis of a metabolish disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
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241..294
/label= CBS
/note= "Cystathione beta synthase domain"
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Pred. No. 7.3e-147;
                                                                                                                                                                                                                                                                                                                                                    Looft C, Kalm E, Milan D, Robic Gellin J, Le Roy P, Chardon P;
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                                                                                                                                                                                                                                                     (INRG ) INRA INST NAT RECH AGRONOMIQUE.
(ANDE/) ANDERSSON L.
(LOOF/) LOOFT C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 9; Page -; 71pp; English.
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96.7%;
                                                                                                                                                       11-SEP-2000; 2000WO-EP09896.
                                                                                                                                                                                             99EP-0402236
                                                                                                                                                                                                                 18-MAY-2000; 2000EP-0401388
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             305 AA;
                                                                                                                                                                                                                                                                                                                                                  Andersson L, Ld
Iannuccelli N,
                                                                                                                                                                                                                                                                                                              (KALM/) KALM E.
                                                                              WO200120003-A2
                                                                                                                                                                                             10-SEP-1999;
                                                                                                                    22-MAR-2001
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DFILVLHRYYRSPLVQIYEIEQHKIETWREIYLQGCFKPLVSISPNDSLFEAVYTLIKNR 304 IHRLPVLDPVSGNVLHILTHKRLLKFLHIFGSLI,PRPSFLYRTIQDLGIGTFRDLAVVLE 364

245

QΥ g δ

61 305 121

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TLCLEGVLSCQPHESLGEVIDRIAREQVHRLVLVDETQHLLGVVSLSDILQALVLSPAGI 484
                                                                                                                6, 2003, 11:01:00
                                                                                                                Search completed: June
Job time: 80.7881 secs
                                                                485 DALGA 489
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365 TAPILTALDIFVDRRVSALPVVNECGQVVGLYSRFDVIHLAAQQTYNHLDMSVGEALRQR 424

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GenCore version 5.1.6

Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on:

June 6, 2003, 10:58:29; search time 31.6865 Seconds

(without alignments)

1483.588 Million cell updates/sec

Title:

US-09-826-581-6

Perfect score: 2538

Sequence: 1 NBFQLEHALRRTPSWSSLGG......LSDILQALVLSPAGIDALGA 489

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 2000000000

Post-processing: Minimum Match 100%

Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Database

hypothetical prote regulatory protein probable 5'-AMP-ac hypothetical prote hypothetical prote probable 5'-AMP-ac conserved hypothet yhcv homolog MTH64 hypothetical prote conserved hypothet hypothetical prote hypothetical prote hypothetical prote conserved hypothet conserved hypothet AMP-activated prot conserved hypothet probable membrane two-component hybr IMP dehydrogenase chloride channel SUMMARIES T10759
T125839
T25839
T25839
T25839
T26822
T126222
T24218
T10971
T16222
T16222 Query Match Length DB Score 138 137 136.5 134 130.5 Result No.

RESULT

two-component hybr hypothetical prote IMP dehydrogenase IMP dehydrogenase IMP dehydrogenase IMP dehydrogenase hypothetical prote conserved hypothet probable acetoin u M71225-related pro yhcv homolog W7H18 IMP dehydrogenase hypothetical prote conserved hypothet conserved hypothet probable transcrip IMP dehydrogenase	ALIGNMENTS rotein kinase (EC 2.7.1) gamma chain - rat us norvegicus (Norway rat) 1999 #sequence_revision 20-Sep-1999 #text_change 21-Jul-2000 0759 eung P. C.F.; Smith, F.C.; Davison, M.D.; Scott, J.; Beri, R.K.; Car 271, 10282-10290, 1996 ber: 206738; MUD:96215327; PMID:8626596 0759 lated from GB/EMBL/DDBJ : mRNA 30 < WADO. ses: EMBL:X95578; NID:91185270; PIDN:CAA64831.1; PID:91185271 rotrimer; Alpha, beta and gamma chains is responsible for the regulation of fatty acid synthesis by phospho CART protein ty acid biosynthesis; phosphotransferase 40.58; Score 1028; DB 2; Length 330; milarity 62.3%; Score 1028; DB 2; Length 330; milarity 62.3%; Score 1028; DB 2; Length 330; milarity 62.3%; Pred. No. 4.1e-72; Conservative 56; Mismatches 63; Indels 0; Gaps 0; PPPEKLGMDDELRKPOAQIYMRFWQEHTCYDAWATSSKLVIFDTMLEIKKAFFALVANGY 224	RAAPLWDSKKOSFVGMLTITDFILVLHRYYRSPLVQIYEIEQHKIETWREIYLQGCFKPL 284 [
AD2103 A64478 A64478 AF31456 AF3148 AF32380 C75148 B69119 B69119 B69119 C75188 C71188 C72264	se (EC 2.7.1) us (NOTWAY rat) nce_revision 20 "; Smith, F.C.; of AMP-activate ; MUD:96215327 GB/EMBL/DDBJ GB/EMBL/DDBJ ain Wistar lpha, beta and ble for the reg n synthesis; phos synthesis; phos A0.5%; Score 1 40.5%; Score 1 40.5	TITDFILLY TITDFINI) KNRIHRLP RNKIHRLP NKTHRLP VLETAPIL VRTTAPIL
001000010000110	e (EC : s (Nort Ce_rev) Smil) / Smil)	MLT
1344 1688 1886 1877 282 282 273 382 382 885 885 885 885 885	A SULT 1 Species: Rattus norvedicus (Noray Dacession: 110759 Mocds, A.: Cheung P. C.F. Smith, F. Ball. Chem. 271, 10282-10290, 1996 Title: Chem. 271, 10282-10290, 1996 Title: Characterization of AMP-actin Reference number: 206738; MUID:9621 Status: translated from GB/EMBL/DDB Molecule type: mRNA Residues: 1-330 (*MOO> Cross-references: EMBL:X95578; NID: Experimental source: strain Wistar Complex: heterotrimer; alpha, beta Bucting: heterotrimer; alpha, beta Bucting: strain wistar Complex: heterotrimer; alpha, beta Bestingtion: is responsible for the Superfamily: CAT3 protein Keywords: fatty acid blosynthesis; Mutches 197; Conservative 56; Matches 197;	RAAPLWDSKKOSFVGMLTITDFI RAAPLWDSKKOSFVGMLTITDFI VSISPNDSLFBAVYTLIKNRIHR VSISPNDSLFBAVYTLIKNRIHR VCISPNASLFBAVYLLKNRIHR VCISPNASLFBAVYTLIKNRIHR VRTIQDLGIGTFRDLAVVLETAP SHELL SHELL AQQTYNHLDMSVGBALRQRTUT AQQTYNHLDMSVGBALRQRTUT AAGTTYNNLDVSVTKALQHRSHY LGVVSLSDILQALVLS 480 KGIVSLSDILQALVLS 480
00000000000000000000000000000000000000	ivated protein kina es: Rattus norvegic 20-Sep-1999 #seque sion: T10759 . Chem. 710, 10282 Chem. 71, 10282 Characterization ence number: 266738 Sion: T10759 s: translated from ule type: mRNA ule type: mRNA ule type: mRNA imental source: str eferences: EMBL:X imental source: str fers nore intion: is responsi family: CAT3 protei rds: fatty acid bio Match Local Similarity es: 197; Conservat es: 197; Conservat es: 197; Conservat	
129.5 126.5 126.5 123.5 123.5 120.5 120.5 119 116.5 116.5 115.5	TIT 1 159 activated p ecies: Ratt ecies: 20-88 ccession: T1 cods, A.: Ch cods, A.: Ch cods, A.: Ch cods: Chem. clain chem. cl	225 R 69 R 69 R 7 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8
8 8 8 8 8 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	RESULT 1 T10759 AMP-activated protein C.Species: Ratus nor C.Species: Ratus nor C.Date: 20-Sep-1999 # C.Accession: T10759 R.Woods, A.: Cheung P. Biol. Chem. 271, 1 A.Title: Charmerterizar A.Reference number: Z.A.Recession: T10759 A.Status: translated A.Molecule type: mRNA-Residues: 1-330 cMCA.Residues:	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0

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submitted to the EMBL Data Library, June 1993
A;Description: Correct end of the ORF for the CDC20 gene of Saccharomyces cerevisiae
A;Reference number: S48507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               probable 5'-AMP-activated, gamma subunit family - fission yeast (Schizosaccharomyoes C; Species: Schizosaccharomyces pombe
C; Species: Schizosaccharomyces pombe
C; Date: 20-Jul-1996 #sequence_revision 13-Mar-1997 #text_change 20-Jun-2000
C; Accession: T38059; S67444
R: McLean, J.; Harris, D.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.
submitted to the EMBL Data Library, March 1996
A; Reference number: 221766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: BMBL:272637; NID:91322666; PIDN:CAA96823.1; PID:91322667; GSPDB:
A;Experimental source: strain S288C
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Residues: 1-274 <MC2>
A;Cross-references: EMBL:269944; NID:91217974; PIDN:CAA93805.1; PID:91217975; GSPDB:
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    186 RFMQEHTCYDAMATSSKLVIFDIMLEIKKAFFALVANGVRAAPLWDSKKQSFVGMLTITD 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                350 DLGIGTFRDLAVVLETAPILTALDIFVDRRVSALPVVNECGQVVGLYSRFDVIHLAAQQT 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              246 FILVLHRYYRSPLVQIYEIEQHKIETWREIYLQGCFKPL------VSISPNDSLF 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  84 FINVIQYYFSNP-----DKFELVDKLQLDG-LKDIERALGVDQLDTASIHPSRPLF 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EAVYTLIKNRIHRLPVLDPVSGN----VLHILTHKRLLKFLHIFGSLLPRPS-FLYRTIQ 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    134 EACLKMLESRSGRIPLIDQDEETHREIVVSVLTQYRILKFV----ALNCRETHFLKIPIG 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 410 YNHLDMSVGEALRQRTLCLEGVLSCQPHESLGEVIDRIAREQVHRLVLVDETQHLLGVVS 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24 KFLNSKTSYDVLPVSYRLIVLDTSLLVKKSLNVLLQNSIVSAPLMDSKTSRFAGLLTTTD 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: EMBL:D16506; NID:g391938; PIDN:BAA03958.1; PID:g2160324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Description: involved in derepression of glucose-repressed genes C; Superfaily: CAT3 protein C; Keywords . nuclear and protein c; Keywords 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14.8%; Score 375.5; DB 2; Length 274;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18.0%; Score 457; DB 1; Length 322; 34.2%; Pred. No. 7.9e-28; ive 66; Mismatches 108; Indels
                                                                                                                                                                                                                                                    R.Lauquin, G.
submitted to the Protein Sequence Database, May 1996
A.Reference number: $64122
A.Accession: $64125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Gene: SGD:SNF4; CAT34; MIPS:YGL115w
A;Cross-references: SGD:S0003083; MIPS:YGL115w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Superfamily: CAT3 protein . Keywords: nucleus; transcription regulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  54/1; 173/3; 226/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 18.0%
Best Local Similarity 34.2%
Matches 106; Conservative
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A,Introns: 12/3; 54/1; 173/3
C,Superfamily: CAT3 protein
                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-322 <LAU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A, Accession: T38059
A, Status: preliminary
A, Molecule type: DNA
A, Residues: 1-274 <MC2>
                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-21 <DOI>
                                                                                                                  A; Accession: S48508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Map position: 7L
C; Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               295
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N;Alternate names: CAT3 protein; protein G2945; protein YGL115w
C;Species: Saccharomyces cerevisiae
C;Species: Saccharomyces cerevisian
C;Species: Saccharomyces cerevision 30-Jun-1989 #text_change 21-Jul-2000
C;Accession: A3806; J10316; S48508; S64125
R;Celenza, J.L.; Eng, F.J.; Carlson, M.
Mol. Cell. Biol. 9, 5045-5054, 1989
A;Title: Molecular analysis of the SNF4 gene of Saccharomyces cerevisiae: evidence for A;Reference number: A33480; MUID:90097921; PMID:2481228
A;Accession: A38906
A;Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241 LIITDFILVLHRYYRS ------PLVQI --YEIEQHKIETWRE-IYLQGCFKPLVS 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           347 TIQDLGIGTFRDLAVVLETAPILTALDIFVDRRVSALPVV-NECGQVVGLYSRFDVIHLA 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ISPNDSLFEAVYTLIKNRIHRLPVI.DPVSGNVLHII.THKRLLKFLHIFGSLLPRPSFLYR 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SPKELGIGTWSGIRVVFPDTQLVDCLDILLNKGVSGLPVVERETFKVVDMYSRFDAVGIA 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        406 AQQIYNHLDMSVGEALRQRTLCLEG-----VLSCQPHESLGEVIDRIAREQVHRLVL 457
                                                                                                                                                                                                                                                                                                                                                                                          A:Molecule type: DNA
A:Residues: 1-478 <MIL>
A:Cross-references: EMBL:U97550; PIDN:AAB52856.1; GSPDB:GN00028; CESP:T20F7.6
A:Experimental source: strain Bristol N2; clone T20F7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein T20F7.6 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C:Accession: T25899
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A; Cross references: GB:M21760; NID:g171164; PIDN:AAA34472.1; PID:g171165
R; Doi, A.; Doi, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Map position: X
A;Introns: 33/3; 112/2; 144/1; 205/3; 263/2; 300/3; 380/3; 402/2; 451/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 478;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19.2%; Score 488; DB 2; Length 471 ilarity 36.7%; Pred. No. 5.4e-30; Conservative 69; Mismatches 106; Indels
                                                                                                                                                                        R.Miller, N.; Gattung, S. submitted to the EMBL Data Library, April 1997
A.Description: The sequence of C. elegans cosmid T20F7.
A.Reference number: Z20107
A.Accession: T25899
A.Status: preliminary; translated from GB/EWBL/UDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 119; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Gene: CESP:T20F7.6
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A;Introns: 5/3; 45/2; 72/1; 105/3; 153/3; 179/2; 200/3; 225/3; 255/3; 349/3; 397/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 AQIYMRFMQEHTCYDAMATSSKLVIFDTMLEIKKAFFALVANGVRAAPLWDSKKQSFVGM 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADPYHTFMKSITCYDLQPTHSSLVVFDGKTKVKAAVHALSQHGHIAAVVTNTDKYQAECV 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EAVYTLIKNRIHRLPVLD---PVSGNVLHILTHKRLLK-------FLHIFGSLL 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRPSFLYRTIQDLGIGTFRD - - LAVVLETAPILTALDIFVDRRVSALPVVNECGQVVGLY 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241 LT----ITDFILVL--HRYYRSPLVQIYEIEQHKIETWREIYLQGCFKPLVSISPNDSLF 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        135 FNMGHCLTAILLVAAGNREVASKTL------VEFLKEIGSGN----IICSGVQNSVW 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           397 SRFDVI-HLAAQQTYNHLDMSVGEALRQRTLCLEGVLS----CQPHESLGEVIDRIAREQ 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      291 ARKDIILEIMSHQGGNFHDM-----LKEPVKILQSLQSRLVYGRSSYTVFETVAKMMTSD 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: EMBL:U67950; PIDN:AAB07568.1; GSPDB:GN00028; CESP:T01B6.3 A;Experimental source: strain Bristol N2; clone T01B6
                                                                                                          C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C;Accession: F25854
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C.Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C.Accession: T24248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 460;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 443;
                                                                                                                                                                                                           R;Johnson, D.
submitted to the EMBL Data Library, August 1996
A;Description: The sequence of C. elegans cosmid T01B6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 217.5; DB 2;
Pred. No. 5e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 222; DB 2; L
Pred. No. 2.1e-09;
9; Mismatches 121;
                                                                                       hypothetical protein T01B6.3 - Caenorhabditis elegans
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submitted to the EMBL Data Library, October 1995
A;Reference number: 219863
A;Accession: T24248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     452 VHRLVLVDETQHLLGVVSLSDIL 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8.7%; Scur.
26.3%; Pred
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 26.3
Matches 85; Conservative
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                                                                                                                                                                                                                                                                                                         A;Reference number: Z20100
A;Accession: T25854
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-443 <JOH>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Gene: CESP:T01B6.3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein [imported] - Arabidopsis thaliana
Cipecies: Arabidopsis thaliana (mouse-ear cress)
Cipecies: Date: Obtain (mouse-ear cress)
Cipecies: Arabidopsis A: Ecker, J. R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, R.; ansen, N.F.; Hudnes, B.; Huizar, L.
Arabidopsis: Allores, D.; Johkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
Arabidopsis: Alabergy S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.J.; Davis, R.W.
Aritle: Sequence and analysis of chromosome I of the plant Arabidopsis.
A; Reference number: A86141; MUID:21016719; PMID:11130712
A; Accession: B86222
A; Status: preliminary
A; Molecule type: Dana, A., Accession: B86222
A; Molecule type: Dana, A., Accession: Bara, 
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                               7:
                                                                                       175 ELRKPGAQIYMRFMQEHTCYDAMATSSKLVIFDTMLEIKKAFFALVANGVRAAPLWDSKK 234
                                                                                                                                                                                                           235 QSFVGMLTITDFILVLHRYYRSPLV--QIYEIEQHKIETWREIYLQ-GCFKP-LVSISPN 290
                                                                                                                                                                                                                                                 66 NKFAGLLTMADFVNVIKYYYQSSFPEAIAEIDKFRLLGLREVERKIGAIPPETIYVHPM 125
                                                                                                                                                                                                                                                                                                                                     291 DSLFEAVYTLIKNRIHRLPVLDPVSGN-----VLHILTHKRLLKFLHIFGSLLPRPSFLY 345
                                                                                                                                                                                                                                                                                                                                                                 223 GVRAAPLWDSKKQSFVGMLTITDFILVLHRY--YRSPLVQIYEIEQHKIETWRE--IYLQ 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                279 GCF-----KPLVSISPNDSLFEAVYTLIKNRIHRLPVL-----DPVSGNVLHILTHK 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             180 ROYDGSGRPYPRPLVQVGPYDNLKDVALKILQNKVAAVPVIYSSLQDGSYPQLLHLASLS 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           326 RLLK-----FLHIFGSLLPRPSFLYRTIQDLGIGTF------RDLAVVLETAPILTA 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                240 GILKCICRYFRHSSSSL----PILQQPICSIPLGTWVPRIGESSSKPLATLRPHASLGSA 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  372 LDIFVDRRVSALPVVNECGQVVGLYSRFDVIHLAAQQTYN--HL-DMSVGEALR--QRTL 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RT-IQDLGIGTFRDLAVVLETAPILTALDIFVDRRYSALPVVNECGOVVGLYSRFDVIHL 404
                                                                                                                             A; Residues: 1-391 <STO>
A; Cross-references: GB: AE005172; NID: q2 442682; PIDN: AAB70406.1; GSPDB: GN00141
C; Genetics:
                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                               Indels
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; Mismatches 106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             405 AAQQTYNHLDMSVGEALRQRTLCLEGVLSCQ 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241 IQDGDYSNLDLSVGEALLKRPANFDGVHTCR 271
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                               64;
31.78;
                               86; Conservative
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Matches 79; Conserv
Best Local Similarity
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112	RESULT 9 146197 1746197 1746197 1746197 1746197 1746197 1746197 1746197 1746197 1746197 1746197 1746197 175Peciess: Arabidopsis thaliana (mouse-ear cress) 175Peciess: Arabidopsis thaliana (mouse-ear cress) 176Colone: Arecession: T46197 177Colone: N.: Robert, C.: Brottier, P.: Wincker, P.: Cattolico, L.: Artigueni 177A 178Accession: T46197 178Accession:	Query Match Query Match Query Match Best Local Similarity 22.5%; Pred. No. 1.4e-07; Matches 89; Conservative 82; Mismatches 140; Indels 84; Gaps Qy 162 SPQAPEPKLGWDDELRKPGAQIYMRFMQEHTCYDAMATSSKLVIFDTM-LEIK-	Qy 214KAFFALVANGVRAAPIMDSKKQSFVGMLTITDFIL-VLHRYYRS	Qy 348 IQDLGIGTFRDLAVVLETAPILTALDIFVDRRVSALPVVNECGO-VVGLYSRFDV-IH ::: :	23.2 Qy 404 LAAQQTYNHIDMSVGBALRQRTLCLEGVLSCQPHESIGEVIDRIA 1 1 1 1 1 1 1 1 1	RESULT 10 T18227 hypothetical protein - yeast (Candida albicans) C:Species: Candida albicans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 C;Accession: T18227
13 RLTMLEKGCDPIAGGSPRNSTTKSPRPDTPASEORRNSTSGRRPSFLSQVRDLHPRT 11: 3 RLTMLEKGCDPIAGGSPRNSTTKSPRPDTPASEORRNSTSGRRPSFLSQVRDLHPRT 60 113 GWDCLPSDCTASAAGSSTDDVELATEFPATEAWECELEGLLERPALCLSDQA 16:	MATSSKLVIFDTMLEIKKAFFALVANGVRAAPLMDSKKOSFVGMLTITDFILVLHRYY	ONATO TO TO THE PARTY OF THE PA		atch 8.4%; Score 214; DB 2; Length 379; cal Similarity 23.5%; Pred. No. 7.1e-09; 85; Conservative 73; Mismatches 122; Indels 82; Gaps	188 MQEHTCYDAMATSSKLV1FDTMLEIKKAFFALVANGVRAAPLWDS 23: 1	
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	60 60 60 60 60 60 60 60 60 60 60 60 60 6	Oy 486 Oy 486 Db 420 BESULT 8 T10971 Pv42 protein	C, Speri C, Date: C, Acces R, Abet A, Refer A, Acces A, Statu A, Molec A, Resid A, Resid	Query M Best Lo Matches	QY Db QY	9y 9y 0y

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otein T8P19.40 - Arabidopsis thaliana (adopsis thaliana (mouse-ear cress) 1000 #sequence_revision 04-Feb-2000 #text_change 04-Feb-2000 197 obert, C.; Brottier, P.; Wincker, P.; Cattolico, L.; Artiguenave, F., Protein Sequence Database, December 1999 3r: 223008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18;
                                                                    SDMQNRGSSRRELVTCYAESPLSEVIEKAVTSHVHRVWVVDQEGLLVGVVSLTDVIR 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APFPKLG------WDDELRKPGAQIYMRFMQEHTCYDAMATSSKLVIFDTM-LEIK- 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --KAFFALVANGVRAAPLWD-----SKKQSFVGMLTITDFIL-VLHRYY----RS 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---KIETWREIY-----LQGCFK--PLVSI 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | :: | : | : | : | .: | 134
AASNGFSHDFTTDVLDNGDSAVTSGNFFEVLTSSELYKNTKVRDISGTFRWAPFLAL 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OSLFEAVYTLIKNRIHRLPVLDPVSGNVLHILTHKRLLKFLHIFGSLLPRPSFLYRT 347
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------NECGQVVGLYSRFDV--IHLAAQQTYNHLD-MSVGEALRQRTL 426
                                                                                                                                                                                                                                 3------VLSCQPHESLGEVIDRIAREQVHRLVLVDETQHLLGVVSLSDILQ 475
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larity 22.5%; Pred. No. 1.4e-07;
Conservative 82; Mismatches 140; Indels 84; Gaps
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s: EMBL:AL133315
urce: cultivar Columbia; BAC clone T8P19
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:||::||::||:|||||||
IHRIYVVDDFGNLEGLITLRDIIARLVHEPSG 406
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                                            Conservative
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Matches 96; Conserv
                        Similarity
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  Query Match
Best Local Simi
Matches 81;
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B. Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Mature 408, 816-820, 2000

A. Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, S.X.; Liu, S.X.; Liu, S.X.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakmo, H.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A. Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A. Reference number: A86141; MuID:21016719; PMID:11130712

A. Accession: F86287

A. Status: preliminary
                                                                                                                                                                                                                                                                                  17;
                                                                                                                                                A;Cross-references: EMBL:AL033501; NID:e1341022; PID:e1341023; PIDN:CAA21985.1
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             235 EFVTQTISKAKRGEEVPVEFIIKLHPKNPFIKFNETDTLFSVÆTL-GNGVHRIAITNEE 293
                                                                                                                                                                                                                                                                                                                      71 PPGQGEGPRSRPAAESTGLEATFPKTTPLAQADPAGVGTPPTGWDCLPSDCTASAAGSST 130
                                                                                                                                                                                                                                                                                                                                                                                                          131 DDVELATEPPAT-----EAWECELEGILEERPALCLSPQAPFPKLGW------ 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                59 TGGSISATAPGSTQHYLHHHPSRKTSIVEILSSPPPLPTDPNDPIHQLSLSRHASTSSNK 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            173 -DDELRKPGAQIYMRFWQEHTC-----YDAMATSSKLVIFDTMLEIKKAFFALVAN 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SSSQSIAPGSTA----ITWHAFSLVDWSEIPLTELTESNKLISIHSSHSVQSAFETLLKY 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              223 GVRAAPLWDSKK--QSFVGMLTI-----TDFILVLHRYYRSPL-----VQIYEIEQH 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             268 -----KIETWREIYLQGCFK-----PLVSISPNDSLFEAVYTLIKNRIHRLPVLDPV 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SGNVLHILTHKRLLKFLHIFGSLLPRPSF-LYRTIQDLGIGTFRDLAVVLETAPILTALD 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            294 GNKITGILSQRRLIKYMWENARRFPSLDFYLTSTLQDLKIGSSNPI-TIYEDQMLIEALH 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      374 IFVDRRVSALPVVNECGQVVGLYSRFDVIHLAAQQTYNHLDMSV----GEALRQRTLCLE 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Residues: 1-352 <STO>
A;Cross-references: GB:AE005172; NID:95103830; PIDN:AAD39660.1; GSPDB:GN00141 C;Genetics:
A;Map position: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein F9L1.27 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Dec-2001
                                                                                                                                                                                                                                                                                                                                                4 PPQPRQMPKSPRLSTST---SSGPSAVPNLLGSPR--PSPPQLQHQPSSASTSSTTSTAT
                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                  78;
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                                                                                                                                                                                                                                      Length 629;
                                                                                                                                                                                                                                    ; Score 196; DB 2; Length 629; Pred. No. 3.6e-07; 80; Mismatches 208; Indels
                                                       A, Accession: T18227
A, Status: preliminary; translated from GB/EMBL/DDBJA; Molecule type: DNA
R;Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, November 1998
                                                                                                                                                                                                                                      7.78;
                                                                                                                                                                                                                                                                              101; Conservative
                                          A; Reference number: 218831
                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 101; Conserv
                                                                                                                              A; Residues: 1-629 <BAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
                                                                                                                                                                                            A; Note: Ca41C10.01c
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Chin. C.W.; Ecker, J.R.; Falm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alcans, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kin C.A.; Li, J.H.; Liu, S.Y.; Liu, Z.A.; Luros, J.S.; Maiti, E.; Kin Rizzo, M.; Rooney, T.; Rowley, D.; Sawano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tall A;Authors: Squence and analysis of chromsome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               182 QIYMRFMQEHTCYDAMATSSKLV-----IFD-----TMLEIKKAFFALVANGVRAAPL 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  129 -----TLNPNTSVLECMEVFSKG-IHRALVPVESSIESNNTIAGVELIESASAYKMLTQM 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30 -----W-----VLHRYRSPLV 259
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          320 HILTHKRILKFILHIFGSL--LPRPSFLYRTIQDL-GI--GTFRDLAVVLETAPILT---- 370
                                                                                                                                                                                                                                                                                                                                                                                                                   281 FKPLVSISPNDSLFEAVYTLIKNRIHR -- LPVLDPVSGN------VLHILTHK 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            326 RLLKFL--HIFGSLLPRPSFLYRTIQDLGIGTFRDLAVVLETAPILTALDIFVDRRVSAL 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                384 PVVN-------ECGQVVGLYSRFDVIHLAAQQTYNHLDMSVGEALRQRTLCL 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              239 PIVHAPDIAQEDHLQLVNGRHRKVIGTFSATDLKGCRLPELQTWLPLTALEFTEKTSGKE 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A, Cross-references: GB: AE005173; NID: 95902384; PIDN: AAD55486.1; GSPDB: GN00141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein F18B13.17 [imported] - Arabidopsis thaliana C.Species: Arabidopsis thaliana (mouse-ear cress) C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001 C:Accession: D96832
                                                                                                                                                                                                      17 TAKDLTVRNRRLVEVPYTATLSHAMNTLVANSISALPVAAPPGHWIGAGGSMIMESDKQT
                                                                                                                                                                                                                                                                                 -----FVGMLTITDFIL-----VLHRYYRSPLVQIYEIEQHKIE---TWREIYLQGC
                                                                                                                                                                                                                                                                                                                         81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              429 EGVLSCQPHESLGEVIDRIAREQVHRLVLVDETQHLLGVVSLSDILQAL 477
       Length 352;
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                                                                    Indels
                                                                                                                                        192 TCYDAMATSSKLVIFDTMLEIKKAFFALVANGVRAAPL-----W---
7.5%; Score 189.5; DB 2; 23.2%; Pred. No. 5.1e-07;
                                                                Mismatches 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7.1%; Score 179; DB 2;
25.3%; Pred. No. 3.9e-06;
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tive 59; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ..
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submitted to the EMBL Data Library, July 1999 A.Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome: A:Reference number: A75001 A.Reference number: A75001 A.Accession: G75056 A:Status: preliminary A.Molecule type: DNA A:Residues: 1-392 < KAM> A:Residues: 1-392 < KAM> A:Cross-references: GB-AJ248287; GB:AL096836; NID:g5458657; PIDN:CAB50348.1; PID:e15: G:Genetics: A:Experimental source: strain Orsay C:Genetics: A:Gene: PAB0961	Query Match 6.4%; Score 161.5; DB 2; Length 392; Best Local Similarity 23.4%; Pred. No. 8.8e-05; Matches 63; Conservative 54; Mismatches 103; Indels 49; Gaps 12; Qy 227 APLWDSKKQSFVGMLTITDFILVLHRYTRSPLVQIYEIEQHKIETWREIY 276	QY 277 LQGCFKPLVSISPNDSLFEAVYTLIKNRIHRLPVLDPVSGNVLHILTHKRLKFLHIFGS Db 74RPAPVVKPTDLSHARLLLFTLRSLPVGEN-RABILGVISDWALLE QY 337 LLPRPSFLYRTIQDLGIGTFRDLAYLETAPILTALDIFVDRNSALPVVNDCGQVYGLY :	OY 397 SREDVIHLAAQQTYNHLDMSVGEALRORTLCLEGVLSCOPHESLGEVID 445	RESULT 15 S46088 hypothetical protein YBR214w - yeast (Saccharomyces cerevisiae) N.Alternate names: hypothetical protein YBR1501 C; Species: Saccharomyces cerevisiae C; Date: 26-Aug-1994 #sequence_revision 09-Sep-1994 #text_change 19-Apr-2002 C; Accession: \$46088; \$46090	R.Rieger, M. Submitted to the Protein Sequence Database, August 1994 A.Reference number: \$45734 A.Accession: \$46088 A.Molecule type: DNA A.Residues: 1.527 <rie> A.Cross-references: EMBL:236083; NID:9536599; PIDN:CAA85178.1; PID:9536600; MIPS:YBR: A.Experimental source: Strain \$288C R.Dubois, E.; El Bakkoury, M.; Glansdorff, N.; Messenguy, F.; Pierard, A.; Scherens,</rie>		Query Match Query Match Best Local Similarity 21.5%; Pred. No. 0.00025; Matches 94; Conservative 63; Mismatches 182; Indels 98; Gaps 17; Qy 71 PPGQGGERSRPAAESTGLEATFPKTPLAQADPAGVGTPPTGWDCLPSDCT 122
Db 195 NI-TGPELVESASAYAMLSQMDLISFFFDQSSQLHGILSHTVTDLSAIHNTVLALITSQAR 253 Qy 371ALDIFVDRRVSALPVVNECGQVVGLYSRFDVIHLAAQQTYN 411	Db 372 GCLQGLVSLTDII-AVVRS 389 RESULT 13 B96720 Nypothetical protein T17F3.17 [imported] - Arabidopsis thaliana C:Species: Arabidopsis thaliana (mouse-ear cress)	C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001 C;Accession: B96720 R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K. ansen, N.F.; Hughes, B.; Huizar, L. Narure 408, 816-820, 2000 A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Bopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali	Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H. A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, Rer, M.; Wu, D.; Yu, G.; Fraser, C.M.; Vent., J.C.; Davis, R.W. A; Title: Sequence and analysis of chromosome l of the plant Arabidopsis. A; Reference number: A86141; MUID:21016719; PMID:11130712 A; Accession: B96720 A; Anolecule type: DNA	A; Residues: 1-447 <sto> A; Cross-references: GB:AE005173; NID:g6358813; PIDN:AAF07393.1; GSPDB:GN00141 C; Genetics: A; Genetics: A; A;</sto>	QY 262 YEIEQHKIETWREIYLQGCFKPLVSISPNDSLFEAVYTLIKNRIHRLPVLDPVSGN 317 Db 194 YEVILQEEPFKSTTVRTILKSFRMAPFIEVSTESSMI.SVMI.LLSKYRLRNVPVIKTGEPD 253 QY 318 VLHILTHKRLIKFLHIFGSILLRPSFI.YRTIQDLGIGTFRDLAVY-LETA 366 CS4 IKNYYTQSAVVHGLEGCKGRDWFDHISALPISDLGIPFMSPNEVISIESE 303	Qy 367 P-ILTALDIFUDRRVSALPVVNECG-QVVGLYSRFDVIHLAAQQTYNHLDM 415	SULT 14 5056 hydrogenase PAB0961 Species: Pytrococcus Date: 20-Aug-1999 #s Accession: G75056 anonymous, Genoscope

123 ASAAGSSTDDVELATEPPATEAWECELEGILEERPALCISPQAPFPKLGW 172	173 DDELRKPGAQIYMRFMQEHTCYDAMATSSKLVIFDTMLEIKKAFFALVANGVRAAPLMDS 232 : : : : : : : : : : : : :	233 KKQSFVGMLTITDFILVLHRYYRSPLVQIYEIEQHKIETWREIXLQGCFKP 283	284 LVSISPNDSLFEAVYLLIKNRIHRLEVLDEVSGNVLHILTHKRLLKFLHIFGSLLP 339 111 1::: :: : 11 1 1 1	340 RPSFLYRTIQDLGIGTFRDLAVVLETAPILTALDIFVDRRVSALPVVNEC 389 ::	390 GQVVGLYSRFDVIHLAAQQTYNHLDMSVGEALRQRTLCLEGVLSCQPHESLG 441 :	442 EVIDRIAREQVHRLVLV 458 42 ::: :: : 380 RTLAKLVATKSHRLWIV 396
ço qo	QY	Qy	QY	çy Q	Qy Db	QY D b

Search completed: June 6, 2003, 11:03:34 Job time : 34.6865 secs --

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GenCore version 5.1.6
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OM protein - protein search, using sw model

6, 2003, 10:57:04; Search time 17.9842 Seconds (without alignments) 1127.761 Million cell updates/sec June Run on:

US-09-826-581-6 2538

1 MEPGLEHALRRTPSWSSLGG........LSDILQALVLSPAGIDALGA 489 Perfect score: Sequence:

BLOSUM62 Scoring table:

Gapop 10.0 , Gapext 0.5

112892 segs, 41476328 residues Searched:

112892 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Listing first 45 summaries Post-processing: Minimum Match 08 Maximum Match 1008

SwissProt_40:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Oguqi9 homo sapien	s sns			P54619 homo sapien	bos 1	O54950 mus musculu	P12904 saccharomyc		kluy		Sacc	Q58622 methanococc	P15889 thermofilum		P42851 pyrococcus		Q58821 methanococc	O58045 pyrococcus	Q9uy49 pyrococcus			Q59011 methanococc	Q9wr15 herpesvirus				Q07152 drosophila			-	4346	050316 chlorobium
SUMMARIES	ID	AAK I_HUMAN	AAKI_PIG	AAKH HUMAN	AAKG_RAT	AAKG_HUMAN	AAKG_BOVIN	AAKG_MOUSE	SNF4_YEAST	YDA1_SCHPO	SNF4_KLULA	AAKG_PIG	YB64_YEAST	YC25_METJA	YR33_THEPE	YE04_METJA	IMDH_PYRFU	YGF6_YEAST	YE26_METJA	IMDH_PYRHO	IMDH_PYRAB	CAPP_SYNP6	YC32_METJA	IMDH_METJA	VGLB_HSVT2	Y100_METJA	Y525_METKA	YE29_HELPY	IMDH_DROME	CCAG_HUMAN	Y922_METJA	Y146_MYCGE	UL52_HSVSA	IMDH_CHLVI
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	l Query Match Length	464	464	569	330	331	330	330	322	334	328	133	527	280	300	421	485	527	168	486	485	1053	296	496	944	509	196	329	537	2377	138	424	835	521
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	Score	2398	2011	1093	1028	1017	1013	687	457	456.5	418.5	267.5	158	149	139	138.5	138	136.5	126.5	126	119	114	113.5	110	108.5	107.5	104.5	104	103	102.5	102	101.5	101.5	101
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٠,	Q09826 schizosacch	Q9wtq2 rattus norv	Q9eq60 rattus norv	Q58139 methanococc	P13199 herpesvirus	Q9z114 helicobacte	P56088 helicobacte	Q96ru2 homo sapien	P13666 oryctolagus	088480 rattus norv	Q62059 mus musculu
PHY2_SYNY3	SD23_SCHPO	PODX_RAT	CCAH_RAT	Y729_METJA	IE63_HSVSA	IMDH_HELPJ	IMDH_HELPY	UBPS_HUMAN	SRCA_RABIT	CABI_RAT	PGCV_MOUSE
~	Н	гH	Н	Н	Н	Н	~	Н	⊣	Н	Н
1276	408	485	2359	124	417	481	481	1077	806	2182	3358
9.6	3.9	3.9	3.9	3.9	3.8	3.8	3.8	3.8	3.8	3.8	3.8
0	5.5	38.5	98.5	86	97.5	97.5	97.5	97.5	26	97	96.5
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ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SENSITIVE LIPASE. THIS IS A REGULATORY SUBUNIT. IT MAY PLAY A ROLE IN THE REGULATION OF ENERGY METABOLISM IN SKELETAL MUSCLE.
SUBUNIT: HETEROTRINER OF AN ALPHA CATALYTIC SUBUNIT, A BETA AND A GAMMA NON-CATALYTIC REGULATORY SUBUNITS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- TISSUE SPECIFICITY: SKELETAL MUSCLE, WITH WEAK EXPRESSION IN HEART AND PANCREAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -i- SIMILARITY: BELONGS TO THE 5'-AMP-ACTIVATED PROTEIN KINASE, GAMMA SUBUNIT FAMILY.
-i- SIMILARITY: CONTAINS 4 CBS DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
TSSUB-SReletal muscle;
MEDILINE-20280150; PubMed-10818001;
Milan D., Jeon J.-T., Looft C., Amarger V., Robic A., Thelander M.,
Rogel-Gaillard C., Paul S., Iannuccelli N., Rask L., Ronne H.,
Lundstroem K., Reinsch N., Gellin J., Kalm E., Le Roy P., Chardon P.,
Andersson L.;
                                                                                                                                                                                    16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
5'-AMP-activated protein kinase, gamma-3 subunit (AMPK gamma-3 chain)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -i- FUNCTION: AMPK IS RESPONSIBLE FOR THE REGULATION OF FATTY ACID SYNTHESIS BY PHOSPHORYLATION OF ACETYL-COA CARBOXILABE. ALSO REGULATES CHOLESTEROL. SYNTHESIS VIA PHOSPHORYLATION AND INACTIVATION OF HYDROXYMETHYLGLUTARYL.-COA REDUCTASE AND HORMONE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "A mutation in PRKAG3 associated with excess glycogen content in pig
                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         [1] SEQUENCE FROM N.A. MEDIATE-20164049; PubMed=10698692; Cheung P.C., Salt I.P., Davies S.P., Hardie D.G., Carling D.; "Characterization of AMP-activated protein kinase gamma-subunit isoforms and their role in AMP binding."; Biochem. J. 346:659-669(2000).
                                                                        464 AA.
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EMBL; AF214519; AAF73987.1; -.
                                                                        PRT;
                                                                                                        09UGI9; 09NRL1;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequ
16-OCT-2001 (Rel. 40, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    skeletal muscle.";
Science 288:1248-1251(2000).
                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                         (AMPK gamma3).
PRKAG3 OR AMPKG3.
                                                                    AAKI_HUMAN
                            AAKI_HUMAN

JUD AAKI_HUMAN

JUD AAKI_HU

DE 5'-AOCT

DE 5'-AOCT

DE 6'OCT

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QHKIETWREIYLQGCFKPLVS1SPNDSLFEAVYTLIKNRIHRLPVLDPVSGNVLHILTHK 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RLLKFLHIFGSLLPRPSFLYRTIQDLG1GTFRDLAVVLETAPILTALDIFVDRRVSALPV 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             386 VNECGQVVGLYSRFDVIHLAAQQTYNHLDMSVGEALRQRTLCLEGVLSCQPHESLGEVID 445
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-OCT-2001 (Rel. 40, Created)
LoCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
5'-AMP-activated protein kinase, gamma-3 subunit (AMPK gamma-3 chain)
                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-20280150; PubMed-10818001;
Milan D., Jeon J.-T., Looft C., Amarger V., Robic A., Thelander M.,
Rogel-Gaillard C., Paul S., Iannuccelli N., Rask L., Ronne H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Euteleostomi;
Sus.
                                                                                                                                                                                                                                                                                                                   ;
0
                                                                                                                                                                                                                                                                                Length 464;
                                                                                                                                                                        T -> A (IN REF. 1).
MQ -> IE (IN REF. 1).
Q -> K (IN REF. 1).
ALGA -> PSGPEKI (IN REF. 1).
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                                                                                                                                                                                                                                              53985C2C77003A63 CRC64;
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Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                   1;
                                                                                                                                                                                                                                                                               94.5%; Score 2398; DB 1; 99.8%; Pred. No. 3.7e-174;
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TISSUE-Skeletal muscle;
                                                                                Fatty acid biosynthesis; Repeat; CBS domain.

147 201 CBS 1.

DOMAIN 228 CBS 2.

DOMAIN 333 356 CBS 3.

DOMAIN 375 428 CBS 4.
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                               InterPro; IPR000644; CBS_domain.
Pfam; PF00571; CBS; 4.
SMART; SM00116; CBS; 4.
                                                                                                                                                                                                                                              51514 MW;
                                                                                                                                                                                                                                                                                                                   463; Conservative
 HGNC:9387; PRKAG3
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356
428
164
398
464
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Mammalia; Eutheria;
                                                                                                                                                                                                                                            464 AA;
                                                                                                                                                                                                                                                                                                   Similarity
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303
375
375
58
163
398
461
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                  604976;
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Q9MYP4;
                                                                                                                                                                        CONFLICT
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   Genew;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  145 WECELEGILEERPALCLSPQAPFPKLGWDDELRKPGAQIYMRFMQEHTCYDAMATSSKLV 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 SGDEL-GLVEEKPAPCPSPEVLLPRLGWDDELQKPGAQVYMHFMQEHTCYDAMATSSKLV 179
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                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: BELONGS TO THE 5'-AMP-ACTIVATED PROTEIN KINASE, GAMMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
Chardon P.,
                Andersson L.; "A mutation in PRKAG3 associated with excess glycogen content in pig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Repeat; CBS domain; Disease mutation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 2011; DB 1; Length 464; Pred. No. 7.4e-145;
Le Roy P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -> Q (IN RN-).
17638CB12A2BA9DF CRC64;
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19; Mismatches
Lundstroem K., Reinsch N., Gellin J., Kalm
                                                                                                                                                                                                                                                                                                                                                                           SUBUNIT FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CBS 2.
CBS 3.
CBS 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL, AF214521; AAF73989.1; -.
EMBL, AF214520; AAF73988.1; -.
Interpro: IPR000644; CBS_domain.
Pfam; PP00571; CBS; 4.
SMART; SW00116; CBS; 4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 79.2%;
86.0%;
                                                               Science 288:1248-1251(2000)
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Best Local Similarity 86.0's
Matches 400; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     biosynthesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      381
453
200
                                                                                                                                                                                                                                                                                                                                        BREEDING INDUSTRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      328
400
200
264 AA;
                                                    skeletal muscle."
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SEQUENCE
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us-09-826-581-6.rsp

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Genew; HGNC:9386; PRKAG2
   385 VVNECGQVVGLYSRFDVIHLAAQQTYNHLDMSVGEALRQRTLCLEGVLSCQPHESLGEVI 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y., Nishikawa T., Nagai K., Sugano S., Aotsuka S., Yoshikawa Y., Matsunawa H., Ishii S., Kawai Y., Salto K., Yamamoto J., Wakamatsu A., Nakamura Y., Nagamari K., Masuno Y., Sasaki N.; "NEDO human cDMA sequencing project.", Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. (ISOFORM B).

MEDLINE-20564210; PubMed-11112354;
Lang T., Yu L., Qiang T., Jiang J., Chen Z., Xin Y., Liu G., Zhao S.;
"Molecular cloning, genomic organization, and mapping of PRKAG2, a heart abundant gamma-2 subunit of 5'-AMP-activated protein Kinase, to human chromosome 7q36.";
Genomics 70:258-263(2000).
                                                                                                                           AAKH HUMAN STANDARD; PRT; 569 AA.
Q9UGJO; Q9UDN8; Q9ULX8;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
5'-AMP-activated protein kinase, gamma-2 subunit (AMPK gamma-2 chain)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 218-569 FROM N.A. Hattori A., Seki N., Hayashi A., Kozuma S., Muramatsu M., Saito T., "Human homolog of AMPK gamma-1 chain.";
                                                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. (ISOFORM A).
MEDLINE-20164049; PubMed-106988692;
Cheung P.C.F., Salt I.P., Davies S.P., Hardie D.G., Carling D.;
Characterization of AMP-activated protein kinase gamma-subunit isoforms and their role in AMP binding.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gollob M.H., Seger J.J., Gollob T.N., Tapscott T., Gonzales O., Bachinski L., Roberts R.;
"Novel PRRAG2 mutation responsible for the genetic syndrome of ventricular preexcitation and conduction system disease with childhood onset and absence of cardiac hypertrophy.";
Circulation 104:3030-3033(2001).
                                               DRIAREQVHRLVLVDETQHLLGVVSLSDILQALVLSPAGIDALGA 489
                                                            Strausberg R.; Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 254-569 FROM N.A.
Walker C., Scott K., Bauer C., Harkins R.;
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VARIANTS HCM/WPWS LEU-350 INS AND ARG-383.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=21264334; PubMed=11371514;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=21614537; PubMed=11748095;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. (ISOFORM B). TISSUE=Placenta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. (ISOFORM B).
                                                                                                                                                                                                                                                                                                                                                    Biochem. J. 346:659-669(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VARIANT WPWS GLY-531
                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
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                                               445
                                                                       420
                                                                                                                                                                                                                    PRKAG2
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J. Clin. Invest. 109:357-362(2002)

I. FUNCTION: AMPK IS RESPONSIBLE FOR THE REGULATION OF FATTY ACID SYNTHEELS BY PHOSPHORYLATION OF ACETYL.-COA CARBOXYLASE. ALSO REGULATES CHOLESPEROL SYNTHESIS VIA PHOSPHORYLATION OF ACETYL.-COA REDUCTASE. ALSO REGULATES CHOLESPEROL SYNTHESIS VIA PHOSPHORYLATION AND HYDROXYMETHYIGLUTARNI-COA REDUCTASE AND HORMONE-SENSITIVE LIPASE. THIS IS A REGULATORY SUBUNIT.

I. SUBUNIT: HETENOTRIMER OF AN ALPHA CATALYIC SUBUNIT, A BETA AND A GAMA NON-CATALYIC REGULATORY SUBUNITS.

I. ALTERNATIVE PRODUCTS: 2 ISOFORMS; A (SHOWN HERE) AND B; ARE PRODUCTS BY ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 be associated with a form of hypertrophic cardiomyopathy (BCM), which is probably due to polysaccharide storage in the heart. Defects in PRKAG2 may not be a frequent cause of HCM where no features of pre-excitation are found in affected individuals. SIMILARITY: BELONGS TO THE 5'-AMP-ACTIVATED PROTEIN KINASE, GAMMA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EXCEPT IN
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Blair E., Redwood C., Ashrafian H., Oliveira M., Broxholme J., Kerr B., Salmon A., Oestman-Smith I., Matkins H.; "Mutations in the gamma(2) subunit of AMP-activated protein Kinase ause familial hypertrophic cardiomyopathy: evidence for the central role of energy compromise in disease pathogenesis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-21686220; PubMed=11827995; Arad M., Benson D.W., Person D.W., Person D.W., Person D.W., Seidman J.G., Seidman W.J., Sparks E.A., Kanter R.J., McGarry K., Seidman J.G., Seidman C.E.; "Constitutively active AMP kinase mutations cause glycogen storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -i- TISSUE SPECIFICITY: ISOFORM B IS UBIQUITOUSLY EXPRESSED EXCEPT
LIVER AND THYMUS. THE HIGHEST LEVEL IS DETECTED IN HEART WITH
ABUNDANT EXPRESSION IN PLACENTA AND TESTIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Karibe A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gollob M.H., Green M.S., Tang A.S.-L., Gollob T., Karibe A., Al Sayegh A.H., Ahmad F., Lozado R., Shah G., Fananapazir L.
Bachinski L.L., Roberts R.;
                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-21279949; Pubmed=11407343;
Gollob M.H., Green M.S., Tang A.S.-L., Gollob T., Karibe A
Al Sayegh A.H., Ahmad F., Lozado R., Shah G., Fananapazir
Bachinski L.L., Roberts R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gollob M.H., Green M.S., Tang A.S.-L., Gollob T., Karibe A Al Sayegh A.H., Ahmad F., Lozado R., Shah G., Fananapazir Bachinski L.L., Roberts R.;
New Engl. J. Med. 345:552-552(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Identification of a gene responsible for familial Wolff-Parkinson-White syndrome."; New Engl. J. Med. 344:1823-1831(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VARIANTS WPWS GLN-302; ASN-400 AND ILE-488.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -! - SIMILARITY: CONTAINS 4 CBS DOMAINS.
                                                                                                                                                                                                                                           Hum. Mol. Genet. 10:1215-1220(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New Engl. J. Med. 346:300-300(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; BC020540; AAH20540.1;
EMBL; AB025580; BAA84695.1;
EMBL; AC006966; AAF03528.1;
                                                                                                                                                                                                                                                                                                                                         VARIANT WPWS GLN-302
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                                                       Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAC52580.1
         01-FEB-1995 (Rel. 31,
01-NOV-1997 (Rel. 35,
16-OCT-2001 (Rel. 40,
                                                                                                                                                                                                                                                                                                                                                                                                           SUBUNIT FAMILY
                                                                                            SEQUENCE FROM N.A.
                                                                             NCBI_TaxID=10116;
                                                                                                     STRAIN-Wistar;
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                                                                                                                                                                                                                                                                                                                                                               SUBUNIT.
                01-NOV-1997
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                                        (AMPKg).
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   10;
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                                                                                                                                                                                                                                                                                                   ----AGVGTPPTGWDCLPSDC---TASAAGSST----DDVELATEPATEAWECELEG 151
                                                                                                                                                                                                                                                                                                                                      188 ENRIYASSSPPDTGQRFCPSSFQSPTRPPLASPTHYAPSKAAALAAALGPAEA-----G 241
                                                                                                                                                                                                                                                                                                                                                      LLEERPALCLSPQAPFPKI,GWDDB-LRKPGAQIYMRFMQEHTCYDAMATSSKLVIFDTML 210
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                                                                                                                                                                                                                                                                                                                                                                                                                          LHIFGSLLPRPSFLYRTIQDLGIGTFRDLAVVLETAPILTALDIFVDRRVSALPVVNECG 390
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                      Repeat; CBS domain; Alternative splicing;
                                                                                                                                                                                                                            ASPTHYAPSKAAALAA -> MLIAVLLLPLRRRWRR
                                                                                                                                                                                       /FTIG=VAR_013268.
R -> G (IN WPWS; ABSENCE OF CARDIAC HYPERTROPHY; ONSET IN CHILDHOOD).
                                                                                                         R -> RL (IN FAMILIAL HCM WITH WPWS; SEVERE).
                                                                                                                                                                                                                                                                          52;
                                                                                                                                  H -> R (IN FAMILIAL HCM WITH WPWS;
                                                                                                                                                                                                                                                          43.1%; Score 1093; DB 1; Length 569; 51.0%; Pred. No. 3.2e-75;
                                                                                                                                                                               N -> I (IN WPWS WITH CARDIAC HYPERTROPHY).
                                                                                                                                                        T -> N (IN WPWS WITH CARDIAC HYPERTROPHY).
                                                                                                                                                                                                                                                                          95; Indels
                                                                                                                                                                                                                                     N REF. 5).
F51C30668C294089 CRC64;
                                                                                    MISSING (IN ISOFORM B)
                                                                                          R -> Q (IN WPWS).
/FTId=VAR_013264.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QVHRLVLVDETQHLLGVVSLSDILQALVLSPAG 483
                                                                                                                                                                       FTIG=VAR_013267.
                                                                                                                                                 /FTId=VAR_013266
                                                                                                                          /FTId=VAR_013265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  330 AA.
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                                                                                                                                         SEVERE)
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              InterPro; IPR000644; CBS_domain.
Pfam; PF00571; CBS; 4.
SMART; SM00116; CBS; 4.
                                                                                                                                                                                                                                           63066 MW;
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                                      Fatty acid biosynthesis;
Disease mutation.
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409
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602743; -.
194200; -.
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AAKG_RAT
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 48-330 FROM N.A., AND PARTIAL SEQUENCE.
STRAIN-Sprague-Dawley; TISSUE-Liver;
MEDLINE-95050763; PubMed-9961907;
Stapleton D., Gao G., Michell B.J., Widmer J., Mitchelhill K.,
Teh T., House C.M., Witters L.A., Kemp B.E.;
"Mammalian 5'-AMP-activated protein kinase non-catalytic subunits are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commer.
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TISSUG SPOETPECTY: HIGHLY EXPRESSED IN HEART AND BRAIN, ALSO
FOUND IN KIDNEY, WHITE ADIPOSE TISSUE, LUNG AND SPLEEN.
SIMILARITY: BELONGS TO THE 5'-AMP-ACTIVATED PROTEIN KINASE, GAMMA
L-NOV-1997 (Rel. 35, Last sequence update)
5-OCT-2001 (Rel. 40, Last annotation update)
-AMP-activated protein kinase, gamma-1 subunit (AMPK gamma-1 chain)
                                                                                                                                                                                                                                                        Eukaryota; Métazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       homologs of proteins that interact with yeast Snf1 protein kinase.";
J. Biol. Chem. 269:29343-29346(1994).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -- FUNCTION: AMPK IS RESPONSIBLE FOR THE REGULATION OF FAITY ACID SYNTHESIS BY PHOSPHORYLATION OF ACETYL-COA CARBOXXLASE. IT ALSO REGULATES CHOLESTEROL SYNTHESIS VIA PHOSPHORYLATION AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBUNIT: HETEROTRIMER OF AN ALPHA CATALYTIC SUBUNIT; A BETA AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Characterization of AMP-activated protein kinase beta and gamma subunits. Assembly of the heterotrimeric complex in vitro."; J. Biol. Chem. 271:10282-10290(1996).
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STRAIN-SPORGUE-Dawley; TISSUE-Liver;
MEDIINE-96224074; PubMed-8621499;
Gao G., Fernandez C.S., Stapleton D., Auster A.S., Widmer J.,
Dyck J.R.B., Kemp B.E., Witters L.A.;
"Non-catalytic beta- and gamma-subunit isoforms of the
5' AMP-activated protein kinase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WEDLINE-96215327; PubMed=8626596; Woods A., Cheung P.C.F., Smith F.C., Davison M.D., Scott J., Beri R.K., Carling D.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             domain.
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Pfam; PF00571; CBS; 4.
SMART; SM00116; CBS; 4.
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DOMAIN
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                285 VSISPNDSLFEAVYTLIKNRIHRLPVLDPVSGNVLHILTHKRLLKFLHIFGSLLPRPSFL 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   345 YRTIQDLGIGTFRDLAVVLETAPILTALDIFVDRRVSALPVVNECGQVVGLYSRFDVIHL 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     405 AAQQTYNHLDMSVGEALRQRTLCLEGVLSCQPHESLGEVIDRIAREQVHRLVLVDETQHL 464
                                                                                                                                                                                                                                                                       Gao G., Fernandez C.S., Stapleton D., Auster A.S., Widmer J., Dyck J.R.B. B. Kemp B.E., Witters L.A.; "Non-catalytic beta-and gamma-subunit isoforms of the 5'-AMP-activated protein kinase.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SENSITIVE LIPASE. THIS IS A REGULATORY SUBUNIT.
-!- SUBUNIT: HEFEROTRIMER OF AN ALPHA CATALYTIC SUBUNIT, A BETA AND A GAMMA NON-CATALYTIC REGULATORY SUBUNITS.
-!- SIMILARITY: BELONGS TO THE 5'-AMP-ACTIVATED PROTEIN KINASE, GAMMA
                                                                                                                                                                                                                                           165 APFPKLGWDDELRKPGAQIYMRFMQEHTCYDAMATSSKLVIFDTMLEIKKAFFALVANGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
5'-AMP-activated protein kinase, gamma-1 subunit (AMPK gamma-1 chain)
                                                                                                                                                                                   Gaps
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-:- FUNCTION: AMPK IS RESPONSIBLE FOR THE REGULATION OF FATTY ACID SYNTHESIS BY PHOSPHORYLATION OF ACETYL-COA CARBOXYLASE. ALSO REGULATES CHOLESTERGL SYNTHESIS VIA PHOSPHORYLATION AND INACTIVATION OF HYDROXYMETHYLGLUTARYL-COA REDUCTASE AND HORMONE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                   0;
                                                                                                                     Length 330;
                                                                                                                                                                                63; Indels
E -> Q (IN REF. 3).
A -> P (IN REF. 3).
36031E526C1F1E97 CRC64;
                                                                                                                     40.5%; Score 1028; DB 1;
62.3%; Pred. No. 1.2e-70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          331 AA.
                                                                                                                                        62.3%; Pred. No. .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBUNIT FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Fetal liver;
MEDLINE-96224074; PubMed-8621499;
   114 E
201 A
37386 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-1996 (Rel. 34, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              465 LGVVSLSDILQALVLS 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  309 KGIVSLSDILQALVLT 324
                                                                                                                                                                                Matches 197; Conservative
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114 1
201 2
330 AA;
                                                                                                                                                 Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Strausberg R.
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15-JUN-2002
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                                                                                                                                                                                                                                                                                                   σ
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   CONFLICT
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                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (AMPKg).
                                                                                                                     Query Match
                                                                                                                                                    Best Local
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s its content is in no way Usage by and for commercial
                                                                                                    entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           183 IYMRFMQEHTCYDAMATSSKLVIFDTMLEIKKAFFALVANGVRAAPLWDSKKQSFVGMLT 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 363 LETAPILTALDIFVDRRVSALPVVNECGQVVGLYSRFDVIHLAAQQTYNHLDMSVGEALR 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  243 ITDFILVLHRYYRSPLVQIYEIEQHKIETWREIYLQGCFKPLVSISPNDSLFEAVYTLIK 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NRIHRLPVLDPVSGNVLHILTHKRLLKFLHIFGSLLPRPSFLYRTIQDLGIGTFRDLAVV 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28 VYTSFWKSHRCYDLIPTSSKLVVFDTSLQVKKAFFRLVTNGVRAAPLMDSKKQSFVGMLT 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              423 QRTLCLEGVLSCQPHESLGEVIDRIAREQVHRLVLVDETQHLLGVVSLSDILQALVLS 480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SYNTHESIS BY PHOSPHORYLATION OF ACETYL-COA CARBOXXLASE. ALSO REGULATES CHOLESTEROL SYNTHESIS VIA PHOSPHORYLATION AND INACTIVATION OF HYDROXYMETHYLGLUTARYL-COA REDUCTASE AND HORMONESENSTIVE LIPASE. THIS IS A REGULATORY SUBUNIT.
SUBUNIT: HETEROTRIMER OF AN ALPHA CATALYTIC SUBUNIT, A BETA AND A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: AMPK IS RESPONSIBLE FOR THE REGULATION OF FATTY ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bos taurus (Bovine).
Enkaryota, Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Davoren
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 40.1%; Score 1017; DB 1; Length 331; 64.8%; Pred. No. 8.4e-70; Live 53; Mismatches 52; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
Benkel B., Kollers S., Fries R., Sazanov A., Yoshida E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0F22B9CA1DBD87AE CRC64;
between the Swiss Institute of Bioinformatics the European Bioinformatics Institute. There an use by non-profit institutions as long as if modified and this statement is not removed. Use
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                              Fatty acid biosynthesis; Repeat; CBS domain.
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CBS 2.
CBS 3.
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                                                                                                                                                                                                                                                                                          InterPro; IPR000644; CBS_domain.
Pfam; PF00571; CBS; 4.
SMART; SM00116; CBS; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                          123 177 CBS
197 250 CBS
271 323 CBS
331 AA; 37579 MW; C
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(Rel. 40, Last sequ
(Rel. 40, Last anno
                                                                                                                                                                                                            EMBL; BC000358; AAH00358.1; -.
                                                                                                                                                                                  EMBL; U42412; AAC50495.1; -.
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                                                                                                                                                                                                                                     HGNC:9385; PRKAG1
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                                                                                                                                                                                                                                                                 MIM; 602742;
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16-OCT-2001
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P58108;
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SNF4_YEAST
P12904;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                             183 IYMRFMQEHTCYDAMATSSKLVIFDTMLEIKKAFFALVANGVRAAPLWDSKKQSFVGMLT 242
                                                                                                                                                                                                                                                                                                                                                                          ITDFILVLHRYYRSPLVQIYE1EQHKIETWREIYLQGCFKPLVSISPNDSLFEAVYTLIK 302
                                                                                                                                                                                                                                                                                                                                                                                         NRIHRLPVLDPVSGNVLHILTHKRLLKFLHIFGSLLPRPSFLYRTIQDLGIGTFRDLAVV 362
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15-DEC-1998 (Rel. 37, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
5'-AMP-activated protein kinase, gamma-1 subunit (AMPK gamma-1 chain)
GAMMA NON-CATALYTIC REGULATORY SUBUNITS.
SIMILARITY: BELONGS TO THE 5'-AMP-ACTIVATED PROTEIN KINASE, GAMMA
                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Cloning, organisation, chromosomal localization and expression analysis of the mouse Pragal gene."; analysis of the mouse Pragal gene."; Cytogenet. Cell Genet. 92:134-138(2001).
-!- FUNCTION: AMPK IS RESPONSIBLE FOR THE REGULATION OF FATTY ACID SYNTHESIS BY PHOSPHORYLATION OF ACETYL-COA CARBOXYLASE. ALSO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Mus mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Shamsadin R., Jantsan K., Adham I., Engel W.;
Libning, organisation, chromosomal localization and expression
analysis of the mouse pread ness ".
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                                                                                                                                                                                                                                                                                  39.9%; Score 1013; DB 1; Length 330; 64.4%; Pred. No. 1.7e-69;
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                                                                                                                                                                                                                                                            F130AC8EE2BFEB89 CRC64;
                                                                                                                                                                                                                                                                                                         52;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   330 AA.
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                                   SIMILARITY: CONTAINS 4 CBS DOMAINS.
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CBS
                                                                                                                                                               InterPro; IPR000644; CBS_domain. Pfam; PF00571; CBS; 4. SMART; SM00116; CBS; 4.
                                                                                                                                                                                                                                                          330 AA; 37481 MW;
                                                                                                                                                    EMBL; AF329081; AAK19307.1; -.
                                                                                                                                                                                                                                                                                           Local Similarity 64.4 les 192; Conservative
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                                                                                                                                                                                                             96
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                       SUBUNIT FAMILY
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054950;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      243 ITDFILVLHRYYRSPLVQIYEIEQHKIETWREIYLQGCFKPLVSISPNDSLFEAVYTLIK 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NRIHRLPVLDPVSGNVLHILTHKRLLKFLHIFGSLLPRPSFLYRTIQDLGIGTFRDLAVV 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              363 LETAPILTALDIFVDRRVSALPVVNECGQVVGLYSRFDVIHLAAQQTYNHLDMSVGEALR 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27 VYTSFMKSHRCYDLIPTSSKLVVFDTSLQVKKAFFALVTNGVRAAPLWDSKKQCFVGMLT 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             423 QRTLCLEGVLSCQPHESLGEVIDRIAREQVHRLVLVDETQHLLGVVSLSDILQALVLS 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SENSITIVE LIPASE. THIS IS A REGULATORY SUBUNIT.
SUBUNIT: HEFERCARIMER OF AN ALPHA CAPLYTIC SUBUNIT, A BETA AND A
GAMMA NON-CATALYTIC REGULATORY SUBUNITS.
SIMILARITY: BELONGS TO THE S'-AMP-ACTIVATED PROTEIN KINASE, GAMMA
REGULATES CHOLESTEROL SYNTHESIS VIA PHOSPHORYLATION AND INACTIVATION OF HYDROXYMETHYLGLUTARYL-COA REDUCTASE AND HORMONE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-89006284; PubMed-3049255;
Schueller H.-J., Entian K.-D.;
"Molecular characterization of yeast regulatory gene CAT3 necessary
for glucose derepression and nuclear localization of its product.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 330;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          57; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             322 CBS 4.
37554 MW; D504707B83512DDC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Saccharomycetales; Saccharomycetaceae; Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          39.3%; Score 997; DB 1; 64.1%; Pred. No. 2.7e-68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nuclear protein SNF4 (Regulatory protein CAT3).
SNF4 OR CAT3 OR YGL115W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-0CT-1989 (Rel. 12, Created)
01-0CT-1989 (Rel. 12, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fatty acid biosynthesis; Repeat; CBS domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         322 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Pred. No. 2.7e
50; Mismatches
                                                                                                                                                                               SUBUNIT FAMILY.
SIMILARITY: CONTAINS 4 CBS DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CBS
CBS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MGD; MGI:108411; Prkagi.
InterPro: IPRO00664; CBS_domain.
Pfam; PF00571; CBS; 4.
SMART; SM00116; CBS; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AF036535; AAB95475.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            122
196
270
330 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    191;
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RR WOOD V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A., WOOD V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A., Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A., Brown S., Chillingworth T., Churcher C.M., Brown D., Brown S., Chillingworth T., Churcher C.M., Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A., Collins M., Connor R., Gronin A., Davis P., Feltwell T., Fraser A., Gollins M., Connor P., Moule S., Mungall K., Murbhy L., Niblett D., Odell C., Admin N., Harris D., Hidalgo J., Hodgen G., Hornsby T., Howarth S., Mungall K., Murbhy L., Niblett D., Odell C., Allones M., Squares R., Seeger K., Sharp S., Skelton J., Simmonds M., Squares R., Squares S., Stevens K., Rathor C., Tivey A., Walsh S.V., Warren T., Whitehead S., Weltpen J., Volckaert G., Aert R., Robben J., Grymonprez B., Weltpens I., Volckaert G., Aert R., Robben J., Grymonprez B., Weltpens I., Volckaert G., Aert R., Robben J., Grymonprez B., Weltpens I., Volckaert G., Aert R., Robben J., Grymonprez B., Weltpens I., Volckaert G., Aert R., Robben J., Grymonprez B., Weltpens I., Volckaert G., Aert R., Robben J., Grymonprez B., Weltpens I., Volckaert G., Aert R., Robben J., Grymonprez B., Weltpens I., Volckaert G., Aert R., Robben J., Grymonprez B., Weltpens I., Volckaert G., Aert R., Robben J., Grymonprez B., Rocket M., Enager M., Schaefer M., Wotler R., Pohl T.M., Borzym K., Langer I., Beck A., Lehrach H., Wealhardt R., Pohl T.M., Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M., Loas M., Rochet M., Galilardin C., Tallada V.A., Garzon A., Thode G., Andore M., Rochet M., Galilardin C., Tallada V.A., Garzon A., Thode G., Moniquez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L., The Genome sequence of Schizosaccharomyces P., Ruture 415:871-880(2002).

Rature 415:871-880(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
       DLGIGTFRDLAVVLETAPILTALDIFVDRRVSALPVVNECGQVVGLYSRFDVIHLAAQQT 409
                                                                                                                                                                                                                                           110 YNHLDMSVGEALRQRTLCLEGVLSCQPHESLGEVIDRIAREQVHRLVLVDETQHLLGVVS 469
                                                                                                                                                                                                                                                                                  190 DLNIITQDNWKSCQMTTPVIDVIQMLTQGRVSSVPIIDENGYLINVYEAYDVLGLIKGGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q10343; Q9UTJ1;
01-0CT-1996 (Rel. 34, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Hypothetical protein CIF12.01c in chromosome I
SPACIF12.01C OR SPACI556.08C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             334 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: CONTAINS 4 CBS DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; Z69944; CAA93805.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                               470 LSDILQALVL 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                  LSDILKYILL 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Schizosaccharomyces.
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                                          134
                                                                                                          350
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YDA1_SCHPO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      294
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBCELLULAR LOCATION: Nuclear.
SIMILARITY: BELONGS TO THE 5'-AMP-ACTIVATED PROTEIN KINASE, GAMMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24 KFLNSKTSYDVLPVSYRLIVLDTSLLVKKSLNVLLQNSIVSAPLWDSKTSRFAGLLTTTD
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                                                            SEQUENCE FROM N.A.
MEDINE-90097921; Pubmed-2481228;
Celenza J.L., Farg F.J., Carlson M.;
"Molecular analysis of the SNF4 gene of Saccharomyces cerevisiae:
evidence for physical association of the SNF4 protein with the SNF1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   J. Biol. Chem. 269:2361-2364(1994).
-!- FUNDATION: THIS PROTEIN CAUSES EXPRESSION OF GLUCOSE-REPRESSIBLE GENES UPON GLUCOSE DEPRIVATION. IT INTERACTS AND HAS FUNCTIONAL RELATIONSHIP TO THE PROTEIN-KINASE SNPI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00571; CBS; 4.
SWART; SW00116; CBS; 4.
Carbohydrate metabolism; Transcription regulation; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              domain of yeast Snfl protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 30-34 AND 316-322.
MEDLINE-94131988; PubMed-7905477;
Mitchelhill K.I., Stapleton D., Gao G., House C., Michell B., Katsis F., Witters L.A., Kemp B.E.;
"Mammalian AMP-activated protein kinase shares structural and functional homology with the catalytic domain of yeast Snfl pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 457; DB 1; Length 322; Pred. No. 2e-27; S: Mismatches 108; Indels :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CBS 1.
CBS 2.
CBS 3.
CBS 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Doi A., Doi K.;
Submitted (JUN-1993) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: CONTAINS 4 CBS DOMAINS.
                                                                                                                                                                                                                                                                       Mol. Cell. Biol. 9:5045-5054(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL, M21760, AAA34472.1; --
EMBL, M30470; AAA35061.1; --
EMBL, Z72637; CAA96823.1; --
EMBL, D16506; BAA03958.1; --
PIR: JT0316; RGBYC3.
PIR: J33409, A33480, A33480, A33480, A33480, A33480, A33480, A3480, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99
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175 CB
246 CB
318 CB
36401 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 1-21 FROM N.A.
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106; Conservative
Gene 67:247-257(1988).
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117
192
259
322 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBUNIT FAMILY
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                                                                                                                                                                                                                                       protein kinase.
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Best Local Si
Matches 106
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SEQUENCE
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RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed, Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                             175 ELRKPGAQIYMRFMQEHTCYDAMATSSKLVIFDTMLEIKKAFFALVANGVRAAPLWDSKK 234
                                                                                                                                                                                                                                                                    235 QSFVGMLTITDFILVLHRYYRSPLV--QIYEIEQHKIETWREIYLQ-GCFKP-LVSISPN 290
                                                                                                                                                                                                                                                                                       291 DSLFEAVYTLIKNRIHRLPVLDPVSGN-----VLHILTHKRLLKFLHIFGSLLPRPSFLY 345
                                                                                                                                                                                                                                                                                                                                              241 IQDGDYSNLDLSVGEALLKRPANFDGVHTCRATDRLDGIFDAIKHSRVHRLFVVDENLKL 300
                                                                                                                                                                                                                                                                                                                                                                                  RT-IQDLGIGTFRDLAVVLETAPILTALDIFVDRRVSALPVVNECGQVVGLYSRFDVIHL 404
                                                                                                                                                                                                                                                                                                                                                                                                                                         405 AAQQTYNHLDMSVGEALRQRTLCLEGVLSCQPHESLGEVIDRIAREQVHRLVLVDETQHL 464
                                                                                                                                                                                                                                        ETQKGALKEIQAFIRSRTSYDVLPTSFRLIVFDVTLFVKTSLSLLTLNNIVSAPLWDSEA 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tomasini L., Ferrero I., Golfrini P.;

Tomasini L., Ferrero I., Golfrini P.;

Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: THIS PROTEIN CAUSES EXPRESSION OF GLUCOSE-REPRESSIBLE
GENES UPON GLUCOSE DEPRIVATION. IT INTERACTS AND HAS FUNCTIONAL
RELATIONSHIP FOR THE PROTEIN-KINASES ENFI (BY SIMILARITY).

-!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).

-!- SIMILARITY: BELONGS TO THE 5'-AMP-ACTIVATED PROTEIN KINASE, GAMMA
                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kluyveromyces lactis (Yeast).
Eukaryota, Fungi: Ascomycota; Saccharomycolina; Saccharomycetes;
                                                                                                                                                                                      15;
                                                                                                                                                          DB 1; Length 334;
                                                                                                                                                                                   73; Mismatches 123; Indels
                                                                                                                             8D32CC6CE53F7916 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Saccharomycetales: Saccharomycetareae; Kluyveromyces.
                                                                                                                                                       18.0%; Score 456.5; DB 1 32.8%; Pred. No. 2.3e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Rel. 40, Created)
(Rel. 40, Last sequence update)
(Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   328 AA
                                                       Hypothetical protein; Repeat; CBS domain.
DOMAIN 33 81 CBS 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBUNIT FAMILY.
SIMILARITY: CONTAINS 4 CBS DOMAINS.
                                                                                     CBS 2.
CBS 3.
CBS 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
EMBL; AL132984; CAB61219.1; -.
InterProx; IRRO00644; CBS_domain.
Pfan; PF00571; CBS; 4.
SMART; SM00116; CBS; 4.
                                                                                                                             37427 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LGVVSLSDILQALV 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          301 EGILSLADILNYII 314
                                                                                                                                                                                   103; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                   170
241
314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nuclear protein SNF4.
                                                                                                                           334 AA;
                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCB1_Tax1D+28985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-0CT-2001
16-0CT-2001
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                                                                                                                             SEQUENCE
                                                                                                                                                         Query Match
Best Local 3
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                                                                                                                 DOMAIN
                                                                                     DOMAIN
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                                                                                                                                                                                   Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                              237 FVGMLTITDFILVLHRYYRSPLVQIYEIEQHKIETWREIYLQGC--FKPLVSISPNDS-- 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    293 -----LFEAVYTLIKNRIHRLPVLDPVSGN----VLHILTHKRLLKFLHIFGSLLPRPS 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              343 FLYRTIQDLGIGTFRDLAVVLETAPILTALDIF-VDRRVSALPVVNECGQVVGLYSRFDV 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             188 YLKRPLRELDIISTNNIMSCOMSTPVIDVIQLLTLAGGVSSVPIVDEQGKLVNVYEAVDV 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        402 IHLAAQQTYNHLDMSVGEALRQRTLCLEGVLSCQPHESLGEVIDRIAREQVHRLVLVDET 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              248 LGLIKGGIYNDLSLSVGEALMRRSDDFEGVFTCTEKHKLSSILDTVRKSRVHRFFVVDSN 307
                                                                                                                                                                                                                                                                                                                                                              INACTIVATION OF HYDROXYMETHYLGLUTARYL-COA REDUCTASE AND HORMONE-
SENSITIVE LIPASE. THIS IS A REGULATORY SUBUNIT.
SUBUNIT: HETEROTRIMER OF AN ALPHA CATALYTIC SUBUNIT, A BETA AND A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
5'-AMP-activated protein kinase, gamma-1 subunit (AMPK gamma-1 chain)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GAMMA NON-CATALYTIC REGULATORY SUBUNITS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Stableton D., Goo G., Michell B.J., Widmer J., Mitchelhill K., Stapleton D., Goo G., Mitchell B.J., Kemp B.E.;
Teh T., House C.M., Witters L.A., Kemp B.E.;
Thammanian 5'-AMP-activated protein kinase non-catalytic subunits are homologs of proteins that interact with yeast Snfl protein kinase.";
J. Biol. Chem. 269:29343-29346(1994).
-!-FUNCTION: AMPK IS RESPONSIBLE FOR THE REGULATION OF FATTY ACID SWITHESIS BY PHOSPHORYLATION OF ACETYL-COA CARBOXYLASE. ALSO REGULATES CHOLESTEROL SYNTHESIS VIA PHOSPHORYLATION AND
                                                                                                                                                                                                                                                                                                 Gaps
                                                                                    Carbohydrate metabolism; Transcription regulation; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
NCBL_TaxID=9823;
                                                                                                                                                                                                                                                                                               27;
                                                                                                                                                                                                                                                        Length 328;
                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                               DC9ED3F85E46BAD3 CRC64;
                                                                                                                                                                                                                                                    ; Score 418.5; DB 1;
; Pred. No. 1.7e-24;
72; Mismatches 121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     133 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (AMPKg) (38 kDa subunit) (Fragments).
                                                                                                                             CBS 1.
CBS 2.
CBS 3.
CBS 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=95050763; PubMed=7961907;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | ||::|||||: : : GFLTGVLTLSDILKYILFA 326
EMBL; AJ277480; CAB89520.1; -.
InterPro; IPR000644; CBS_domain.
Pfam; PF00571; CBS; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      462 QHLLGVVSLSDILQALVLS 480
                                                                                                                         94 CBS
180 CBS
252 CBS
324 CBS
37163 MW; I
                                                                                                                                                                                                                                                      16.5%;
31.0%;
                                                                                                                                                                                                                                                                       Best Local Similarity 31.0 Matches 99; Conservative
                                                                SMART; SM00116; CBS;
                                                                                                       Repeat; CBS domain.
DOMAIN 40 9
DOMAIN 122 16
DOMAIN 198 25
                                                                                                                                                                                                           328 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sus scrofa (Pig).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Liver;
                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAKG_PIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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us-09-826-581-6.rsp

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----QHIPLSQLIEQNKLIFVPGSISVEEAFNTLIKYHLNSIPV--- 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        71 PPGQGEGPRSRPAAESTGL--EATFPKTTPLAQADPAG-----VGTPPTGWDCLPSDCT 122
                                                                                                                                                                                                                                                                                                                                                                                                                     123 ASAAGSSTDDVELATEFPATEAWECELEGLLEERPALCLS----PQAPFPKLG-----W 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 AAAPGPGC----AATPAP-----LRDEKPQFKLSAVPMTQTPSQCLSCVHAQKW 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               173 DDELRKPGAQIYMRFMQEHTCYDAMATSSKLVIFDTMLEIKKAFFALVANGVRAAPLWDS 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           233 KKQSFVGMLTITDF-----ILVLHRYYRSPLVQIYEIEQHKIETWREIYLQGCFKP 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --ESFPGDMNCFTFDYNDLNSYLLLVLNKITVSNKQLTADCQNGKPVPVGEMVKLTPKNP 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      284 LVSISPNDSLFEAVYTLIKNRIHRLPVLDPVSGNVLHILTHKRLLKFL----HIFGSLLP 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   340 RPSFLYRTIQOLGIG-----TFRDLAV--VLETAPILTALDIFVDRRVSALPVVNEC 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---LINSSLQDLHIGVLNIQSKPTSRQSRVISIQGEEPLIMGLYKMHVERISSIAVIDKQ 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               390 GQVVGLYSRFDVIHLAAQQIYNHLDMS----VGEALRQRTLCLE----GVLSCQPHESLG 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            320 GNLLGNISVIDVKHVTRTSQYPLLHKTCRHFISVILNSRGLETGKDSFPIFHVYPSSSLA 379
                                                                                                                                                                                                                                                                                                                                                                                    9 PPSQSNSSNNLPTSRHASIVEMLSTPPLLPHVQVNDTDDKEQPEESTPPT-----AT
                                                                                                                                                                                                                                                                                                                              98;
                                                                                                                                                                                                                                                                                                Length 527;
                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                DC2741550A69C154 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Archaea; Euryarchaeota; Methanococci; Methanococcales;
                                                                                                                                                                                                                                                                                                         21.5%; Pred. No. 0.00018;
tive 63; Mismatches 182;
                                                                                                                                                                                                                                                                                            6.2%; Score 158; DB 1;
21.5%; Pred. No. 0.00018;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   280 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Methanocaldococcaceae; Methanocaldococcus.
                                                                                                                                                                                                                  Hypothetical protein; Repeat; CBS domain.
DOMAIN 196 251 CBS 1.
DOMAIN 283 335 CBS 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN-JAL-1 / DSM 2661 / ATCC 43067;
MEDLINE-96337999; PubMed=8688087;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                     SGD; S0000418; SDS24.
InterPror; IPRO00644; CBS_domain.
Pfam; PPO0571; CBS; 4.
SWART; SM00116; CBS; 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : :: : !!! :!
380 RTLAKLVATKSHRLWIV 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                058622;
15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequ
                                                                                                                                                                                                                                                                527 AA; 57187 MW;
                                                                                                                         EMBL; Z36083; CAA85178.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical protein MJ1225 MJ1225.
                                                                                                                                                                                                                                                                                                            3est_Local Similarity 21.5
Matches 94; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Rel. 40,
                                                                                                                                        PIR; S46088; S46088
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 263 EIEQHKIETWREIYLQGCFKPLVSISPNDSLFEAVYTLIKNRIHRLPVLDPVSGNVLHIL 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             323 THKRLLKFLHIFGSLLPRPSFLYRTIQDLGIGTFRDLAVVLETAPILTALDIFVDRRVSA 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        383 LPVVNECGQVVGLYSRFDVIHLAAQQTYNHLDMSVGEALRQRTLCLEGVLSCQPHESLGE 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16
                                                                                                                                                                                                                                                                                                                                                                                                                    -----LVQIY 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----XPVIDPESGNTLYIL 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ------RVSA
                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dubois E., el Bakkoury M., Glansdorff N., Messenguy F., Pierard A. Scherens B., Vierendeels F.; Submitted (AUG-1994) to the EMBL/GenBank/DDBJ databases.
-!- SIMILATIY: TO YESST YGLOSEC AND S. POMBE SDS23.
-!- SIMILARITY: CONTAINS 2 CBS DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----YFEGVL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                         Indels 149;
                                                                                                                                                                                                                                                                                                                         10.5%; Score 267.5; DB 1; Length 133; 28.1%; Pred. No. 1.3e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-0CT-1994 (Rel. 30, Created)
01-0CT-1994 (Rel. 30, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
Hypothetical 57.2 kDa protein in MET8-HPC2 intergenic region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (AUG-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                             133
14763 MW; 84C0C3D41E845CEF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Sacch
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      103 ------KLVVVDENDVVKGIVSLSDILQALVLT 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   443 VIDRIAREQVHRLVLVDETQHLLGVVSLSDILQALVLS 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LPVV-----IYSKFDVINLAAEKSH-----
                                                                       Fatty acid biosynthesis; Repeat; CBS domain.
NON_TER 1
                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            527 AA.
              -:- SIMILARITY: CONTAINS 4 CBS DOMAINS.
Interpro; PRO00664; CBS_domain.
PF0m; PF00571; CBS; 1.
SMART; SM00116; CBS; 1.
                                                                                                         CBS 1.
CBS 2.
CBS 3.
                                                                                                                                                                                                                                                                                                                                                                                                                  1 LVVFDTSLOVKSA-----
                                                                                                                                                                                                                                                                                                                                                       32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19 ELEEHK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 114-527 FROM N.A
                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                       >42
91
127
127
25
43
74
81
95
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YBR214W OR YBR1501.
                                                                                                                                                                                                                                                                                            133 AA;
                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                         ^26
62
62
95
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=S288c;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-S288C;
                                                                                                                                                                                                                                                                                                                                                         78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YB64_YEAST
P38314;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rieger M.;
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NON_CONS
NON_CONS
                                                                                                                                                                                                                                                                           NON_TER
SEQUENCE
                                                                                                                                                                                   NON_CONS
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                                                                                                                                                                       NON_CONS
                                                                                                                                                                                                                  NON_CONS
                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                           Best Local
                                                                                                         DOMAIN
                                                                                                                                       DOMAIN
DOMAIN
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17;

Gaps

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454 RLVLVDETQHLLGVVSLSDIL 474
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR; S08244; S08244.
InterPro: JPR000644; CBS_domain.
Pfam; PP00571; CBS; 4.
SMART; SM00116; CBS; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   300 AA; 33437 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical protein; Repeat;
DOMAIN 8 61 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X14835; CAA32944.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical protein MJ1404.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 5.5%;
Best Local Similarity 23.4%;
Matches 47; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Methanococcus jannaschii
              NCBI_TaxID=2269;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YEO4_METJA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YE04_METJA
              OX RRAPREN RRAPREN RRAPREN RRAPREN RRAPREN RRAPREN RRAPREN RRAPREN RAPREN RAPRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
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                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   54 SMDIVDFMGGGSKYNLIREKHERNFLAAINEPVREIME-----ENVITLKENAD 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         293 LFEAVYTLIKNRIHRLPVLDPVSGNVLHILTHKRLLKFLHIFGSLLPRPSFLYRTIQDLG 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           103 IDEALETFLTKNVGGAPIVND-ENQLISLITERDVIRAL------LDKIDENEV 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              353 IGTF--RDLAVVLETAPILTALDIFVDRRVSALPVVNECGQVVGLYSRFDVIH-LAAQQT 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            150 IDDYITRDVIVATPGERLKDVARTMVRNGFRKLPVVSE-GRLVGIITSTDFIKLLGSDWA 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          410 YNHLDMSVGEA-----LRQRTLCLEGVLSCQPHESLGEVIDRIAREQVHRLVLVDETQHL 464
Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D., Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D., Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I., Overbeek R., Kirkness E.F., Weinstcock G., Merrick J.M., Glodek A., Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D., Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C., Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M., Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    183 IYMRFMQEHTCYDAMATSSKIVIFDTMLEIKKAFFALVANGVRAAPLWDSKKQSFVGMLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MFVRVMK-----IAQNKKIVTVYPTTTIRKALMTMNENKYRRLPVVNAGNNKVVGIIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             243 ---ITDFI-----LVLHRYYRSPLVQIYEIEQHKIETWREIYLQGCFKPLVSISPNDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CBS domain; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 280;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  126; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Hypothetical 33.4 kDa protein in ribosomal RNA operon.
Thermofilum pendens.
Archaea; Cremarchaeota; Thermoprotei; Thermoproteales; Thermofilum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31719 MW; 614AE160DC92E45F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5.9%; Score 149; DB 1;
Similarity 19.6%; Pred. No. 0.00035;
51; Conservative 72; Mismatches 126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   300 AA.
                                                                                                                                                                                                                                                                                                      -1- SIMILARITY: CONTAINS 4 CBS DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR000644; CBS_domain.
Pfam; PF00571; CBS; 4.
SMART; SM00116; CBS; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; U67563; AAB99228.1; -.
                                                                                                                                                                                                                                                                            Science 273:1058-1073(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  465 LGVVSLSDILQ 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        267 KGIITEKDVLK 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   280 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TIGR; MJ1225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61;
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P15889;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        279 GCFKPLVSISPNDSLFEAVYTLIKNRIHRLPVLDPVSGNVLHILTHKRLLKFL--HIFGS 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   337 LLPR--PSFLYRTIQDLGIGTFR-DLAVVLETAPILTALDIFVDRRVSALPVVNECGQVV 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  394 GLYSRFDVIHLAAQQTYNHLDMSVGEALRQRTLCLEGVLSCQPHESLGEVIDRIAREQVH 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 128 GIVSERHVISLLA-----NVETHVKVKEIMTSEVVYLSPMDSLFEGMRVMSERRIR 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-HVV3 / DSM 2475;
Kjems J., Leffers H., Olesen T., Ingelore H., Garrett R.A.;
"Sequence, organisation and transcription of the ribosomal RNA operon
and the downstream tRNA and protein genes in the archaebacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
MEDLINE=96337999; bubmd=8688087;
Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5.5%; Score 139; DB 1; Length 300;
23.4%; Pred. No. 0.0022;
Ive 52; Mismatches 86; Indels 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              D811A313D37A4293 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Archaea; Euryarchaeota; Methanococci; Methanococcales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                421 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CBS domain.
CBS 1.
CBS 2.
CBS 3.
CBS 3.
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                                                                                                             Thermofilum pendens.";
Syst. Appl. Microbiol. 13:117-127(1990)
-:- SIMILARITY: CONTAINS 4 CBS DOMAINS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        282 KPLVSISPNDSLFFAVYTLIKNRIHRLPVLDPVSGNVLHILTHKRLLKFLHIFGSLLPRP 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    342 SFLYRTIQDLGIGTFRDLAV------VLETAPILTALDIFVDRRVSALPVVNECGQV 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          52 EYYLISMRDLLLASSTDEEVRSLMYKAHCVHEDTPFLDAVCEMLDSGQRAAPIVNNVGKM 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               393 VGLYSRFDVIHLAAQQTYNHLDMSVGEALRQRTLCLEGVLSCQPHESLGEVIDRIAREQV 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15 KDVVTVTPDTPVSKALGIMEENGFHHLIVVDKKDG-------KE 51
Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D., Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C., Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M., Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.; "Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 421;
                                                                                                                                                                                                                                                                                                                                                                                                                                     CBS domain; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        78 121 CBS 2.
134 186 CBS 3.
212 264 CBS 4.
421 AA, 47609 NW, FF89C9E64060202F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 5.5%; Score 138.5; DB 1; Best Local Similarity 21.2%; Pred. No. 0.0039; Matches 43; Conservative 48; Mismatches 73;
                                                                                                              Science 273:1058-1073(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           453 HRLVLVDETQHLLGVVSLSDILQ 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CBS 1.
CBS 2.
CBS 3.
CBS 4.
                                                                                                                                                                                                                                                                                                                                                                      InterPro: JP6000644; CBS_domain.
Pfam: PF00571; CBS: 4.
SMART: SM00116; CBS: 4.
Hypothetical protein: Repeat: CBS cDOMAIN 78 121 CBS 1.
DOMAIN 134 186 CBS 3.
DOMAIN 212 264 CBS 4.
                                                                                                                                                                                                                                                                                                                                       EMBL; U67581; AAB99421.1; -.
                                                                                                                                                                                                                                                                                                                                                           TIGR; MJ1404;
                                                                                                      jannaschii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         qq
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Search completed: June 6, 2003, 11:01:28 Job time: 19:9842 secs Page

protein

Run on:

Sequence:

Minimum DB Maximum DB

Database

Result . Ю

Searched:

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Q8txy3 methanopyru
Q9car3 arabidopsis
Q9car3 arabidopsis
Q9uyr4 pyrococcus
Q8xyb6 pyrobaculum
Q8tk4 saccharomyc
O58317 pyrococcus
Q9xy6 arabidopsis
Q97x4 aulfolobus
Q8u3y0 pyrococcus
Q8u3y0 pyrococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                Q811XO dictyosteli
027292 methanobact
02740 methanobact
Q81250 methanopru
Q96y62 sulfolobus
Q8yql0 anabaena sp
029410 archaeoglob
Q8wx4 methanopru
Q97aj9 thermoplasm
                                                                                      Q8rzi9 oryza sativ
Q9m727 lycopersico
Q9xi37 arabidopsis
Q9ssd0 arabidopsis
                     Q41108 phaseolus v
Q9s7w6 arabidopsis
O94035 candida alb
                                                                                                                                                                                 Q94d32 oryza sativ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   116 RSPRRMSFSG-----SRKTSSSKESSPNSNPSTSPGGIRFFSR-----SRKTSSVSSS 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               71 PPGQGEGPRSRP-AAESTGLEATFPKTTPLAQADPAGVGTPPTGWD-CLPSDCTA-SAAG 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        128 SSTDDVELATEPPATEAWECELEGLLEERPALCLSPQAPFPKLGWDDELRKPGAQIYMRF 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  163 PSTPTOVTKOHPFPLESYKOEPERPESRIYASSSP----PDTGQRFCLAFQSPARPPLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11 RTPSWSSLGGSEHQEMSFLEQENSSSWPSPAVTSSSERIRGKRRAKALRWTRQKSVEEGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              42.8%; Score 1085.5; DB 11; Length 566;
49.2%; Pred. No. 6.8e-80;
tive 79; Mismatches 126; Indels 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Strausberg R.; Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases. EMBL. BC015283, AAH15283.1; InterPro: 1PR006644; CBS_domain. Pfont: PF00571; CBS; 4. Hypothetical_protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            al protein.
566 Aa; 62997 MW; 754DE4D696102C7D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                   Q973T4
Q8U3Y0
Q97V95
                                                                                                                                                                                                                                                                                                                                                                                                                                                     QBT1X0
027292
026740
QBTZ50
Q96Y62
Q8YQL0
029410
                       Q41108
Q9S7W6
O94035
                                                                                                                                     Q9XI37
Q9SSD0
                                                                                                                                                                                 Q94D32
Q8TXY3
                                                                                        Q8RZ19
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                                                                                                                                                                                                                              Q9CAR3
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    Matches 234; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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   \texttt{0.48} \texttt{V.} \texttt{0.} \texttt{0.} \texttt{0.4444} \texttt{0.} \texttt{0
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Q91WG5;
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094d2 drosophila
089xt8 drosophila
085x7 drosophila
09bh16 caenorhabdi
0818x7 dictyosteli
002168 caenorhabdi
091601 caenorhabdi
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091602 arabidopsis
09fv59 arabidopsis
09fvy5 arabidopsis
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0925v0 mus musculu
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1589.904 Million cell updates/sec
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                                                                                                                                                                                                                                                                                          ........LSDILQALVLSPAGIDALGA
                                                                                                                                                6, 2003, 10:58:04 ; Search time 63.373 Seconds
                  GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                      671580 segs, 206047115 residues
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                                                                                                           - protein search, using sw model
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Q925V0
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08SXT8
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Gapop 10.0 , Gapext 0.5
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2538
1 MEPGLEHALRRTPSWSSLGG.
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                                                                                                                             ELRKPGAQIYMRFMQEHTCYDAMATSSKLVIFDTMLEIKKAFFALVANGVRAAPLWDSKK 234
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                                                                     LPVLDPVSGNVLHILTHKRLLKFLHIFGSLLPRPSFLYRTIQDLGIGTFRDLAVVLETAP 367
                                                                                                                                                                       368 ILTALDIFVDRRVSALPVVNECGQVVGLYSRFDVIHLAAQQTYNHLDMSVGEALRQRTLC 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  355 TFRDLAVVLETAPILTALDIFVDRRVSALPVVNECGQVVGLYSRFDVIHLAAQQTYNHLD 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             415 MSVGEALRQRTLCLEGVLSCQPHESLGEVIDRIAREQVHRLVLVDETQHLLGVVSLSDIL 474
             LVLHRYYRSPLVQIYEIEQHKIETWREIYLQGCFKPLVSISPNDSLFEAVYTLIKNRIHR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QSFVGMLTITDF1LVLHRYYRSPLVQIYE1EQHKIETWREIYLQGCFKPLVSISPNDSLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EAVYTLIKNRIHRLPVLDPVSGNVLH1LTHKRLLKFLHIFGSLLPRPSFLYRTIQDLGIG
                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster (Fruit fly).
Mkaryota: Metazoa; Arthropoda: Tracheata; Hexapoda: Insecta;
Pterygota: Neoptera: Endopterygota: Diptera: Brachycera; Muscomorpha;
Ephydroidea: Drosophilidae: Drosophila.
                                                                                                                                                                                                                               428 LEGVLSCQPHESLGEVIDRIAREQVHRLVLVDETQHLLGVVSLSDILQALVLSPAG 483
                                                                                                                                                                                                                                                DB 5; Length 647;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             70; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yoshida E.N., Benkel B.F., Fong Y., Hickey D.A.;
Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
EMBL, AF094764, AAC95306.1;
EMBL, AF094763, AAC95305.1;
FlyBase; FBqn0025803; SNF4A-gamma.
Interpro; IPR0000664; CBS_domain.
Ffam; PF00571; CBS; 4.
SMART; SM00116; CBS; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    647 AA; 71592 MW; B792BE1089730B52 CRC64;
                                                                                                                                                                                                                                                                                                                                                           01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-UN-2002 (TrEMBLrel. 21, Last annotation update)
SNF4Amp-activated protein kinase gamma subunit.
SNF4A-GAMMA OR CG17299.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2.2e-62;
                                                                                                                                                                                                                                                                                                                                   647 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34.3%; Score 871.5;
53.1%; Pred. No. 2.2e
ive 74; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            164; Conservative
                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      475 QALVLSPAG 483
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                       248
                                                                                                                 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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REDLING-20196005; Pubbmed-10731132;
RADAMEMERKELEY:
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Galle R.F.,
Gocyge R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.C., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Ballew R.M., Basu A., Baxerdale J., Bayraktaroglu L., Beasley E.M.,
Ballew R.W., Basu A., Baxerdale J., Bayraktaroglu L., Beasley E.M.,
RA Ballew R.W., Basu A., Baxerdale J., Bayraktaroglu L., Beasley E.M.,
Ballew R.W., Basu A., Barsardale J., Bayraktaroglu L., Beasley E.M.,
RA Ballew R.M., Basu A., Bouk J., Brokstein P., Benchtier P.,
Burtis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I.,
RA Burtis K.C., Busam D.A., Deut E., Deverport L.B., Davies P.,
RA Burtis K.C., Busam D.A., Deut E., Deverport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahler H., Cadieu E., Cabries P.,
RA Dodson K., Doug L.E., Downes M., Dugan-Rocha S., Dukov B.C., Dunn P.
Durbin K.J., Evangelista C.C., Ferrac C., Ferrac S., Fleischmann W.,
RA Cong F., Gorrell J.H., Gu Z., Genbart W.M., Glasser K.,
RA Gods K., Correll J.H., Gu Z., Gand M.-H., Ibegwam C.,
RA Jalli M., Kalush F., Karpen G.H., Kez J., Kennison J.A., Kecthum K.A.,
RA Lasko P., Lei Y., Levitsky A.A., Li J.J., Hernandez J.R., Houck J.M.,
RA Lei W. Murph B., Murphy B., Murphy D.M., Moshrefi A.,
Rakotiov G., Milshina N., Murphy B., Murphy D.M., Nebson D.L.,
Rangelin D.R., Nelson K.A., Nixon K., Nuxskern D.R., Shoel B.,
Rangelin D.R., Nelson K.A., Nixon K., Nuxskern D.R., Shoel B.,
Shue B.C., Siden Kasaman D.A., Weinscock G.M., Weissenbach J.,
Rangelin D.R., Nelson K.A., Worley K., Shon B.,
Shue B.C., Stapleron G., Stapleton M., Strong R., Shon B.,
Shue B.C., Stapleron G.M., Wenter E., Wang G., Zhoo Q., Zhoo G., Zhoo G., Shoo Q., Shoo G., Stene R., Rond R., Shoo B., Sho
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          175 ELRKPGAQIYMRFMQEHTCYDAMATSSKLVIFDTMLEIKKAFFALVANGVRAAPLWDSKK 234
                                                                                                                                                                                                                                         Pterygota; Neoptera; Endopteryota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                       SNF4A-GAMMA OR SNF4AGAMMA OR CG17299.
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 634;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; lrmcvc.
Pfam; PF00571, CBS; 4.
SMART; SM0116; CBS; 4.
Caa AA: 70174 MW; 3FFD0D53E54BBE7C CRC64;
                                                                                      01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34.3%; Score 869.5; DB 5; 53.1%; Pred. No. 3.1e-62; ive 73; Mismatches 71;
                                         634 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AE003733; AAF55864.1; -. FlyBase; FBgn0025803; SNF4A-gamma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 53.19
hes 164; Conservative
                                         PRELIMINARY;
                                                                                                                                                         SNF4AGAMMA protein.
                                                                                                                                                                                                                                                                                                                                                           STRAIN-BERKELEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                       Q9VDD2
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Matches
RESULT 3
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ELRKPGAQIYMRFMQEHTCYDAMATSSKLVIFDTMLEIKKAFFALVANGVRAAPLWDSKK 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         295 EAVYTLIKNRIHRLPVLDPVSGNVLHILTHKRLLKFLHIFGSLLPRPSFLYRTIQDLGIG 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   355 TFRDLAVVLETAPILTALDIFVDRRVSALPVVNECGQVVGLYSRFDVIHLAAQQTYNHLD 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       415 MSVGEALRQRILCLEGVLSCQPHESLGEVIDRIAREQVHRLVLVDETQHLLGVVSLSDIL 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster (Fruit fly).

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophilia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   235 QSFVGMLTITDFILVLHRYYRSPLVQIYEIEQHKIETWREIYLQGCFKPLVSISPNDSLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Y11B2A.8 protein.
Y11B2A.8.
Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E., George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G., Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S., Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M., Celniker S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1400;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AY070541; AAL48012.1; -. SEQUENCE 1400 AA; 152380 MW; 411B93CC6B9EC7AF CRC64;
                                                                                                                                                                                                                                                                                                                                                21, Created)
21, Last sequence update)
21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9e-62;
                                                                                                                                                                                                                                                                                       1400 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34.3%; Score 869.5; I
53.1%; Pred. No. 9e-63
live 73; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            372 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-2001 (TrEMBLrel, 17, 01-JUN-2001 (TrEMBLrel, 17, 01-JUN-2002 (TrEMBLrel, 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              164; Conservative
                                                                                                                                                                                                                                                                                                                                                    01-JUN-2002 (TrEMBLrel).
01-JUN-2002 (TrEMBLrel).
01-JUN-2002 (TrEMBLrel).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1214 LYLVLRPSG 1222
                                          483
                                                                                     475 QALVLSPAG 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        [1]
SEQUENCE FROM N.A.
                                              QALVLSPAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=BERKELEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SNF4 AGAMMA.
                                          475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29BHL6;
                                                                                                                                                                                                                                                                                       Q8SZS7
                                                                                                                                                                                                                                                                                                                           Q8SZS7
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Q8SZS7
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                                                                                                                                           267
                                                                                                                                                                                                               354
                                                                                                                                                                                                                                               414
                                                                                                                                                                                                                                                                                                                                                                                                                        387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        474
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DLEEDDSQIFVKFFRFHKCYDLIPTSAKLVVFDTQLLVKKAFYALVYNGVRAAPLWDSEK 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 115 MSVGEALRQRILCLEGVLSCQPHESLGEVIDRIAREQVHRLVLVDFTQHLLGVVSLSDIL 474
                                                                                                               EAVYTLIKNRIHRLPVLDPVSGNVLHILTHKRLLKFLHIFGSLLPRPSFLYRTIQDLGIG
                                                                                                                                                                                                                                                                                                                                             355 TFRDLAVVLETAPILTALDIFVDRRVSALPVVNECGQVVGLYSRFDVIHLAAQQTYNHLD
                                                                                                                                                                                                                                                                                                                                                                                    415 MSVGEALRQRTLCLEGVLSCQPHESLGEVIDRIAREQVHRLVLVDETQHLLGVVSLSDTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                QSFVGMLTITDFILVLHRYYRSPLVQIYEIEQHKIETWREIYLQGCFKPLVSISPNDSLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                175 ELRKPGAQIYMRFMQEHTCYDAMATSSKI,VIFDTMLEIKKAFFALVANGVRAAPLWDSKK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QSFVGMLTITDFILVLHRYYRSPLVQIYE1EQHKIETWREIYLQGCFKPLVSISPNDSLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QQFVGMLTITDF1K1LQMYYKSPNASMEQLEEHKLDTWRSV-LHNQVMPLVSIGPDASLY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                600 TYNNIETADETTSIITALKKFVERRVSALPLVDSDGRLVDIYAKFDVINLAAEKTYNDLD
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Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
George R., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G.,
Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S.,
Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 5; Length 906;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-00N-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         906 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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SEQUENCE 906 AA; 99970 MV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ||| |:|
448 LYLVLRPSG 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QALVLSPAG 483
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NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Celniker S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SNF4 AGAMMA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Si
Matches 164;
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SINNYINHSSISTVSEGLEN-----LULKSGIKKI--DSETEKYIEEGKQVFVNFLKGH 274
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            451 TPLVEVLELLSEKKISAVPIIDSETSKIVDVYSKSDVTLMSKQGILSPSDLNLPVHQVLS 510
                                    89 LEATFPKTT------PLAQ---ADPA-GVGTPPTGWDCLPSDCTASAAGSSTDDVE 134
                                                                                                 163 LPSTDNKSSTNTNNNNENPLKQTISSSPSKSTTTTTTSTSTTTTPSLSSLSSNNNNNSN 222
                                                                                                                                                                    135 LATEFPATEAWECELEGLLEERPALCLSPQAPFPKLGWDDELRK---PGAQIYMRFMQEH 191
                                                                                                                                                                                                                                                                                            TCYDAMATSSKLVIFDIMLEIKKAFFALVANGVRAAPLWDSKKQSFVGMLTITDFILVLH 251
                                                                                                                                                                                                                                                                                                                                                                                                                        252 RYYRSPLVQ--IYEIEQHKIET-WREIYLQGCFKP--LVSISPNDSLFEAVYTLIKNRIH 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   366 APILTALDIFVDRRVSALPVV-NECGQVVGLYSRFDVIHLAAQQTYN------HLDMS 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            417 VGEALRQRILCLEGVLSCQPHESLGEVIDRIAREQVHRLVLVDETQHLLGVVSLSDILQA 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; 197550; ARK18981.2; ...
InterPro; IPROA0664; CBS_domain.
Pfam; PF00571; CBS; 4.
SMART; SM00116, CBS; 4.
Hypothetical protein.
SEQUENCE 423 AA; 47451 MW; 6997065D515E7B21 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Miller N., Gattung S.;
"The sequence of C. elegans cosmid T20F7.";
Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUL-1997 (TrEMBLrel. 04, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 47.5 kDa protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=BRISTOL N2;
MEDLINE=99069613; Pubmed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Caenorhabditis elegans.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. STRAIN=BRISTOL N2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=6239;
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LL 569
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                                                                                                                                                                                                                                                                                            192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         188 MQEHTCYDAMATSSKLVIFDTMLEIKKAFFALVANGVRAAPLWDSKKQSFVGMLTITDFI 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             365 TAPILTALDIFVDRRVSALPVVNECGQVVGLYSRFDVIHLAAQQTYNHLDMSVGEALRQR 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        105 NSIEQPSPSFISSSQ--DGVLTVDPLAVDGEKGNKESQSPPNGDNQILNNNNMFFKDITS 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     248 LVLHRYY -- RSPLVQIYEIEQHKIETWREIY - LQGCFKPLVSISPNDSLFEAVYTLIKNR 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                305 IHRLPVLDPVSGNVLHILTHKRLLKFLHIFGSLLPRPSFLYRTIQDLGIGTFRDLAVVLE 364
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Gloeckner G., Eichinger L., Szafranski K., Pachebat J., Dear P.,
Gloeckner G., Eichinger L., Parta G., April J.F., Guigo R., Kumpf K.,
Lehmann R., Baumgart C., Parta G., April J.F., Guigo R., Kumpf K.,
Tunggal B., Cox E., Quail M.A., Platzer M., Rosenthal A., Noegel A.A.;
"Sequence and Analysis of Chromosome 2 of Dictyostellum.";
Schence and Analysis of the EMBL/Genbank/DDBJ databases.
EMBL; AC115599; AAL92329.1;
SEQUENCE 577 AA; 64209 MW; 3FBCS6EA649B25A9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEWFEGVQTCLETDSLFQVLEAIVKAEVHRLIVTDQDKKVVGVVSLSDILKNLVLDP 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TLCLEGVLSCQPHESLGEVIDRIAREQVHRLVLVDETQHLLGVVSLSDILQALVLSP 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33 NSSSWPSPAVTSSSERIRGKRRAKALRWTRQKSVEEGEPPGQGEGP----RSRPAAESTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29.0%; Score 736.5; DB 5; Length 372; 49.8%; Pred. No. le-51; ive 63; Mismatches 83; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 5; Length 577;
                                                                                                                                                                                                                                                                                                                    'Genome sequence of the nematode C.elegans: A platform for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 151; Conservative 100; Mismatches 178; Indels
                                                                                                                                                          Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 372 AA; 41376 MW; 81A39670877167DF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last Sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
50.F4/AMP-activated protein kinase gamma subunit.
50.Etyostellum discoideum (Slime mold).
Eukaryota: Mycetcozoa; Dictyostellida; Dictyostellum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22.0%; Score 559.5; DB 5
31.3%; Pred. No. 4.7e-37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               577
   Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                       MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                Science 282:2012-2018(1998).
EMBL; AL132904; CAG35836.1; -.
Interpror; IPR000644; CBS_domain.
Pfam; PF00571; CBS; 4.
SMART; SM00116; CBS; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                148; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                            investigating biology.
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Best Local Similarity
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                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                          NCBI_TaxID=6239;
                                                                                                                               Sulston J.E.
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QQTYNHLDMSVG--EALRQRT----LCLEGVLSCQPHESLGEVIDRIAREQVHRLVLVDE 460
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                                                                                                                                                                                                                       288 SPNDSLFEAVYTLIKNRIHRLPVLDPVSGNVLHILTHKRLLKFLHIFGSLLPRPSFLYRT 347
                                                                                                                                                                                                                                                  348 IQDLGIGTFRDLAVVLETAPILTALDIFVDRRVSALPVVNE-CGQVVGLYSRFDVIHLAA 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     354 AAFSDHIDLSVSVTRAIQERDYQNGIRRDGVVTANYTTTLWSLIEIFIDKNVHRIFMVDD 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      112 TGWDCLPSDCTASAAGSS---TDDVELATEFPATEAWECELEGLLEERPALCLSPQAPFP 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         169 KL-GWDDELRKPGAQIYMRFMQEHTCYDAMATSSKLVIFDTMLEIKKAFFALVANGVRAA 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        228 PLWDSKKQSFVGMLTITDFILVLHRY--YRSPLVQIYEIEQHKIETWRE--IYLQGCF-- 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             282 -----KPLVSISPNDSLFEAVYTLIKNRIHRLPVL----DPVSGNVLHILTHKRLLK- 329
        183 IYMRFMQEHTCYDAMATSSKLVIFDTMLEIKKAFFALVANGVRAAPLWDSKKQSFVGMLT
                                      243 ITDFILVLHRY--YRSPLVQI------YEIEQHKIETWRE-IYLQGCFKPLVSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 21, Last annotation update)
01-UNN-2002 (TrEMBLrel. 21, Last annotation update)
Atig09020/F7019_11.
Arabidopsis thaliana (Mouse-ear cress).
Berarydota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Shinn P., Chen H., Cheuk R., Kim C.J., Koesema E., Meyers M.C., Banh J., Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y., Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J. Liu S.X., Miranda M., Narusaka M., Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A., Shinozaki K., Oravis R.W., Theologis A., Ecker J.R.; Shinozaki K., Vandanted (OCT., Toriumi M., Yamada K., Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.; Submitted (OCT., 2001) to the EMBL/Genbank/DDBJ databases.

EMBL: AF439826; AAL2448.1; --
InterPro: IPR000644; CBS_domain.
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SEQUENCE 487 AA: 53466 MW; 4545FE3BF2C4EBEC CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      414 RTILKGIISLSDVIEFLVLRP 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        461 TQHLLGVVSLSDILQALVLSP 481
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Matches
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                                                                                                          182 QIYMRFMQEHTCYDAMATSSKLVIFDTMLEIKKAFFALVANGVRAAPLWDSK-KQSFVGM 240
                                                                                                                                                                                                                 241 LTITDFILVLHRYYRS------PLVQI--YEIEQHKIETWRE-IYLQGCFKPLVS 286
                                                                                                                                                                                                                                             |::|||| |:: || |: : || | | |:||| || |:|||| LSVTDFIKVMLKIYRERTKCEKESTELDMTQIANEEIGNLSIRQYRELVKKEGNLRPLVS 157
                                                                                                                                                                                                                                                                                                                      ISPNDSLFEAVYTLIKNRIHRLPVLDPVSGNVLHILTHKRLLKFLHIFGSLLPRPSFLYR 346
                                                                                                                                                                                                                                                                                                                                                    347 TIQDLGIGTFRDLAVVLETAPILTALDIFVDRRVSALPVV-NECGQVVGLYSRFDVIHLA 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SPKELGIGTWSGIRVVFPDTQLVDCLDILLNKGVSGLPVVERETFKVVDMYSRFDAVGIA 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    406 AQQTYNHLDMSVGEALRQRTLCLEG------VLSCQPHESLGEVIDRIAREQVHRLVL 457
                                                                                                                                                           EAFARLLWINQCYEAMPSSSKMVVFDQGLLMHKAFNGLLAQSTRHVLLSDPDFGGKLDGI 97
                                                           Gaps
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                                                         30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Genome sequence of the nematode C. elegans: a platform for investigating biology, The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
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        Length 423;
                                                         106; Indels
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InterPro: IPR000644; CBS_domain.
Pfam; PF00571; CBS; 4.
SMART; SM0116, CBS; 4.
SKART; SM0116, CBS; 3.
Hypothetical protein.
SEQUENCE 448 AA; 51514 KW; B689218979299479 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ryan E., Wohldman P., Walker C., Fielder T.;
"The sequence of C. elegans cosmid Y41G9A.";
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 51.5 kDa protein.
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     DB 5;
     : Score 488; DB 5;
Pred. No. 2e-31;
69; Mismatches 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VDETQHLLGVVSLSDILQALVLSP 481
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=99069613; PubMed=9851916;
     19.2%;
36.7%;
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Matches 106; Conservative
                                                         119; Conservative
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Query Match
Best Local Similarity
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STRAIN=BRISTOL N2;
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us-09-826-581-6.rspt

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[1]
SEQUENCE FROM N.A.
Victoria L., Mar A
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                                                                                                                                                      377 DRRVSALPVVNECGQVVGI,YSRFDVIHLAAQQTYN--HL-DMSVGEALR--QRTLCLEGV 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -GWDDELRKPGAQIYMRFMQEHTCYDAMATSSKLVIFDTMLEIKKAFFALVANGVRAAPL 229
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kleinow T., Bhalerao R., Breuer F., Umeda M., Salohert K., Koncz C., "Functional identification of an arabidopsis snf4 ortholog by screening for heterologous multicopy suppressors of snf4 deficiency in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        269 EVSSIPVVDDNDSLIDIYSRSDITALAKDKAYAQIHLDDMTVHQALQLGQDASPPYGIFN
                                                                 ----FLHIFGSLLPRPSFLYRTIQDLGIGTF------RDLAVVLETAPILTALDIFV
                                                                                                            316 ICRYFRHSSSSL----PILQQPICSIPLGTWVPRIGESSSKPLATLRPHASLGSALALLV
                                                                                                                                                                                  | | | | | : : | | : : | | : : | | : : | | SGVDLELSRHRISV---LLSTRTAYELLPESGKVIALDVNLPVKQAFHILYEQGIPLAPL
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Bubrayota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                         01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Putative activator subunit of SNF1-related protein kinase SNF4.
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EMBL, AF250335; AAG10141.1; -.
InterPro; IPR000644; CBS_domain.
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Matches 118; Conservative
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SMART; SM00116; CBS;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     296 AVYTLIKNRIHRLPVLDPVSGN-----VLHILTHKRLLK-----FLHIFGSL----- 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -LPRPSFLYRTIQDLGIGTFRDLAVVLETAPILTALDIFVDRRVSALPVVNECGQVVGLY 396
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Zea mays (Maize).
Eukaryota: Viridiplantae; Streptophyta; Embryophyta: Tracheophyta;
Spermatophyta: Magnoliophyta: Liliopsida; Poales; Poaceae; PACC clade;
Panicoideae; Andropogoneae; Zea.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
Pantcoideae; Andropogoneae; Zea.
NCBL_TaxID=4577;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 497;
Victoria L., Mar A., Tatjana K., Csaba K., Montserrat P.;
"Domain fusion between Snfl related kinase subunits during
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EMBL; AF276085; AAG31751.1; -.
InterPro; IPR00644; CBS_domain.
Pfam; PF00571; CBS; 3.
SWART; SW00116; CBS; 3.
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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Last annotation update)
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Pred. No. 8.5e-20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13.7%;
29.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99; Conservative
                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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12;

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223 GVRAAPLWDSKKQSFVGMLTITDFILVLHRY--YRSPLVQIYEIEQHKIETWRE--IYLQ 278
                                                                                                                                                           279 GCF-----KPLVSISPNDSLFEAVYTLIKNRIHRLPVL-----DPVSGNVLHILTHK 325
                                                                                                                                                                                                                                                                                      372 LDIFVDRRVSALPVVNECGQVVGLYSRFDVIHLAAQQTYN--HL-DMSVGEALR--QRTL 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         156 RPALCLSPQAPPPKLGWDDELRKPGAQIYMRFMQEHTCYDAMATSSKLVIFDTMLEIKKA 215
                                                                                                                                                                                                                          326 RLLK----FLHIFGSLLPRPSFLYRTIQDLGIGTF-----RDLAVVLETAPILTA 371
                                                                                                                                                                                                                                                        240 GILKCICRYFRHSSSSL----PILOOPICSIPLGTWVPRIGESSSKPLATLRPHASLGSA 295
                                                                                                                                                                                                                                                                                                        34 RPCRIFSNEGAYEVLSAFDRHADP----YHTFMKSITCYDLQPTHSSLVVFDGKTKVKAA
                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                               47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
                            9.6%; Score 243.5; DB 10; Length 391;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8.9%; Score 227; DB 5; Length 423; 25.9%; Pred. No. 3.7e-10; Live 61; Mismatches 135; Indels
                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "The sequence of C. elegans cosmid T01B6.";
Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; U67950; AAK84564.1; -.
InterPro; IPR000644; CBS_domain.
391 AA; 43032 MW; 26D6D08280587B74 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00571; CBS; 4. SEQUENCE 423 AA; 47571 MW; C38F5C7D18DDB167 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                              89;
                                              1.5e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        423 AA
                                                              53; Mismatches
                                                                                                                                                                                                                                                                                                                                                      427 CLEGVLS-----CQPHESLGEVIDRIA 448
                                                                                                                                                                                                                                                                                                                                                                        |::|:|:|356 PPYGIFNGQRCHMCLRSDSLVKVMERLA 383
                                              Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical protein T01B6.3.
                                             29.5%;
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                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Waterston R.; "Direct Submission.";
                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-BRISTOL N2;
Johnson D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. STRAIN=BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=6239;
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Best Local S
Matches 90
SEQUENCE
                               Query Match
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                                                                                                                                                                                                                          13;
                                                                                                                                                                                                                                                        187 FMQEHTCYDAMATSSKLVIFDTMLEIKKAFFALVANGVRAAPLWDSKKQSFVGMLTITDF 246
                                                                                                                                                                                                                                                                                        225
                                                                                                                                                                                                                                                                                                                                                                                                                    285 IAVKLLQNGISTVPVIYSSSSDGSFPQLLHLASLSGILKCICRYFKNSTGNL----PILN 340
                                                                                                                                                                                                                                                                                                                    247 ILVLHRY--YRSPLVQIYEIEQHKIETWREIYLQ-----GCFKP---LVSISPNDSLFE 295
                                                                                                                                                                                                                                                                                                                                                      284
                                                                                                                                                                                                                                                                                                                                                                                    296 AVYTLIKNRIHRLPVLDPVSGN-----VLHILTHKRLLK-----FLHIFGSLLPRPSFLY 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                    RTIQDLGIGTF ---- RDLAVVLETAPILTALDIFVDRRVSALPVVNECGQVVGLY 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                341 QPVCSIPLGSWVPKIGDLNSRPLAMLRPNASLSSALNMLVQACVSSIPIVDDNDSLLDTY 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SRFDVIHLAAQQTYNHL---DMSVGEALR-----QR-TLCLEGVLSCQPHE 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SRSDITALAKAKVYTHVRLDEMTIHQALQLGQDANTPFGFFNGQRCQMCLRS-----D 453
                                                                                                                                                                                                                                                                                                                                          YLSLHTCYDLLPDSGKVIALDINLPVKQSFHILHEQGIPVAPLWDSFRGQFVGLLSPLDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana (Mouse-ear cross).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Epermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN-CV. COLUMBIA;
SOBOTINE B.I., Vysotskaia V.S., Toriumi M., Yu G., Oji, O, Buehler E.,
Conway A.B., Conway A.R., Dewar K., Feng J., Kim C., Kurtz D., Li Y.,
Shinn P., Sun H., Davis R.W., Ecker J.R., Federspiel N.A.,
Theologis A.;
                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "The sequence of BAC F7G19 from Arabidopsis thaliana chromosome 1."; Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
          Victoria L., Mar A., Tatjana K., Csaba K., Montserrat P.; "Domain fusion between Snfl related kinase subunits during plant
                                                                                                                                                                                                                          61;
                                                                                                                                                                                           Length 496;
                                                                                                                                                                                 13.6%; Score 34.v.
28.7%; Pred. No. 1.1e-19;
*ive 77; Mismatches 105; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AC000106; AAB70406.1; -.
InterPro; IPR000644; CBS_domain.
Pfam; PP00571; CBS; 2.
SMART; SM00116; CBS; 1.
                                             evolution.";
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                          496 AA; 54799 MW; 316F8282B3B55D8A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SLGEVIDRIAREQVHRLVLVDE-TQHLLGVVSLSDILQALV 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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                                                                         EMBL; AF276086, AAG31752.1; -.
InterPro: JPR000644; CBS_domain.
Pfam; PF00571; CBS; 3.
SMART; SM00116; CBS; 3.
                                                                                                                                                                                                                        98; Conservative
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STRAIN=CV. COLUMBIA;
Theologis A.;
                                                                                                                                                                                                          Similarity
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                                                                                                                                                          SEQUENCE
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13;

216 FFALVANGVRAAPLMDSKKQSFVGMLTITDFILVLHRYYRSPLVQIYEIEQHKI 269	90 VHALSQHGHIAAVVTNTDKYQAECVFNWGHCLTAILLVAAGNREVASKTL 140	270 ETWREIYLQGCFKPLVSISPNDSLFEAVYTLIKNRIHRLPVLDPVSGNVLHILTHKR 326	N99	327 LLKFLHJEGSLLPRPSFLYRTIQDLGIGTERDLAVVLETAPILTA 371	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	372 LDIFVDRRVSALPVVNECCQVVGLYSRFDVI-HLAAQQTYNHLDMSVGEALRQRTLCLEG 430	246 IKLMSERKMSTIPVVNDFKQIVNMLARKDILLEIMSHQGGNFHDMLKEPVKILQS 300	431 VLSCQPHESLGEVIDRIAREQVHRLVLVDETQHLLGVVSLSDIL 474	301 LQSRLVYGRSSYTVETVAKMMTSDKSSLPIIDEGKRILAVVSCSDIL 348
δλ	QO	Qy	qa	Qy	QQ	QY	qq	ΟY	qa

Search completed: June 6, 2003, 11:02:49 Job time : 66.373 secs

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INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 328 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LIBRARY: PENITUTO1
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Sequence 21, Appl
Sequence 21, Appl
Sequence 7, Appli
Sequence 5, Appli
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Sequence 1, Appli
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33, Appli
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494.132 Million cell updates/sec
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2538
1 MEPGLEHALRRTPSWSSIGG......LSDILQALVLSPAGIDALGA 489
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Sequence 2, 1
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Sequence 4, P
Sequence 2, P
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Sequence 3
Sequence 3
Sequence 5
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-272-796-7

US-09-359-161-6

US-08-181-989-21

US-09-359-161-7

US-09-359-161-7

US-09-359-161-3

US-09-359-161-3

US-09-426-998-5

US-09-426-998-5

US-09-426-998-5

US-09-45-37A-287

US-09-55-746-3

US-09-55-745-3

US-09-55-746-3

US-08-45-3

US-09-57-746-4

US-09-579-181-2

US-09-579-181-1

US-09-579-181-1
                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                 262574 seqs, 29422922 residues
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Maximum Match 100%
Listing first 45 summaries
                                          OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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length: 2000000000
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Perfect score:
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Sequence 4, Appli Sequence 4, Appli Sequence 12, Appli Sequence 12, Appli Sequence 2, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 2, Appli		
29 90.5 3.6 909 4 US 009-448-R68-4 31 90.5 3.6 1618 1 US 07-853-913-4 32 90.5 3.6 1618 1 US 07-853-913-4 33 90 3.5 595 4 US 08-764-920-12 34 90 3.5 619 1 US 08-86-76-76-2 35 90 3.5 619 1 US 08-46-7682A-3 36 90 3.5 619 2 US 08-246-682A-3 37 90 3.5 619 2 US 08-246-682A-3 38 90 3.5 619 2 US 08-247-411A-3 39 90 3.5 619 2 US 08-247-491A-3 41 90 3.5 619 2 US 08-46-695-2 42 90 3.5 648 1 US 08-112-949-2 43 90 3.5 648 1 US 08-712-949-2 44 90 3.5 648 1 US 08-712-949-2 45 90 3.5 648 1 US 08-714-22-2 45 90 3.5 648 1 US 08-714-22-2	ALIGNMENTS	RESULT 1 US-08-878-99-7 Sequence 7, Application US/08878989 Patent No. 5885803 GENERAL INFORMATION: APPLICANT: Bandman, Olga APPLICANT: Hillman, Jennifer L. APPLICANT: Guegler, Karl G. APPLICANT: Golly, Newl C. APPLICANT: Golly, Newl C. APPLICANT: Goll, Surya K. APPLICANT: Blah, Purvi TITLE OF INVENTION: KINASES NUMBER OF SEQUENCES: 21 CORRESPONDENCE ADDRESS: ADDRESSEE: Incyte Pharmaceuticals, Inc. STATE: Golly Alto CITY: Pal Alto STATE: Golly Alto COUNTYR: LEM Compatible OOPERATING SYSTEM: MEDIUM TYPE: Diskette COMPUTER: LEM Compatible OPERATING SYSTEM: BELICATION NUMBER: US/08/878,989 FILING DATE: CLASSIFICATION DATA: APPLICATION NUMBER: US/08/878,989 FILING DATE: CLASSIFICATION DATA: APPLICATION NUMBER: FILING DATE: FILI

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                                                                                                                                                                                                                                       64 PLWESKKQSFVGMLTITDFINILHRYYKSPWVQIYELEBHKIETWRELYLQETFKPLVNI 123
                                                                                                       169 KLGWDDE-LRKPGAQIYMRFMQEHTCYDAMATSSKLVIFDTMLEIKKAFFALVANGVRAA 227
                                                                                                                                                                228 PLWDSKKQSFVGMLTITDFILVLHRYYRSPLVQIYEIEQHKIETWREIYLQGCFKPLVSI 287
                                                                                                                                                                                                                         288 SPNDSLFEAVYTLIKNRIHRLPVLDPVSGNVLHILTHKRLLKFLHIFGSLLPRPSFLYRT 347
                                                                                                                                                                                                                                                                                 IQDLGIGTFRDLAVVLETAPILTALDIFVDRRVSALPVVNECGQVVGLYSRFDVIHLAAQ 407
                                                                                                                      Gaps
                                                                           1;
                                            42.6%; Score 1080.5; DB 2; Length 328; 63.3%; Pred. No. 2.3e-111;
                                                                           48; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: COTIEY, Neil C.
APPLICANT: Guegler, Karl G.
APPLICANT: Gal, Preeti
APPLICANT: Goli, Surya K.
TITLE OF INVENTION: BISEASE ASSOCIATED PROTEIN
TITLE OF INVENTION: KINASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                          67; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY AGENT INFORMATION:
NAME: Billings, Lucy J J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0321 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Incyte Pharmaceuticals,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US/09/272,796
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APPLICATION NUMBER: 08/878,989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 7, Application US/09272796; Patent No. 6207148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hillman, Jennifer L.
Corley, Neil C.
                                                                                                                                                                                                                                                                                                                                                                                                    468 VSLSDILQALVLSPAG 483
                                                                                                                                                                                                                                                                                                                                                                                                                     3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM Compatible
                                                                          Matches 200; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bandman, Olga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Ph
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM:
                                                            Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 3174 Por
CITY: Palo Alto
STATE: CA
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; CLONE: 1452972
US-08-878-989-7
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US-09-272-796-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       288 SPNDSLFEAVYTLIKNRIHRLPVLDPVSGNVLHILTHKRLLKFLHIFGSLLPRPSFLYRT 347
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QTYNHLDMSVGEALRQRTLCLEGVLSCQPHESLGEVIDRIAREQVHRLVLVDETQHLLGV 467
                                                                                                                                                                                                                                                                                                                                                63
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APPLICANT: Downie, Bruce
APPLICANT: Gee, Oliver
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Regulation of Source-Sink Relationships and Responses
TITLE OF INVENTION: Lo Stress Conditions in Plants
FILE REFERENCE: 023070-095900US
                                                                                                                                                                                                                                                                                                                           228 PLWDSKKQSFVGMLTITDFILVLHRYYRSPLVQIYEIEQHKIETWREIYLQGCFKPLVSI
                                                                                                                                                                                                                                                                                                          169 KLGWDDE-LRKPGAQIYMRFWQEHTCYDAMATSSKLVIFDTMLEIKKAFFALVANGVRAA
                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: gamma subunit of AMP-activated protein kinase; OTHER INFORMATION: (AMPK-gamma)
US-09-359-161-6
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                                                                                                                                                                                                                            DB 4; Length 328;
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                                                                                                                                                                                                                                                                    48; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63;
                                                                                                                                                                                                                        ; Score 1080.5; DB 4
; Pred. No. 2.3e-111;
67; Mismatches 48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/359,161A
CURRENT FILING DATE: 1999-07-21
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 6, Application US/09359161A Patent No. 6342656 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           468 VSLSDILQALVLSPAG 483
                                                                                                                                                                                                                            42.6%;
INFORMATION FOR SEQ ID NO: 7
SEQUENCE CHARACTERISTICS:
LENGTH: 328 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT ORGANISM: Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Bradford, Kent J. APPLICANT: Dahal, Peetambar APPLICANT: Yang, Hong
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Best Local Similarity 62.39
Matches 197; Conservative
                                                                                                                                                                                                                                                                  200; Conservative
                                                                                STRANDEDNESS: single
                                                                                                                                         LIBRARY: PENITUT01
CLONE: 1452972
                                        LENGTH: 328 aming TYPE: amino acid
                                                                                                       linear
                                                                                                                                                                                                                                               Similarity
                                                                                                                        IMMEDIATE SOURCE:
                                                                                                       TOPOLOGY:
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Best Local Si
Matches 200;
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FILING DATE: 8 JAN 1996
ATTORNEY/AGENT INFORMATION:
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                                                                                                                193; Conservative
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        MEDLAL.
LIBRARY: Gene...
.vo. 1335856
                                                                                 Query Match
Best Local Similarity
Matches 193; Conserv
    IMMEDIATE SOURCE:
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                                                 US-08-878-989-21
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                                    CLONE:
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                                                                                                                                           189 SKSLEELQIGTYANIAMVRTTTPVYVALGIFVQHRVSALPVVDEKGRVVDIYSKFDVINL 248
                                                                                                                                                                                                                                                  105 AAQQTYNHLDMSVGEALRQRTLCLEGVI,SCQPHESLGEVIDRIAREQVHRLVLVDETQHL 464
                                                                                                                                                                                      345 YRTIQDLGIGTFRDLAVVLETAPILTALDIFVDRRVSALPVVNECGQVVGLYSRFDVIHL 404
                                                                                                                                                                                                                                                                       165 APFPKLGWDDELRKPGAQIYMRFMQEHTCYDAMATSSKLVIFDTMLEIKKAFFALVANGV 224
                                                             RAAPLWDSKKQSFVGMLTITDFILVLHRYYRSPLVQIYEIEQHKIETWREIYLQGCFKPL 284
                  GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Galdan, Jennifer L.
APPLICANT: Guegler, Karl G.
APPLICANT: Guegler, Karl G.
APPLICANT: Gald, Surya K.
APPLICANT: Gald, Surya K.
APPLICANT: Shah, Purvi
ITILE OF INVENTION: DISEASE ASSOCIATED PROTEIN
ITILE OF INVENTION: KINASES
NUMBER OF SEQUENCES:
ADDRESSEE: INCYL PHARMACCULICALS, INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: FastSEQ for Windows Version 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 21, Application US/08878989 Patent No. 5885803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Billings, Lucy J J
REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                  465 LGVVSLSDILQALVLS 480
                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 21:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IBM Compatible
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LENGTH: 331 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
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TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
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                                                                                                                                                                                                                                                                               303 NRIHRLPVLDPVSGNVLHILTHKRLLKFLHIFGSLLPRPSFLYRTIQDLGIGTFRDLAVV 362
                                                                                                                                                                                                                                                                                                          363 LETAPILTALDIFVDRRVSALPVVNECGQVYGLYSRFDVIHLAAQQTYNHLDMSVGEALR 422
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
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APPLICANT: Dartmouth College, St. Vincents Institute of APPLICANT: Medical Research, Kemp et al.
TITLE OF INVENTION: No. 6124125el AMP Activated Protein Kinase NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
    Length 331;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 331;
                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
COMPUTER: IBM PC
40.1%; Score 1017; DB 2;
64.8%; Pred. No. 2.7e-104;
Live 53; Mismatches 52;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: WINDOWS 95
SOFTWARE: WORDPERFECT 6.0 FOR WINDOWS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/101,146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Jane Massey Licata, Esq. STREET: 66 E. Main Street
CITY: Marlton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DC-0050
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; Patent No. 6124125
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (856) 810-1515
TELEFAX: (856) 810-1454
INFORMATION FOR SEQ ID NO: 64:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: October 7, 1998 CLASSIFICATION: 435 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            32,257
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us-09-826-581-6.rai

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LIBRARY: GenBank
CLONE: 1335856
                                                                               Similarity
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        ; LIBRARY:
; CLONE: 1
US-09-272-796-21
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                                                                Query Match
                                                                                  Best Local
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                                                183 IYMRFWQEHTCYDAMATSSKLVIFDTMLEIKKAFFALVANGVRAAPLWDSKKQSFVGMLT 242
                                                                                                              243 ITDFILVLHRYYRSPLVQIYEIEQHKIETWREIYLQGCFKPLVSISPNDSLFEAVYTLIK 302
                                                                                                                              303 NRIHRLPVLDPVSGNVLHILTHKRLLKFLHIFGSLLPRPSFLYRTIQDLGIGTFRDLAVV 362
                                                                                                                                                                                                                                       363 LETAPILTALDIFVDRRVSALPVVNECGQVVGLYSRFDVIHLAAQQTYNHLDMSVGEALR 422
                                                                                                                                                                                                                                                       28 VYTSFWKSHRCYDLIPTSSKLVVFDTSLQVKKAFFALVTNGVRAAPLMDSKKQSFVGMLT 87
                                                                                                                                                                                                                                                                                                   423 QRTLCLEGVLSCQPHESLGEVIDKIAREQVHRLVLVDETQHLLGVVSLSDILQALVLS 480
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Pred. No. 2.7e-104;
3: Mismatches 52; Indels
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APPLICANT: Hillman, Jennifer L.
APPLICANT: Corley, Neil C.
APPLICANT: Gold, Warl G.
APPLICANT: Gold, Surya K.
APPLICANT: Gold, Surya K.
APPLICANT: Shah, Purvi
TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN
TITLE OF INVENTION: KINASES
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
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FastSEQ for Windows Version 2.0
                53; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Incyte Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PF-0321 US
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APPLICATION NUMBER: US/09/272,796
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 21, Application US/09272796 Patent No. 6207148 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 08/878,989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Billings, Lucy J J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3174 Porter Drive
   64.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 331 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 415-845-4166
                   193; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IMMEDIATE SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               USA
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183 IYMRFMQEHTCYDAMATSSKLVIFDTMLEIKKAFFALVANGVRAAPLWDSKKQSFVGMLT 242
                                                                                                                                                                                                                                                   243 ITDFILVLHRYYRSPLVQIYEIEQHKIETWREIYLQGCFKPLVSISPNDSLFEAVYTLIK 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             186 RFMQEHTCYDAMATSSKLVIFDTMLEIKKAFFALVANGVRAAPLWDSKKQSFVGMLTITD 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84 FINVIQYYFSNP-----DKFELVDKLQLDG-LKDIERALGVDQLDTASIHPSRPLF 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             295 EAVYTLIKNRIHRLPVLDPVSGN----VLHILTHKRLLKFLHIFGSLLPRPS-FLYRTIQ 349
                                                                                                                                                                                                                                                                                   88 ITDFINITHRYYKSALVQIYELEBHKIETWREVYLQDSFKPLVCISPNASLFDAVSSLIR 147
                                                                                                                                                                                                                                                                                                                                                                         303 NRIHRLPVLDPVSGNVLHILTHKRLLKFLHIFGSLLPRPSFLYRTIQDLGIGTFRDLAVV 362
                                                                                                                                                                                                                                                                                                                                                                                                            363 LETAPILTALDIFVDRRVSALPVVNECGQVVGLYSRFDVIHLAAQQTYNHLDMSVGEALR 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   246 FILVLHRYYRSPLVQIYEIEQHKIETWREIYLQGCFKPL------VSISPNDSLF 294
                                                                                                                                                                                      87
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Regulation of Source-Sink Relationships and Responses TITLE OF INVENTION: to Stress Conditions in Plants
FILE REFERENCE: 023070-095900US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         423 QRTLCLEGVLSCQPHESLGEVIDRIAREQVHRLVLVDETQHLLGVVSLSDILQALVLS 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 18.0%; Score 457; DB 4; Length 322; Best Local Similarity 34.2%; Pred. No. 4.7e-42; Matches 106; Conservative 66; Mismatches 108; Indels 30; Gaps
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      Length 331;
                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Bradford, Kent J.
APPLICANT: Dahal, Peetambar
APPLICANT: Yang, Hong
APPLICANT: Cooley, Michael
APPLICANT: Downie, Bruce
APPLICANT: Gee, Oliver
APPLICANT: The Regents of the University of California
40.1%; Score 1017; DB 4;
64.8%; Pred. No. 2.7e-104;
Live 53; Mismatches 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/359,161A
CURRENT FILING DATE: 1999-07-21
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 7, Application US/09359161A ; Patent No. 6342656
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                                                                Matches 193; Conservative
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----LSLWTLSPNTSIVDCMEVFSKG-IHRAMV--PVNGRLENVVGVELTESASCYRM 186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     80 ESDKQTGAVRKHYIGMVTMLDILAYIAGNGYRDDDDDLTKKMMVPVSSIIGHCLES---- 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              276 YLQGCFKPLVSISPNDSLFEAVYTLIKNRIHRLPVLDPVSG---NVL------HI 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LTHKRLLKFLHIFGSLLPRPSFLYRTIQDLGIGTFRDLAV-VLETAPILTALDIFVDRRV 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     187 LIQMDLLRFLNDQQEL---KAIMSHKVSDKQLQAITDTVFGVINKAKVIDVIKCMRTASL 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----QVVGLYSRFDVIHLAAQQTYNHLDMSVGEALRQRT 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LCLEGV------LSCQPHESLGEVIDRIAREQVHRLVLVDETQHLLGVVSLSDI 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20 OMLKDKOVKDLIIDKRRLVEVPYTATLADTINTLMANKVVAVPVAAPPGHWIGAGGSMIL 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Lycopersicon esculentum sucrose non-fermenting protein OTHER INFORMATION: kinase activation subunit 4 (LeSNF4)
                                                                                                            APPLICANT: Bradford, Kent J.
APPLICANT: Bradford, Kent J.
APPLICANT: Dahal, Peetambar
APPLICANT: Yang, Hong
APPLICANT: Young, Hong
APPLICANT: Downie, Bruce
APPLICANT: Gooley, Michael
APPLICANT: Gee, Oliver
APPLICANT: Gee, Oliver
TITLE OF INVENTION: Regulation of Source-Sink Relationships and Responses
TITLE OF INVENTION: to Stress Conditions in Plants
TITLE OF INVENTION: 10 Stress Conditions in Plants
CURRENT APPLICATION NUMBER: US/09/359,161A
CURRENT FILLING DATE: 1999-07-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              186 REMQEHTCYDAMATSSKLVIFDTMLEIKKAFFALVANGVRAAPL------W------
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APPLICANT: PYATI, JAXASHREE
APPLICANT: ZHU, JESSICA Y
APPLICANT: ERLANDER, WARK G
APPLICANT: GLINDO, JOSE E
TITLE OF INVENTION: DNA ENCODING HUMAN ALPHAIG T-TYPE CALCIUM
TITLE OF INVENTION: CHANNEL (ALPHAIG-C)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 373;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7.5%; Score 190; DB 4; Length 37:
22.4%; Pred. No. 2.9e-12;
ive 66; Mismatches 126; Indels
                                             ; Sequence 3, Application US/09359161A; Patent No. 6342656; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 5, Application US/09426998 Patent No. 6358706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT ORGANISM: Lycopersicon esculentum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   82; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 7
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                          US-09-359-161-3
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Best Local 8
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APPLICANT: Bradford, Kent J.
APPLICANT: Bradford, Kent J.
APPLICANT: Dahal, Peetambar
APPLICANT: Cooley, Michael
APPLICANT: Cooley, Michael
APPLICANT: Downle, Bruce
APPLICANT: Downle, Bruce
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Regulation of Source-Sink Relationships and Responses;
TITLE OF INVENTION: Costress Conditions in Plants
CURRENT APPLICATION NUMBER: US/09/359,161A
CURRENT FILING DATE: 199-07-21
NUMBER OF SEQ ID NOS: 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----NECGQVVGLYSRFDV--IHLAAQQTYNHLD-MSVGEALRQRTL 426
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                                      190 DLNITTQDNMKSCQMTTPVIDVIQMLTQGRVSSVPIIDENGYLINVYEAYDVLGLIKGGI 249
                                                                                                                   77 DKQTGAVRKHYIGMVTMLDILAHIAGDDHLSCGDNITQ--DLDQRMSDSVSSIIGHSFEG 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           280 CFKPLVSISPNDSLFEAVYTLIKNRIHRLPVLDPVSG---NV------LHILTH 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       325 KRLLKFLHIFGSLLPRPSFLYRT1QDLGIGTFRDLAVVLETAPILTALDIFVDRRVSALP 384
350 DLGIGTFRDLAVVLETAPILTALDIFVDRRVSALPVVNECGQVVGLYSRFDVIHLAAQQT 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16
                                                                                        410 YNHLDMSVGEALRQRTLCLEGVLSCQPHESLGEVIDRIAREQVHRLVLVDETQHLLGVVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17 LKEKKVKDMMVGKKRLVEVPYTASLAQIMNTLVANKIVAVPVAAPPGQWIGAGGSMIVES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  233 KKQS-----FVGMLTITDFILVL----HRYYRSPLVQIYEIEQHKIETWREIY----LQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 379;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 214; DB 4; Length 379
Pred. No. 6.4e-15;
Mismatches 122; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Phaseolus vulgaris I. Pv42
                                                                                                                                                                                                                                                                                                                                           Sequence 5, Application US/09359161A Patent No. 6342656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 23.5%; Pr
Matches 85; Conservative 73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8.48;
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ORGANISM: Phaseolus vulgaris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Ver. 2.1 SEQ ID NO 5
                                                                                                                                                                                    470 LSDILQALVL 479
                                                                                                                                                                                                            310 LSDILKYILL 319
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                                                                                                                                                                                                                                                                                                  RESULT 8
US-09-359-161-5
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76 EGPRSRRAAEST-GLEAT-----FPKTTPLAQAD------PAGVGTPPTGWD---C 116
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                                                                                                                                                                                                                                                                                                                                                                                                                          138 APCSRGRPCAAP------PPSPAW------PARSSAGSAPSP 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   117 LPSD----CTASAAGSSTDDVELATEFPATEAWECELEGLLEERPALCLSPQAPFP 168
                                                                                                                                                                                                                                                                                                                Length 187;
                                                                                                                                                                                                                                                                                                                                                           46; Indels
TITLE OF INVENTION: VIRULENCE-ASSOCIATED NUCLEIC ACID TITLE OF INVENTION: SEQUENCES AND USES THEREOF FILE REFERENCE: 00786/361002 CURRENT APPLICATION NUMBER: US/09/199,637A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Hustad, Carolyn M.
APPLICANT: Ghidyal, Namit
TITLE OF INVENTION: Human E3 Ubiquitin Protein
TITLE OF INVENTION: Ligase
                                                                                                                                                                                                                                                                                                                  Score 101; DB 4;
Pred. No. 0.0069;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                           14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2: ZENECA Pharmaceuticals, Inc. 1800 Concord Pike
                                                                                                                                                                       FastSEQ for Windows Version 4.0
                                                                              CURRENT FILING DATE: 1998-11-25
PRIOR APPLICATION NUMBER: 60/066,517
PRIOR FILING DATE: 1997-11-25
NUMBER OF SEQ ID NOS: 437
SOFTWARE FEASEEQ for Windows Version 4
SEQ ID NO 287
LENGTH: 187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/073,839
FILING DATE: 05-FEB-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3, Application US/09070060; Patent No. 5976849; GENERAL INFORMATION:
                                                                                                                                                                                                                                    ; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-199-637A-287
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FELECOMMUNICATION INFORMATION:
TELEPHONE: 302.886.4889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX:
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                  / Match 4.0%;
Local Similarity 25.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Higgins, Patrick H
REGISTRATION NUMBER: 39,7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 852 amino acids
                                                                                                                                                                                                                                                                                                                                                           44; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 11
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STREET: 18
CITY: Wilm
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US-09-070-060-3
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Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1395 AQGLKLVVETLMSS-----LKPI-GN1VVI-----CCAFFIIFGILGVQLFKGKFFVC 1441
                                                                                                                                                                                                                                                                             30;
                                                                                                                                                                                                                                                                                                                                                                                                    62 RQKSVEEGEPPGQ~----GEGPRSRPAAESTGLEATFPKTTPLAQADPAGVGTPPTG-- 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     114 -----WDCLPSDC-----TASAAGSSTDDVE-----LATEFPATEAWE 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     147 CELEGLIE--ER------PALCLSPQAPFPKLGWDDELRKPGA--QIYMRFMQEHTC 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       194 YDAMATSSKLVIFDTMLEI------KKAFFALVANGVRAAPL-----W 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        231 DSKKQSFV-GMLTITDFILVLHRYYRSPLVQIYEIEQHKIETWREIYLQGCFKPLVSISP 289
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                                                                                                                                                                                                                                                                                                                      2 EPGLEHALRRTPSWSSLGGSEHQEMSFLEQENSSSWPSPAVTSSSERIRGKRRAKALRWT
                                                                                                                                                                                                                                    Query Match 4.0%; Score 102; DB 4; Length 2273; Best Local Similarity 19.5%; Pred. No. 0.4; Matches 122; Conservative 77; Mismatches 194; Indels 234; Gaps
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  FILE REFERENCE: ORT-1057
CURRENT APPLICATION NUMBER: US/09/426,998
CURRENT FILING DATE: 1999-10-26
NUMBER OF SEO 1D NOS: 5
SOFTWARE: PATENTIN VER. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 287, Application US/09199637A Patent No. 6355411
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ausubel, Frederick
Goodman, Howard M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rahme, Laurence G.
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Cao, Hui
                                                                                                                                                                       ORGANISM: HOMO SAPIENS
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                                                                                                                                LENGTH: 2273
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APPLICANT:
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APPLICANT:
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                                                                                                                                                   TYPE: PRT
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                                                                                                          SEQ ID NO 5
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329 FTRTTTWQRPTLESVRNYEQWQLQ---RSQLQGAMQQFNQRFIYGNQDLF 375
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APPLICANT: TAKKER FOGED, Niels
APPLICANT: PETERSON. Svend
TITLE OF INVENTION: A PASTEURELLA VACCINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 1800 Diagonal Road, Suite 500 CITY: Alexandria
                                                                                                                                                                                                                                      FILE REFERENCE: UTSW0708
CURRENT APPLICATION NUMBER: US/09/562,737
CURRENT FILING DATE: 2000-05-01
NUMBER OF SED ID NOS: 132
SOFFWARE: PatentIN Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PC-DOS/MS-DOS
                                                                                                                   Sequence 33, Application US/09562737
Patent No. 6428967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-07-582-945-2
; Sequence 2, Application US/07582945
; Patent No. 5369019
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ZIF: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                APPLICANT: Herz, Joachim
APPLICANT: Gotthardt, Michael
                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Sequence US-09-562-737-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 Similarity 24.5
46; Conservative
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CLASSIFICATION: 424
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                             GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                LENGTH: 830
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : | : : | : : | : : | : | : | 193 SNGGFKPSRPPRPRPASVNGSPSA----TSESDGSSTGSLPPTNTNTTSE 248
                                                                                                                                                                                                                                                                                                                                                                    249 GATSGLIIPLT-----ISGGSGPRP---LNPVFQAPLPP-GWEQRVDQHGRVYYVDHVE 298
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                193 SNGGFKPSRPPRPSRPPPTPRRPASVNGSPSA----TSESDGSSTGSLPPTNINTNTSE 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          135 LATE---FPATEAWECELEGLLEERPALCLSP--QAPFPKLGWDDELRKPGAQIYMRFMQ 189
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                                                                                                                                                                                                         ESTGLEATFP----KTTPLAQAOPAGVCTPPTGWDCLPSDCTASAAGS-----STDDVE 134
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                                                                                                                                                                                                                                                                                                                                                                                                                             190 EHTCYDAMAISSKLVIFDTMLEIKKAFFALVANGVRAAPL---WDSKKQSFVGMLTITDF 246
                                                                                                                                                                                29 LEQENSSSWPSPAVTSSSERIRGKRRAKALRWTRQKSVEEGEPPGQGEGPR----SRPAA 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29 LEQENSSSWPSPAVTSSSERIRGKRRAKALRWTRQKSVEEGEPPGQGEGPR----SRPAA
                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 247 ILVLHRYYRSPLVQIYEIEQHKIETWREIYLQGCFKPLVS--ISPNDSLF 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          247 ILVLHRYYRSPLVQIYEIEQHKIETWREIYLQGCFKPLVS--ISPNDSLF 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     72;
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                                                                                                    DB 2; Length 852;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Score 97; DB 3; Length 852; Pred. No. 0.26; 40; Mismatches 114; Indels
                                                                                                                       ; Pred. No. 0.26;
40; Mismatches 114; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION HUMAN E3 UBIQUITIN PROTEIN LIGASE
FILE REPRENCE: PHM. 70112.N1
CURRENT APPLICATION NUMBER: US/09/357,746
CURRENT APPLICATION NUMBER: US/09/357,746
EARLIER APPLICATION NUMBER: US NO. 6087122 60/073,839
EARLIER APPLICATION NUMBER: US NO. 608712209/070,060
EARLIER RILING DATE: 1998-02-05
EARLIER RILING DATE: 1998-04-30
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FASTSEQ for Windows Version 3.0
                                                                                                    Score 97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3, Application US/09357746 Patent No. 6087122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3.8%; 22.1%;
                                                                                                Query Match
Best Local Similarity 22.1%
Matches 64; Conservative
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Best Local Similarity 22.1°
Matches 64; Conservative
  unknown
                    ; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-09-070-060-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  299 KRTTWD----
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  STRANDEDNESS:
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328 -----VGQDDVN--SEYESGSEWEPDLSEDADYPWLLSNLVSAMISEGSSPIDCPGQCL 379
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      275 SETELELSNDGGSSSG-RSQHLTNSIE-EARSPASEPEPESEP--LHEPPRRTAFLP--- 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  122 TASAAGSSTDDVELATEFPATEAWECEL-------EGLLEER-----PALCL 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 EPGLEHALRRIPSWSSLGGSEHQEMSFLEQENSSSWPSPAVISSSERIRGKRRAKALRWT 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         48; Gaps
                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Description of Artificial Sequence: Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                      3.8%; Score 96; DB 4; Length 830; 24.5%; Pred. No. 0.32; iive 20; Mismatches 74; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      74; Indels
TITLE OF INVENTION: LDL Receptor Signaling Pathways
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/07/582,945
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22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       162 PNEQIY----HSRVIADILYARS---VWD---EFKKYFM------EYWQKYAQLYT 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 239 GML------PLVQIYEIEQH 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 268 KIETWREI-YLQGCFKPLVSISPNDSLFEAVYTLIKNRIHRLPV------- 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         311 -LD------PVSGNVLHILTHKRLLKFLHIFGSLLPRPSFLYRTIQDLGI--- 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       :| :: | :: |: | 322 GIDKALQYIAEESPEWPANKYILYNPTH---LETENLFNIMMKRTE--QRALEDSDVQIR 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11 |: :||| :: :|| :: :| :: | :: :| :: | :: :| :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---QALA 486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 3.7%; Score 94.5; DB 1; Length 1285; Best Local Similarity 19.9%; Pred. No. 1; Matches 81; Conservative 58; Mismatches 109; Indels 159; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      437 KYGIGSLVQSALFTGINLIPVISETAEILSSFSRTEEDIPAFFTEE-----
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NAME: BENT, Stephen A.
RECISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30307/112 PLVI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1285 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear

MOLECULE TYPE: protein

US-07-582-945-2
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Search completed: June 6, 2003, 11:04:13 Job time : 31.1173 secs

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6, 2003, 11:02:59; Search time 40.2504 Seconds (without alignments) 1254.259 Million cell updates/sec
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2538
1 MEPGLEHALRRTPSWSSLGG......LSDILQALVLSPAGIDALGA 489
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                  protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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Perfect score:
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Maximum DB
                                                    OM protein
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                                                                             Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Sequence 6, Appli		S			Sequence 50, Appl		Sequence 6006		S	Sequence 1,	Sequence 5,	Sequence 10	Sequence 33,		Sequence 4919			5 0000000000000000000000000000000000000
	ID	US-09-826-581-6	US-09-925-297-46	US-10-108-605-71	US-10-108-605-19	US-09-864-761-3	US-10-001-873-50	US-09-975-719-28	US-09-738-626-60	US-09-272-809-2	US-10-052-092-12	US-10-211-613-1	US-09-971-490-5	US-10-097-534-10	US-10-211-962-33	US-09-746-491-8	US-09-738-626-49	US-10-211-962-37	US-10-257-963-12	110-00-175-264-2
	DB	10	10	6	6	10	0	σ	σ	10	6	6	6	σ	σ	10	6	6	6	10
	Match Length DB	489	344	1207	980	91	1134	187	440	1276	701	701	1139	739	830	1604	622	830	419	017
* Ouerv	Match	100.0	40.1	35.2	4.5	4.5	4.2	4.0	4.0	3.9	3.9	3.9	3.8	3.8	3.8	3.8	3.8	3.7	3.7	0
	Score	2538	1017	892.5	115	114	105.5	101	100.5	100	99.5	99.5	97.5	76	96	96	95.5	94	93.5	0.5
Result	No.	П	7	3	4	5	9	7	8	σ	10	11	12	13	14	15	16	17	18	C

AQIYMRFMOBHTCYDAMATSSKLVIFDTMLEIKKAPFALVANGVRAAPLMDSKKQSFVGM 240

TROKSVEEGEPPGGGEGPRSRPAAESTGLEATFPKTTPLAQADPAGVGTPPTGWDCLPSD 120 121 CTASAAGSSTDDVELATEPPATEAWECELEGILEERPALCLSPQAPFPKLGWDDELRKPG 180

61

Qy g δy g ΩŽ 121 181 181

qq

δŽ Q

Sequence 5, Appli Sequence 24, Appl Sequence 24, Appl Sequence 31, Appl Sequence 8, Appli Sequence 4, Appli Sequence 4, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 5, Appli Sequence 1, Appli	TED PROTEIN KINASE GAMMA 3 St. Length 489; Indels 0; Gaps 0;
9 US-09-819-104A-5 12 US-10-042-417-44 9 US-10-007-270-24 9 US-11-052-092-31 10 US-09-904-987-5 110 US-09-9853-033-4 9 US-10-226-296-4 9 US-10-226-318-4 9 US-10-226-318-4 9 US-10-226-318-4 9 US-10-226-318-4 10 US-09-887-1 9 US-10-136-891-2 10 US-09-894-125-4 10 US-09-840-125-4 10 US-09-840-125-4 10 US-09-840-125-4 10 US-09-840-125-4 10 US-09-840-125-4 10 US-09-840-125-4 10 US-09-819-104A-5 10 US-09-819-104A-5 110 US-09-819-104A-5 110 US-09-819-104A-5 110 US-09-819-1242-14028 110 US-09-819-1242-14028 110 US-09-819-1242-14028 110 US-09-819-1242-14028 110 US-09-818-221-4 9 US-10-048-221-12	MMENTS JMAN AMP-ACTIVAT 581 55 4.0 4.0 No. 1.5e-209; natches 0; 1
20 93.5 3.7 2462 22 22 92.5 3.6 1069 22 3.6 1069 22 22 22 22 3.6 1069 22 22 22 22 22 22 22 22 22 22 22 22 22	RESULT 1 US-09-226-581-6 Sequence 6, Application US/09826581 Patent No. US202020142310A1 PAPPLICANT: Andersson, Leif APPLICANT: Andersson, Leif APPLICANT: Anthund, L. Holger APPLICANT: Marklund, L. Holger TITLE OF INVENTION: VARIANTS OF THE HI FILE REFRENCE: 11145-007001 CURRENT PILLIG DATE: 2001-04-05 PRIOR APPLICATION NUMBER: US 60/195,6 PRIOR PILLIG DATE: 2001-04-07 NUMBER OF SEQ ID NOS: 14 SOFTWARE: FastSEQ for Windows Version SEQ ID NO 6 LENGTH: 489 TYPE: PRT ORGANISM: Homo sapiens US-09-226-581-6 Best Local Similarity 100.0%; Pred. Matches 489; Conservative 0; Misi

```
APPLICANT: Stam, Lynn
APPLICANT: Bachmann, Jane
APPLICANT: Bachmann, Jane
APPLICANT: Bachmann, Jane
APPLICANT: Bachmann, Jane
APPLICANT: Randar, Kim
TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FROM DROSOPHILA MELANOGASTER THAT ENCO:
TITLE OF INVENTION: PROTEINS ESSENTIAL FOR LARVAL VIABILITY AND USES THEREOF
FILE REFERENCE: 3133B
CURRENT APPLICATION NUMBER: US/10/108,605
PRIOR FILING DATE: 2002-03-27
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2000-01-14
NUMBER OF SEQ ID NOS: 361
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APPLICANT: Kandar, Kim
TILLE OF INVENTION: NUCLEIC ACID SEQUENCES FROM DROSOPHILA MELANOGASTER THAT ENCO.
TITLE OF INVENTION: PROTEINS ESSENTIAL FOR LARVAL VIABILITY AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SSS EKTYNDLDVSLRKANEHRNEWFEGVOKCNLDESLYTIMERIVRAEVHRLVVVDENRKVIG 1012
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               227 APLWDSKKQSFVGMLTITDFILVLHRYYRSPLVQIYEIEQHKIETWREIYLQGCFKPLVS 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    287 ISPNDSLFEAVYTLIKNRIHRLPVLDPVSGNVLHILTHKRLLKFLHIFGSLLPRPSFLYR 346
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 109 T-PPTGWDCLPSDCTASAAGSSTDDVELATEF-PATEAWECELEGLLEERPALCLSPQAP 166
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             167 FPKLGWDDELRKPGAQIYMRFWQEHTCYDAMATSSKLVIFDTMLEIKKAFFALVANGVRA 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           654 IE-----QWKRQQQLL-----PRS-----GRKISLHFYSNHAGRLVLGGG
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                                                                                                                                                                                                                                                                                                                                                                                                           35.2%; Score 892.5; DB 9; 40.6%; Pred. No. 1.1e-67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7 HALRRIPSWSSLGGSEHQEMSFLEQENSSSWPSPAVTS--
                                                                                                                                                                                                                                                                                                                                                                                                                                                  93; Mismatches 121;
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APPLICANT: Broadus, Julie
APPLICANT: Stam, Lynn
                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Drosophila melanogaster
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|013 IISLSDILLYLVLRPSG 1029
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SEQ ID NO 71
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APPLICANT: Broadus, Julie
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US-10-108-605-195
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                                                                                             VVLETAPILTALDIFVDRRVSALPVVNECGQVVGLYSRFDVIHLAAQQTYNHLDMSVGEA 420
                                                                                                                                                                       41 VYTSFMKSHRCYDLIPTSSKLVVFDTSLQVKKAFFALVTNGVRAAPLWDSKKQSFVGMLT 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     183 IYMRFMQEHTCYDAMATSSKLV1FDTMLEIKKAFFALVANGVRAAPLWDSKKQSFVGMLT
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TITLE OF INVENCETION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PALOS
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64.8%; Pred. No. 3.6e-79;
live 53; Mismatches 52;
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CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05989
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124, 270
PRIOR FILING DATE: 1999-03-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 461, Application US/09925297 Patent No. US20020081659A1 GENERAL INFORMATION:
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Patent No. US20020160934A1
GENERAL INFORMATION:
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 461
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                                                                                                                                                                                                                                                                                                             PAGIDALGA 489
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Sequence 50, Application US/1001873
Sequence 50, Application US/1001873
Patent No. US200201603881
GENERAL INPORMATION:
APPLICANT: Recipon, Herve
APPLICANT: Chen, Sei-Yu
APPLICANT: Liu, Chenghua
APPLICANT: Liu, Chenghua
APPLICANT: Turner, Leah
TITLE OF INVENTION: Compositions and Methods Relating to Lung Specific Genes and
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HER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 7
HER INFORMATION: EXPRESSED IN BAT74, SIGNAL = 7
HER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 7.6
HER INFORMATION: EXPRESSED IN HBLIO, SIGNAL = 6.5
HER INFORMATION: EXPRESSED IN HBLIA, SIGNAL = 6.5
HER INFORMATION: EXPRESSED IN HBLIA, SIGNAL = 4.8
HER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 4.7
HER INFORMATION: EXPRESSED IN HEARY, SIGNAL = 5.9
HER INFORMATION: EXPRESSED IN HERRY, SIGNAL = 5.9
HER INFORMATION: EXPLESSED IN HERRY, SIGNAL = 5.9
HER INFORMATION: EXTLANDAN HIT: BROSSE, EVALUE 2.000e-15
HER INFORMATION: EXTLANDAN HIT: BROSSE, EVALUE 2.000e-15
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LENGTH: 91
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PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR PILLING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
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Best Local Similarity
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TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
TITLE ACOMICA'S 1

CURRENT APPLICATION NUMBER: US/09/864,761

CURRENT FILING DATE: 2001-05-23

PRIOR PELICATION NUMBER: US 60/2180,312

PRIOR PELICATION NUMBER: US 60/207,456

PRIOR FILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-06-05-86

PRIOR FILING DATE: 2000-08-03

PRIOR FILING DATE: 2000-08-03

PRIOR FILING DATE: 2000-08-03

PRIOR FILING DATE: 2000-08-03
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     199 TSSKLVIFDIMLEIKKAFFALVANGVRAAPLWDSKKQSFVGMLTITDFIL--VLHRYYRS 256
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              308 LPVL-------DPVSGNVLHILTHKRLLKFLHIFGSLLP--RPSFLYRTIQD 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              305 VIMIQDDERYLLDVFAVLTDPTFGDAKRRDTVLFLKEFCNYAQNLQPQGKDSF-YKTLTC 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    351 LGIGTFRDLAVVLE-----TAPILTALDIFVDRRVSALPVVNECGQVVGLYSRFDV-- 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           402 --IHLAAQQTYNHLDMSVGEALRQRTLCLEGVLS--CQPHESL---GEVIDRIAREQVHR 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           245 QLAKFREAVPIKNLDLLAKIHQTFRVQYIQDIILPTPSVFVEDNMLNTLSSFIFFNKVEI 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4.5%; Score 115; DB 9; Length 980;
22.5%; Pred. No. 0.49;
tive 66; Mismatches 187; Indels 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          455 LV-----LVD-----ETQHLLGVVSLSDILQALV 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      471 LVAPVILNTIGDRPQNEDYQTAQLLGIV--LDILSFCV 506
                                   CURRENT APPLICATION NUMBER: US/10/108,605
CURRENT FILING DATE: 2002-03-27
FRIOR APPLICATION NUMBER: US 09/761,142
PRIOR FILING DATE: 2001-01-16
PRIOR PILING DATE: 2000-01-14
NUMBER OF SEQ ID NOS: 361
SOFWWARE: PATENTIN VET: 2.1
SEQ ID NO 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 33979, Application US/09864761 Patent No. US20020048763A1 GENERAL INFORMATION: APPLICANT: Penn, Sharron G. APPLICANT: Hank, David R. APPLICANT: Hanzel, David K. APPLICANT: Chen, Wensheng
                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT / ORGANISM: Drosophila melanogaster US-10-108-605-195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 22.59
Matches 103; Conservative
              FILE REFERENCE: 31133B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -09-864-761-33979
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287 ISPNDSLFEAVYTLIKNRIHRLPVLDPVSGNVLHILTHKRLLKFLHIFGS-----LLPR 340
       180 GAQIYMRFWQEHTCYDAMAISSKLVIFDTMLEIKKAFFALVANGVRAAPLWDSKKQSFVG 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98 AIVVVSLLTFAVVGVFGRT----VGRKNPYSVMLRSAVVLSGLAKILGPIARGLIWIGNI 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        154 IAPGPGFRNGPYA---TEVELREMVDIAQEHGIVEIEERRMIQSVFDLASTIVRQVMVPR 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    341 PSFLYRTIQDLGIGTFRDLAVVLETAPILTALDIFVDRRVSALPVVNE-CGQVVGLYSRF 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   211 PEMIW----IESG------KTAGQATAL--CVRSGHSRIPVIGENVDDIIGIVYLK 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           400 DVIHLAAQQTYNHLD----MSVGEALRQRTLCLEGVLSCQPHESLGEVIDRIAREQVHRL 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         47 GSASLLRVIDERALHINM-----LIMLRTLLDASAAVFA----GAIAVNVMDSWAWGIVL 97
                                                                      117 LPSD----CTASAAGSSTDDVELATEFPATEAWECELEGLLEERPALCLSPQAPFP 168
                                                                                                             138 APCSRGRPCAAP------PPSPAW------PARSSAGSAPSP 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          240 MLTITDFI--LVLHRYYRSPLVQIYEIEQHKIETWREIYLQGCFK---PLVS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4.0%; Score 100.5; DB 9;
19.8%; Pred. No. 2.6;
tive 62; Mismatches 130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 2000-04-07
PRIOR PLILING DATE: 2000-04-07
PRIOR PLILING DATE: 2000-08-03
PRIOR PLILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PATENTIN NOS: 7059
SOFTWARE: PATENTIN NOS: 7059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      456 VLVDETQHLLGVVSLSDILQALV 478
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304 ILVDEYGGVAGLISIEDILEEIV 326
                                                                                                                                                                                                                         ; Sequence 6006, Application US/09738626; Publication No. US20020197605A1
GENERAL INFORMATION: APPLICANT: NARAGANA, SATOSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Corynebacterium glutamicum
US-09-738-626-6006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 9
US-09-272-809-2
; Sequence 2, Application US/09272809
                                                                                                                                                                                                                                                                                                                      MIZOGUCHI, HIROSHI
                                                                                                                                                                                                                                                                                                                                      ANDO, SEIKO
HAYASHI, MIKIRO
OCHIALI, KEIKO
YOKOI, HARUHIKO
TATEISHI, NAOKO
SENOH, AKIHIRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 19.89
nes 64; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IKEDA, MASATO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE: 249-125
                                                                                                                                                                                 RESULT 8
US-09-738-626-6006
                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
APPLICANT:
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APPLICANT:
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                76 EGPRSRPAAEST-GLEAT-----FPKTTPLAQAD------PAGVGTPPTGWD---C 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PSPAGGCGG----GLLEAQALSATGQSCAEPSECPDFVEGPEPRVDSPGRTEPCTAALDL 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        88 GLEATFPKTTPLAQADP--AGVGTPPTGWDCLPSDCTASAAGSSTDDVELATEFPATEAW 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    146 ECELEGILLEERPALCLSPQAPFPKLGWDDELRKPGAQIYMRFMQEHTC-YDAMATSSKL- 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    204 -----VIFDTMLEIKKAFFALVANGVRAAPLWDSKKQSFVGMLTITDFILVLHRYY 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     255 RSPLVQIYEIEQHKIETWREIYLQGCFKPLVSISPNDSLFEAVYTLIKNRIHRLPVLDPV 314
                                                                                                                                                                                                                                                                                                                                                                                                                                    ----PAAEST 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         38 PSPAVTSS-----KSVEEGEPPGQG 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19 PAPCTTRSCPPRSGRGRGTSRSAGSDR-RGRRANGARRWTRRLPPRPGRSLADAAPAPCA 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                             Length 1134;
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                                                                                                                                                                                                                                                                                                                                                                                     46; Mismatches 113; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                 38 PSPAVISSSERIRGKRRAKALRWTRQKSVEEGEPPGQGEGPRSR---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Ausubel, Frederick M.
APPLICANT: Rahme, Laurence G.
TITLE OF INVENTION: VIRULENCE-ASSOCIATED NUCLEIC ACID
TITLE OF INVENTION: SEQUENCES AND USES THEREOF
FILE REPERENCE: 00786/36/1003
CURRENT APPLICATION NUMBER: US/09/975,719
CURRENT FILING DATE: 2001-10-10
PRIOR PILING DATE: 1998-11-25
PRIOR APPLICATION NUMBER: US 60/189,637
PRIOR FILING DATE: 1998-11-25
                                                                                                                                                                                                                                                                                                                                             DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 4.0%; Score 101; DB 9; Best Local Similarity 25.0%; Pred. No. 0.68; Matches 44; Conservative 14; Mismatches 46.
FILE REFERENCE: DEX-0275
CURRENT APPLICATION NUMBER: US/10/001,873
CURRENT FILING DATE: 2001-11-20
PRIOR FILING DATE: 2000-11-20
PRIOR FILING DATE: 2000-11-20
PRIOR FILING DATE: 2000-11-22
NUMBER OF SEQ ID NOS: 55
SOFTWARE: PATENTIN VUMBER: 60/252,496
SOFTWARE: PATENTIN VUMBER: 60/252,496
SOFTWARE: PATENTIN VUMBER: 60/252,496
SOFTWARE: PATENTIN VOICE 10 NOS: 55
SOFTWARE: PATENTIN VOICE 10 NOS: 50
                                                                                                                                                                                                                                                                                                                                           Score 105.5;
Pred. No. 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 437
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 287, Application US/09975719
Publication No. US20030022349A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                           1 4.2%;
Similarity 23.3%;
                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 23.38
Matches 70; Conservative
                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-975-719-287
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ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   D,
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APPLICANT: WU, Jiong
TITLE OF INVENTION: Monoclonal Antibodies Specific for Phosphorylated Estrogen Rec
TITLE OF INVENTION: (Ser 118) and Uses Thereof
FILE REFERENCE: CST-202
CURRENT APPLICATION NUMBER: US/10/211,613
CURRENT FILING DATE: 2002-08-02
PRIOR APPLICATION NUMBER: US 60/310,066
PRIOR PILING DATE: 2001-08-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             214 KAFFALVANGVRAAPLWDSKKQSFVGMLTITDFILVLHRYYRSPLVQIYEIEQHKIETWR 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              274 EIYLQG----CFKPLVSISPNDSLFEAVYTLI-----KNRIHRLPVLDPVSGNVLH 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    321 ILT------HKRLLKFLHIFGSLLPRPSFLYRTIQDLGIGTFRDLAVVLETAPILTA 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     372 LDIFVDRRVSALPVVNECGQVVGLYSRFDVIHLAAQQTYNHLDMSVGEALRQRTLCLEGV 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94 PKTTPLAQADPAGVGTPPTGWDCLPSDCTASAAGSSTDDVELATEFPATEAWECELEGLL 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33 DPTRPFSEASMMGLLT-------NLADRELVHMI----NWAKRVPGFV 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   154 EERPALCLSPQAPFFKLGWDDELRKPGAQIYMRFMQEHTCYDAMATSSKLVIFDTMLEIK 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                37 WPSPAVTSSSERIRGKRRAKALRWTRQKSVE---EGEPPGQGEGPRSRPAAESTGLEATF 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----ILYSEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ILLNSGVYTFLSSTLKSLEEKDHIHRVLDKITDTLIHLMAKAGLTLQQQH 607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 432 L------LVDETQH 463
                                                                                                                                                                                                                                                                                                                                               DB 9; Length 701;
                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                          3.9%; Score 99.5; DB 9;
17.2%; Pred. No. 6.4;
tive 66; Mismatches 126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    292 WPSPLMIK----RSKKNSLALSLTADQMVSALLDAEPP-
CURRENT APPLICATION NUMBER: US/10/052,092
CURRENT FILING DATE: 2002-01-18
PRIOR APPLICATION NUMBER: US 60/262,990
PRIOR FILING DATE: 2001-01-19
PRIOR FILING DATE: 2001-07-09
PRIOR FILING DATE: 2001-07-09
NUMBER OF SEQ ID NOS: 49
SOFTWARE: Patentin version 3.1
SEQ ID NO 12
LENGTH: 701
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/10211613 Publication No. US2003009641A1
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SOFTWARE: Patentin version 3.1
SEQ ID NO 7
LENGTH: 701
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CROSBY, Katherine
                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 17.28
Matches 81; Conservative
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ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                    ORGANISM: human
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APPLICANT:
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APPLICANT: Allred, D.
APPLICANT: HOPP, Toraten A.
APPLICANT: O'CONNELL, Peter
TITLE OF INVENTION: Methods and Composition in Breast Cancer Diagnosis and Therapeuti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         607 RLTLESDLRQALINQEFVLYY-----QPQVALITICKLIGVE----ALVRWQHPRLG 653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   704 ARQEQDEKWLNSVLECLKRTGMPPEDLELEITESLMMEDIKGTVVLLHRLREEGVQVAID 763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              79 RSRPAA---ESTGLEATFPKTTPLAQADPAGVGTPPTGWDCLP-----SDCTAS 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           276 RGQPSAAMEPMAAVQSTWEKPRPFTSVAP----LPPT--NCVPHGYTLGELEQRSDWIAP 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        165 APFPKL--GWDDELRK----PGAQIYM-----RFWQEHTCYDAMATSSKLVIFDTML 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      280 CFKPL-----VSISPNDSLFEAVYTLIK-------NRIHR----LPVLD 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        313 -- PVSGNVLHILTHKRILKFTHIFGSLLPRFSFLYRTIQDLGIGTFRDLAVVLETAPIL- 369
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QVAPDVFIP-LAEELGLINHLGQWV-----LETACATHQHFFRETGRRLRMAVNIS 703
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          125 AAGSSTDDVE--LATEFPATEAWECELEGLLEER--------PALCLSPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       211 EIKKAFFALVANGVRAAPLWDSKKQSFVGMLTITDFILVLHRYYR---------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 214; Gaps
                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Description of Unknown Organism:cph2 Locus SLL0821
US-09-272-809-2
                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1276;
                                                                                                                                                                                                                                                                                                                                                                                                                3.9%; Score 100; DB 10; Length 1:
20.3%; Pred. No. 14;
tive 72; Mismatches 165; Indels
                      GENERAL INFORMATION:
APPLICANT: Lagarias, John C.
TITLE OF INVENTION: Phytofluors as fluorescent labels
FILE REFERENCE: 2500:118050
CURRENT APPLICATION NUMBER: US/09/272,809
CURRENT FILING DATE: 1998-03-19
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 20.39
Matches 115; Conservative
    Patent No. US20020022339A1
                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Unknown
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Sequence 10, Application US/10097534

Sequence 10, Application US/10097534

Publication No. US20030049607A1

GENERAL INPORMATION:

APPLICANT: MOSCOMITZ, HAIM

APPLICANT: MOSCOMITZ, HAIM

APPLICANT: REISS, YUVAL

APPLICANT: REISS, YUVAL

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE MODULATION OF VIRAL

TITLE OF INVENTION: MATURATION

FILE REFERENCE: PLV-001.01

CURRENT PEPLICATION NUMBER: 60/275, 224

PRIOR FILING DATE: 2001-03-12

PRIOR FILING DATE: 2001-03-12

PRIOR FILING DATE: 2001-03-12

PRIOR FILING DATE: 2001-07-31

PRIOR PLING DATE: 2001-07-31

SEQUENCE FILING DATE: 2001-03-13

NUMBER OF SEQ IN NOSS: 71

SECTION NUMBER: 60/340,170

PRIOR PLING DATE: 2001-12-07

SECTION OF THE MOSS: 71

SECTION OF THE MOSS: 71
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                                                                                                    514 PLTSSRSSMEM-PSQPAPRIVIDEEINFVKTCLQRWRSEIEQDIQDLKTCIASTTQTIEQ 572
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94 PKTTPLAQADPAGVGTPPTGWDCLPSDCT---ASAAGSSTDDVELATEFPATEAWECELE 150
                                                                                                                                                                  GLLEERPALCLSPQAPFPKLGWDDE-----LRKPGAQIYMRFWQEHTCYDAMATSSKL 203
                                                                                                                                                                                                                                                                204 VIFDTMLE------WDS-KKQ 235
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40; Mismatches 114; Indels
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22.1%; Pred. No. 1
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Matches 64; Conserv
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----ILYSEY 331
                                                                                                                                                                                                                                         PKTTPLAQADPAGVGTPPTGWDCLPSDCTASAAGSSTDDVELATEFPATEAWECELEGLL 153
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                                                                                                                                                                                                                                                                                                                                  154 EERPALCLSPQAPFPKLGWDDELRKPGAQIYMRFMQEHTCYDAMATSSKLVIFDTMLEIK 213
                                                                                                                                                                                                                                                                                                                                                                                 369 D----LTLHDQVHLLECAW------LEILMIGLVWRSMEHPVKLLFAPNLL--- 409
                                                                                                                                                                                                                                                                                                                                                                                                                                214 KAFFALVANGVRAAPLWDSKKQSFVGMLTITDFILVLHRYYRSPLVQIYEIEQHKIETWR 273
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                                                                                                                                            37 WPSPAVTSSSERIRGKRRAKALRWTRQKSVE---EGEPPGQGEGPRSRPAAESTGLEATF 93
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APPLICANT: Curtis, Rory A. J.
APPLICANT: Curtis, Rory A. J.
APPLICANT: Bandaru, Rajasekhar
TITLE OF INVENTION: 48120, 23479 AND 46689, NOVEL HUMAN HYDROLASES
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: 10448-100001
CURRENT APPLICATION NUMBER: US/09/971,490
CURRENT FILING DATE: 2001-10-05
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                                                                                                Indels 197;
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                                              Length 701;
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                                                                                                                                                                                      292 WPSPLMIK-----RSKKNSLALSLTADOMVSALLDAEPP-----
                                              / Match
3.9%; Score 99.5; DB 9;
Local Similarity 17.2%; Pred, No. 6.4;
les 81; Conservative 66; Mismatches 126;
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19.8%; Pred. No. 19;
tive 59; Mismatches
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 60/238,170
PRIOR FILING DATE: 2000-10-05
PRIOR APPLICATION NUMBER: 60/237,991
PRIOR FILING DATE: 2000-10-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 5, Application US/08971490 Publication No. US20030032091A1 GENERAL INFORMATION:
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US-09-971-490-5
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Best Local Similarity
Matches 76; Conserva
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  US-10-211-613-1
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Best Local
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389 TVFFSIFMSFWGHGLPGALEAGSATLAHHWDCSDFQDQEAMPSSAPHHWDC-----SDF 442
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                                                                                                                                                                                                                                                                                       443 QDQEVMPS-SALHHWDCSDFQDQEECPHLQFAALALQ-MTQNPVTG----LKEP---- 490
                                                                                                                                                                                                                                                                                                                                186 RFMQEHTCYDAMATSSKLVIFDTMLEIKKAFF--ALVANGV-------RAAP 228
                                                                                                                                                                                                                                                                                                                                                        229 LWDSKKQSFVGMLTITDFILV-----LHRYYRSPLVQIYEIEQHKIETWREIYLQG 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                         548 LWGNG-----GPKALSKVLCVCQQQCGPGGCHIQVTQQLIIIMVGKQLLNHMEEFVGLGG 602
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    389 CGQVVG-----LYSRFDVIHLAAQQTYNH 412
                                         ---EAATPAAA-----GERRLRQRRWRENFQRN 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  280 -----CFKPL----VSISPNDSLFEAVYTLIKNRIHRLPVLDPVSGNVLHILTHKRLL 328
  12 TPSW----SSLGGSEHQEMSFLEQENSSSWPSPAVTSSSERIRGKRRAKALRWTR--QKS 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       651 KY------QRPMAGRGWTSGSDCSCWRPCELILPRTNARSRLGYW-----LNG
                                                                                VEEG--EPPGQGEGPRSRPAAESTGLEATFP-----KTTPLAQ--
                                                                                                                                                                  -ADPAGVGTPPTGWDC-
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                                         396 TPRWVRLRARLGG------
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Job time: 43.2504 secs
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APPLICANT: Burgess, Catherine E.
APPLICANT: Burgess, Catherine E.
TITLE OF INVENTION: NO. US20020137202A1el Proteins and Nucleic Acids Encoding Same FILE REFERENCE: 15966-621
CURRENT APPLICATION NUMBER: US/09/746,491
CURRENT FILING DATE: 2000-12-20
PRIOR FILING DATE: 1999-12-21
NUMBER OF SEQ ID NOS: 72
SOFTWARE: Patentin Ver. 2.0
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Query Match
Best Local Similarity 19.0%; Pred. No. 43;
Matches 107; Conservative 60; Mismatches 167; Indels 230;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           48;
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                                                                                             Sequence 33, Application US/10211962
| Publication No. 220030082640a1
| GENERAL INFORMATION:
| APPLICANT: Herz, Joachim
| APPLICANT: Herz, Joachim
| APPLICANT: Herz, Joachim
| TITLE OF INVENTION: LDL Receptor Signaling Pathways
| FILE REFERENCE: UTSW0708
| CURRENT APPLICATION UNMBER: US/10/211,962
| CURRENT APPLICATION UNMBER: US/09/562,737
| PRIOR PILING DATE: 2000-05-01
| PRIOR FILING DATE: 2000-05-01
| NUMBER OF EQ ID NOS: 132
| SEQ ID NO 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-746-491-8; Sequence 8, Application US/09746491; Patent No. US20020137202A1
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ORGANISM: Artificial Sequence
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	PRKAG3. Homo sapi	Human AMPK gamma s	Pig PRKAG3 polymor	Pig AMPK gamma sub	Pig wild-type PRKA	Pig PRKAG3 polymor	Pig PRKAG3 polymor	Sus scrofa Prkad3	Pig PRKAG3 polymor	Novel human diagno
SUMMARIES		AAE00223	AAE22985	AAE00222	AAE22984	AAE22987	AAE22988	AAE00224	AAE22986	ABG03666
DB	22	22	23	22	23	23	23	22	23	22
% Query re Match Length DB I	489	464	464	464	464	464	464	514	464	171
% Query Match	100.0	98.1	67.3	66.4	66.4	66.4	66.4	66.4	63.6	30.1
Score	214	210	144	142	142	142	142	142	136	64.5
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                                 New variants of human AMP-activated protein kinase gamma3 subunit associated with a metabolic disease e.g. diabetes or obesity and method for determining a risk estimate of diseases in subject by detecting the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human: gamma subunit; adenosine monophosphate-activated kinase; AMPK; PRKAG3; diabetes; Obesity; myopathy; cardiovascular disease; anorectic; genetic testing; carbohydrate metabolism disorder; skeletal muscle; cystathione beta synthase; CBS; cardiant; gene therapy.
                                                                                                               This sequence is encoded by the full length CDNA encoding the human AMP-activated protein kinase gamma 3 subunit (PRKAG3). Detecting the presence of the PRKAG3 DNA, or a variant, is useful in determining a risk estimate of a metabolic disease, such as diabetes or obesity, in a subject. The variation may occur in exons 3, 4 or 10. In exon 3 variation may be a substitution of a G for a C at nucleotide 320, resulting in the amino acid substitution P71A; in exon 4 variation may be a substitution of a T for a C at nucleotide 50; and in exon 10 variation may be a substitution of a T for a C at nucleotide 1037, resulting in the amino acid substitution R340W. There may also be nucleotide variation in intron 6. The numbering of these variations is based on the full length cDNA, rather than on
                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human AMPK gamma subunit muscle-specific isoform, complete PRKAG3.
                                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                                                                Length 489;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label= CBS
/note= "Cystathione beta synthase domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "Cystathione beta synthase domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label= CBS
/note= "Cystathione beta synthase domain"
                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label= CBS
/note= "Cystathione beta synthase domain"
                                                                                                                                                                                                                                                                                                                                                                        1 GKRRAKALRWTRQKSVEEGEPPGQGEGPRSRPAAESTGLEA 41
                                                                                                                                                                                                                                                                                                             Score 214; DB 22;
Pred. No. 6.3e-19;
                                                                                                                                                                                                                                                                                                                                       ..
                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "RN- mutation site"
                                                                                                                                                                                                                                                               position 1 of the open reading frame.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
172..225
                                                                                                                                                                                                                                                                                                                                                                                                                                               AAE00223 standard; Protein; 464 AA.
                                                                                              Disclosure; Fig 5; 25pp; English.
                                                                                                                                                                                                                                                                                                            100.0%;
ilarity 100.0%;
Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11-SEP-2000; 2000WO-EP09896.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label= CBS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13-JUN-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       382
2001-657170/75
                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                       489 AA;
            N-PSDB; AAH43685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200120003-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22-MAR-2001.
                                                                                                                                                                                                                                                                                                                                     41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAE00223;
                                                                                                                                                                                                                                                                                                                                                                                    51
                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Domain
                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 2
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(AMP)-activated kinase (AMPK) gamma subunit muscle-specific isoform, complete PRKAG3. Mutation in Prkag3 results in an altered regulation of carbohydrate metabolism, particularly in skeletal muscle. PRKAG3 is useful as therapeutic for treating carbohydrate metabolism disorders such as diabetes, obesity, and disorders associated with muscle metabolism such as myopathy and cardiovascular diseases, to modulate AMPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         a genetic polymorphic marker linked to a sequence encoding PRKAG3, are useful for detecting a dysfunction of carbohydrate metabolism resulting from the expression of a functionally altered allele of PRKAG3.

Transgenic animal and host cell transformed with PRKAG3 or a heterotrimeric AMPK consisting of PRKAG3 or its mutant, are useful for screening compounds able to modulate AMPK activity. Nucleic acid encoding PRKAG3 is useful for detecting mutations in a Prkag3 gene, or in a sequence encoding the first cystathione beta synthase (CBS) domain of PRKAG3 and is useful in gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                           New variants of the gamma subunit of vertebrate adenosine monophosphate-activated kinase for diagnosis or treatment of disorders associated with energy metabolism such as diabetes, obesity, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   activity, and for restoring a normal AMPK function. PRKAG3 sequence and its functionally altered mutants are useful for the diagnostic evaluation, genetic testing and prognosis of a metabolic disorder, preferably a carbohydrate metabolism disorder. Primers that can detect
                                                                                                                                                                                                                                               Rogel-Gaillard C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "Wild type Asn is substituted with Thr due
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98.1%; Score 210; DB 22; Length 464; 97.6%; Pred. No. 1.9e-18; ive 0; Mismatches 1; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GKRRAKALRWIRQKSVEEGEPPGQGEGPRSRPAAESIGLEA 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence is human adenosine monophosphate
                                                                                                                                                                                                                                        lm E, Milan D, Robic A,
Le Roy P, Chardon P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pig PRKAG3 polymorphic variant (PRKAG3-30).
                                                                                            INRG ) INRA INST NAT RECH AGRONOMIQUE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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                                                                                                                                                                                                                                                  Kalm E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 5; Fig 3; 71pp; English
10-SEP-1999; 99EP-0402236.
18-MAY-2000; 2000EP-0401388.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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40; Conservative
                                                                                                                                                                                                                                               Looft C,
                                                                                                                                                                                                                                                                                                                                     WPI; 2001-244810/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           464 AA;
                                                                                                                     ANDERSSON
                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAD03320.
                                                                                                                                                     (LOOF/) LOOFT C. (KALM/) KALM E.
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                                                                                                                                                                                                                                               Andersson L, Lo
Iannuccelli N,
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diabetes, obesity, and disorders associated with muscle metabolism such as myopathy and cardiovascular diseases, to modulate AMFK activity, and for restoring a normal AMFK function. PRKAG3 sequence and its functionally altered mutants are useful for the diagnostic evaluation, genetic testing and prognosis of a metabolic disorder, preferably a carbohydrate metabolism disorder. Primers that can detect a genetic polymorphic marker linked to a sequence encoding PRKAG3, are useful for detecting a dysfunction of carbohydrate metabolism resulting from the expression of a functionally altered allele of PRKAG3. Transquic animal and host cell transformed with PRKAG3 or a resulting from the annual and host cell transformed with PRKAG3 or a resulting animal and host cell transformed with PRKAG3 or a page 100 metabolism resulting are supplied to the presence of t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence is pig adenosine monophosphate (AMP)-activated kinase (AMFK) gamma subunit muscle-specific isoform, complete PRKAG3. Prkag3 gene is located in the RN locus of chromosome lb. Mutation in Prkag3 results in an altered regulation of carbohydrate metabolism, particularly in skeletal muscle. PRKAG3 is useful as therapeutic for treating carbohydrate metabolism disorders such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    heterotrimeric AMPK consisting of PRKAG3 or its mutant, are useful for screening compounds able to modulate AMPK activity. Nucleic acid encoding PRKAG3 is useful for detecting mutations in a Prkag3 gene, or in a sequence encoding the first cystathione beta synthase (CBS) domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New variants of the gamma subunit of vertebrate adenosine monophosphate-activated kinase for diagnosis or treatment of disorders associated with energy metabolism such as diabetes, obesity, and
      "Cystathione beta synthase domain"
                                             /label= CBS
/note= "Cystathione beta synthase domain"
                                                                                                                                  /note= "Cystathione beta synthase domain"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Robic A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ooft C, Kalm E, Milan D, Robic Gellin J, Le Roy P, Chardon P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 142; DB 22;
Pred. No. 8.4e-10;
3; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of PRKAG3 and is useful in gene therapy.
                                                                                                                                                                                                                                                                                                                                                                             (INRG ) INRA INST NAT RECH AGRONOMIQUE. (ANDE/) ANDERSSON L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAE22984 standard; Protein; 464 AA.
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68.3%;
                                                                                                                                                                                                                                                                   11-SEP-2000; 2000WO-EP09896,
                                                                                                                                                                                                                                                                                                           10-SEP-1999; 99EP-0402236
18-MAY-2000; 2000EP-0401388
                                                                                                              /label= CBS
                        .382
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                                                                                       400..453
         /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Looft C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Query Match
Best Local Similarity
Loca 28; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-244810/25.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAD03319
                                                                                                                                                                                                                                                                                                                                                                                                                                            (KALM/) KALM E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Iannuccelli N,
                                                                                                                                                                             WO200120003-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Andersson L,
                                                                                                                                                                                                                        22-MAR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 myopathy
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                                                                                                                                                                                                                                                                                                                                                                                                                       LOOF/
                           Domain
                                                                                          Domain
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      XX PC
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                                                                                                                                                                                                                                                                                                                                                                                                                 Screening animals to determine those likely to produce larger litters and improved meat quality traits involves assaying for the presence of polymorphisms in the AMP activated protein kinase regulatory gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     those more likely to produce large litters and improved meat quality traits. The method involves assaying for the presence of a genotype in the sample of genetic material obtained from animal. The genotype is characterised by polymorphism(s) in the AMP activated protein kinase regulatory gamma subunit (PRRAG3) gene. The method is used for screening animals e.g., pigs to determine those most likely to exhibit improved meat quality traits and to produce larger litters. The present sequence is pig PRRAG3 polymorphic variant (PRRAG3-30).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     invention relates to a method for screening animals to determine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gamma subunit; adenosine monophosphate-activated kinase; AMPK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pig AMPK gamma subunit muscle-specific isoform, complete PRKAG3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "Cystathione beta synthase domain"
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  to single nucleotide polymorphism (SNP)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GKRRAKALRWTRQKSVEEGEPPGQGEGPRSRPAAESTGLEA 41
                                                                                                                                                                                                                                                                                                         Rothschild MF, Ciobanu DC, Malek M, Plastow G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 144; DB 23;
Pred. No. 4.7e-10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "RN- mutation site"
253..307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 91-93; 109pp; English.
                                                                                                                                                                                                                                                              (10WA ) UNIV IOWA STATE RES FOUND INC
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                                                                                                                                                                      08-SEP-2000; 2000US-231045P.
08-JAN-2001; 2001US-260239P.
18-JUN-2001; 2001US-299111P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67.3%;
68.3%;
                                                                                                                              10-SEP-2001; 2001WO-US28283
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/label= CBS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28; Conservative
                                                                                                                                                                                                                                                                                                                                               WPI; 2002-393850/42.
N-PSDB; AAD36457.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       464 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Misc-difference
                                        WO200220850-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        chromosome 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    subunit gene
                                                                                   14-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sus scrofa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Domain
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Rogel-Gaillard C;

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Gaps

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Indels

Length 464;

pig;

09-AUG-2002

Sus scrofa

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Screening animals to determine those likely to produce larger litters and improved meat quality traits involves assaying for the presence of polymorphisms in the AMP activated protein kinase regulatory gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a method for screening animals to determine those more likely to produce large litters and improved meat quality traits. The method involves assaying for the presence of a genotype in the sample of genetic material obtained from animal. The genotype is characterised by polymorphism(s) in the AMP activated protein kinase regulatory gamma subunit (PRRAG3) gene. The method is used for screening animals e.g., pigs to determine those most likely to exhibit improved meat quality traits and to produce larger litters. The present sequence is pig PRRAG3 polymorphic variant (PRRAG3-199).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AMP activated protein kinase regulatory gamma subunit; PRKAG3 gene;
                                                                                                                                                                                                                                                                         /note= "Wild type Val is substituted with Ile due
                                                                                                                 AMP activated protein kinase regulatory gamma subunit; PRKAG3 screening; meat quality; single nucleotide polymorphism; SNP;
                                                                                                                                                                                                                                                                                               to single nucleotide polymorphism (SNP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GKRRAKALRWIRQKSVEEGEPPGQGEGPRSRPAAESTGLEA 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Malek M, Plastow G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 142; DB 23;
Pred. No. 8.4e-10;
                                                                            Pig PRKAG3 polymorphic variant (PRKAG3-199).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pig PRKAG3 polymorphic variant (PRKAG3-200).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 100-102; 109pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (IOWA ) UNIV IOWA STATE RES FOUND INC.
                                                                                                                                                                                                                                    Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAE22988 standard; Protein; 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66.48;
68.38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ciobanu DC,
                                                                                                                                                                                                                                                                                                                                                                                                                  10-SEP-2001; 2001WO-US28283.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   08-SEP-2000; 2000US-231045P.
08-JAN-2001; 2001US-260239P.
18-JUN-2001; 2001US-299111P.
                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       L Similarity 68.3
28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-393850/42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               464 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAD36459
                                                                                                                                                                                                                                                        Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rothschild MF,
                                                                                                                                                                                                                                                                                                                                      WO200220850-A2
                                    09-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  subunit gene
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                                                                                                                                                                                                                                                                                                                                                                           14-MAR-2002
                                                                                                                                                                                                 Sus scrofa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Si
Matches 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
AAE22987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAE22988;
                                                                                                                                                              variant.
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δŽ
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Screening animals to determine those likely to produce larger litters and improved meat quality traits involves assaying for the presence of polymorphisms in the AMP activated protein kinase regulatory gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a method for screening animals to determine those more likely to produce large litters and improved meat quality traits. The method involves assaying for the presence of a genotype in the sample of genetic material obtained from animal. The genotype is characterised by polymorphism(s) in the AMP activated protein kinase regulatory gamma subunit (PRRAG3) gene. The method is used for screening animals e.g., pigs to determine those most likely to exhibit improved meat quality traits and to produce larger litters. The present sequence is pig wild-type PRRAG3 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                            AMP activated protein kinase regulatory gamma subunit, PRKAG3 gene; screening; meat quality; single nucleotide polymorphism; SNP; pig.
                                                                                                                                                                                                             /note= "Wild type Asn is replaced with Thr during single nucleotide polymorphism (SNP)"
                                                                                                                                                                                                                                                                                                 during
                                                                                                                                                                                                                                                                                                                                                       Val is replaced with Ile during polymorphism (SNP)"
                                                                                                                                                                                                                                                                                                                                                                                                              /note= "Wild type Arg is replaced with Gln during single nucleotide polymorphism (SNP)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .;
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                                                                                                                                                                                                                                                                                         /note= "Wild type Gly is replaced with Ser single nucleotide polymorphism (SNP)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26 GDQGNKASRWTRQEDVEEGCPPGPREGPQSRPVAESTGQEA 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 142; DB 23;
Pred. No. 8.4e-10;
3; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (IOWA ) UNIV IOWA STATE RES FOUND INC.
                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                     "Wild type V
nucleotide p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAE22987 standard; Protein; 464 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 2; Fig 1; 109pp; English.
                                                     Pig wild-type PRKAG3 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66.4%;
68.3%;
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08-JAN-2001; 2001US-260239P.
18-JUN-2001; 2001US-299111P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 68.39,
".hes 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                         single
200
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N-PSDB; AAD36456.
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                                                                                                                                                                                                                                                                         Misc-difference
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subunit gene

Sequence

RESULT 6 AAE22987 ID AAEX

Op δλ

14-MAR-2002

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Gaps

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Length 464; Indels

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The present sequence is pig adenosine monophosphate (AMP)-activated kinase (AMPK) gamma subunit muscle-specific isoform, PRKAG3 splice variant. Prkag3 gene is located in the RN locus of chromosome 15.

Mutation in prkag3 results in an altered requlation of carbohydrate metabolism, particularly in skeletal muscle PRKAG3 is useful as therepetic for treating carbohydrate metabolism disorders such as diabetes, obesity, and disorders associated with muscle metabolism such as myopathy and cardiovascular diseases, to modulate AMPK certuity, and for restoring a normal AMPK function. PRKAG3 sequence and its functionally altered mutants are useful for the diagnostic evaluation, genetic testing and prognosis of a metabolic disorder. Preferably a carbohydrate metabolism disorder. Primers that can detect a genetic polymorphic marker linked to a sequence encoding PRKAG3, are useful for detecting a dysfunction of carbohydrate metabolism resulting from the expression of a functionally altered allele of PRKAG3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Transgenic animal and host cell transformed with PRRAG3 or a heterotrimeric AMPK consisting of PRKAG3 or its mutant, are useful for screening compounds able to modulate AMPK activity. Nucleic acid encoding PRRAG3 is useful for detecting mutations in a Prkag3 gene, or in a sequence encoding the first cystathione beta synthase (CBS) domain of PRKAG3 and is useful in gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      New variants of the gamma subunit of vertebrate adenosine monophosphate-activated kinase for diagnosis or treatment of disorders associated with energy metabolism such as diabetes, obesity, and
                                                                                                                                                                                                                                                                                                     lm E, Milan D, Robic A, Rogel-Gaillard C;
Le Roy P, Chardon P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AMP activated protein Kinase regulatory gamma subunit; PRKAG3 gene; screening; meat quality; single nucleotide polymorphism; SNP; pig;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 66.4%; Score 142; DB 22; Length 514; Best Local Similarity 68.3%; Pred. No. 9.3e-10; Matches 28; Conservative 3; Mismatches 10; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GKRRAKALRWIRQKSVEEGEPPGQGEGPRSRPAAESTGLEA 41
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                                                                                                                                                                                               NAT RECH AGRONOMIQUE.
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                                                                                                                                                                                                                                                                                                                  Kalm E,
                                                                         11-SEP-2000; 2000WO-EP09896.
                                                                                                                       10-SEP-1999; 99EP-0402236.
18-MAY-2000; 2000EP-0401388.
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                                                                                                                                                                                                                                                                                                                                        Gellin J,
                                                                                                                                                                                                                                                                                                                    Looft C,
                                                                                                                                                                                                                                                                                                                                                                                    2001-244810/25.
                                                                                                                                                                                          (INRG ) INRA INST
(ANDE/) ANDERSSON
(LOOF/) LOOFT C.
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                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAD03321
                                                                                                                                                                                                                                                                    (KALM/) KALM E.
                                                                                                                                                                                                                                                                                                                                      Iannuccelli N,
                                                                                                                                                                                                                                                                                                                    Andersson L,
                         22-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAE22986;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Screening animals to determine those likely to produce larger litters and improved meat quality traits involves assaying for the presence of polymorphisms in the AMP activated protein kinase regulatory gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a method for screening animals to determine those more likely to produce large litters and improved meat quality traits. The method involves assaying for the presence of a genotype in the sample of genetic material obtained from animal. The genotype is characterised by polymorphism(s) in the AMP activated protein kinase regulatory gamma subunit (PRKAG3) gene. The method is used for screening animals e.g., pigs to determine those most likely to exhibit improved meat quality traits and to produce larger litters. The present sequence is pig PRKAG3 polymorphic variant (PRKAG3-200).
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screening; meat quality; single nucleotide polymorphism; SNP; pig;
                                                                                                                                                              /noce= "Wild type Arg is substituted with Gln due to single nucleotide polymorphism (SNP)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Malek M, Plastow G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 105-107; 109pp; English.
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                                                                                                                     Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                   10-SEP-2001; 2001WO-US28283.
                                                                                                                                                                                                                                                                                                                                                                                                      08-JAN-2001; 2001US-260239P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rothschild MF, Clobanu DC,
                                                                                                                                                                                                                                                                                                                                                                                 2000US-231045P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      464 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAD36460.
                                                                                                                       Key
Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                 08-SEP-2000;
                                                                                                                                                                                                                                                                                        14-MAR-2002.
                                                                         Sus scrofa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sus scrofa.
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                            variant.
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The cand gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy tenchiques to restore normal activity of (II) or to treat disease states involving quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful for treating inaging of sites expressing (II). (I) and (II) are useful for treating clisorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations are proposed applications of the expension of the product of the expension of the exp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence; corn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human adiagnostic amino acid sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                          New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 RRAKALRWIRQKSVEEGEPPGQGEG----PRSRPAAESIGLE 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5; Mismatches 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zea mays protein fragment SEQ ID NO: 44011.
                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 20; SEQ ID No 34025; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 64.5;
Pred. No. 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAG35967 standard; Protein; 61 AA.
                                                                                                                                        Tang YT;
31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30.1%;
37.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-FEB-2000; 2000EP-0301439.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99US-0121825.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 37.2
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2ea mays subsp. mays.
                                                                                                                                        Liu C,
                                                                                                                                                                                                WPI; 2001-639362/73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         171 AA;
                                                                                     (HYSE-) HYSEQ INC
                                                                                                                                                                                                                              N-PSDB; AAS67853
                                                                                                                                                                                                                                                                                                                                                             biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18-OCT-2000
                                                                                                                                        Drmanac RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAG35967;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 11
AAG35967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Screening animals to determine those likely to produce larger litters and improved meat quality traits involves assaying for the presence of polymorphisms in the AMP activated protein kinase regulatory gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      those more likely to produce large litters and improved meat guality traits. The method involves assaying for the presence of a genotype in the sample of genetic material betained from animal. The genotype is characterised by polymorphism(s) in the AMP activated protein kinase regulatory gamma subunit (PRKAG3) gene. The method is used for screening animals e.g., pigs to determine those most likely to exhibit improved meat quality traits and to produce larger litters. The present sequence is pig PRKAG3 polymorphic variant (PRKAG3-52).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a method for screening animals to determine
                                                                                                          /note= "Wild type Gly is substituted with Ser due to single nucleotide polymorphism (SNP)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GKRRAKALRWTRQKSVEEGEPPGQGEGPRSRPAAESTGLEA 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Malek M, Plastow G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (IOWA ) UNIV IOWA STATE RES FOUND INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 36; Page 96-97; 109pp; English.
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                                         Location/Qualifiers
52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABG03666 standard; Protein; 171
                                                                                                                                                                                                                                                                                                        10-SEP-2001; 2001WO-US28283.
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                                                                                                                                                                                                                                                                                                                                                                08-SEP-2000; 2000US-231045P.
                                                                                                                                                                                                                                                                                                                                                                                           2001US-260239P.
2001US-299111P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rothschild MF, Ciobanu DC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 65.9 es 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2002-393850/42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               464 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAD36458
                                                                                Misc-difference
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                                                                                                                                                                                                W0200220850-A2
                                                                                                                                                                                                                                                                                                                                                                                                                      18-JUN-2001;
                                                                                                                                                                                                                                                                                                                                                                                              08-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            subunit gene
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  Sus scrofa.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    56
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ABG03666

á q ä

Gaps

14-JUL-1999; 990S-0144005. 15-JUL-1999; 990S-0144005. 16-JUL-1999; 990S-0144005. 19-JUL-1999; 990S-0144006. 19-JUL-1999; 990S-0144322. 19-JUL-1999; 990S-0144331. 19-JUL-1999; 990S-0144332. 20-JUL-1999; 990S-0144335. 20-JUL-1999; 990S-0144335. 20-JUL-1999; 990S-0144335. 22-JUL-1999; 990S-0144335. 22-JUL-1999; 990S-0144814. 21-JUL-1999; 990S-0144814. 22-JUL-1999; 990S-0145086. 22-JUL-1999; 990S-0145086. 22-JUL-1999; 990S-0145086. 22-JUL-1999; 990S-0145086. 23-JUL-1999; 990S-0145086. 23-JUL-1999; 990S-0145087. 23-JUL-1999; 990S-0145086. 23-JUL-1999; 990S-014519. 24-JUL-1999; 990S-014519. 25-JUL-1999; 990S-014519. 26-JUL-1999; 990S-014518. 27-JUL-1999; 990S-014518. 27-JUL-1999; 990S-014518. 27-JUL-1999; 990S-014518. 28-JUL-1999; 990S-014518. 28-JUL-1999; 990S-014518. 28-JUL-1999; 990S-014519. 28-JUL-1999; 990S-014519. 28-JUL-1999; 990S-014433. 28-JUL-1999; 990S-0144328. 28-JUL-1999; 990S-0144328. 28-JUL-1999; 990S-0144328. 28-JUL-1999; 990S-0144328. 28-JUL-1999; 990S-0144328. 28-JUL-1999; 990S-0144328. 28-JUL-1999; 990S-014938. 28-JUL-1998; 990S-	
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990x-0123180 990x-012348 990x-0123548 990x-0125788 990x-0127472 990x-012744 990x-012744 990x-012744 990x-012744 990x-012746 990x-012746 990x-012746 990x-012786	990S-0140854 990S-0140855 990S-0140853 990S-014182 990S-014182 990S-014287 990S-0142390 990S-0142390 990S-0142390 990S-0142390 990S-0142390 990S-0142390
05-MAR-1999; 23-MAR-1999; 24-MAR-1999; 25-MAR-1999; 25-MAR-1999; 26-APR-1999; 26-APR-1999; 27-APR-1999; 28-APR-1999; 28-APR-1999; 28-APR-1999; 28-APR-1999; 30-APR-1999;	23-JUN 1999; 24-JUN 1999; 28-JUN 1999; 29-JUN 1999; 30-JUL 1999; 01-JUL 1999; 06-JUL 1999; 06-JUL 1999; 09-JUL 1999; 12-JUL 1999; 13-JUL 1999;

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                                                                                                                                                                                                                                This is the amino acid sequence of a truncated form of human hepatocyte nuclear factor 1 alpha (HNF-1 alpha, see also AAW71559) that arises from a trameshift mutation at codon Pro-379 of the coding region of the HNF-1 alpha gene (see AAV52656). The mutation has been detected in patients with the MODY3 (maturity onset diabetes of the young) form of diabetes. The invention concerns the identification of genes responsible for non-insulin dependent diabetes mellitus (NIDDM) for use in diagnostics and therapeutics. It demonstrates that the MODY3 locus is the HNF-1 alpha gene, the MODY4 locus is the HNF-1 alpha gene (see AAV52730) and the MODY1 locus is the HNF-4 alpha gene (see AAV52730) and the MODY1 locus contemplates methods of screening for modulators of HNF function also contemplates methods of screening for modulators of HNF function use useful for treating diabetes by modulating HNF function in an
                                                                                                                                                       Isolated nucleic acid encoding hepatocyte nuclear factor 1-alpha and 1-beta - useful for detecting susceptibility for non-insulin dependent diabetes, especially maturity-onset diabetes of the young
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hepatocyte nuclear factor 1 alpha; HNF-1 alpha; MODY3; human; transcription factor; maturity onset diabetes of the young; diabetes; NIDDM; diagnosis; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 61.5; DB 19; Length 415;
Pred. No. 13;
4; Mismatches 18; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "DNA binding domain with POU-like and homeodomain-like motifs"
                                                                             Horikawa Y, Kaisaki PJ, Menzel S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human hepatocyte nuclear factor 1 alpha (R131Q mutant).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 KRRAKALRWIRQKSVEEGEPPGQGEGPRSRPAAESIGL 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "transactivation domain"
Misc-difference 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'note= "dimerisation domain"
                                                                                                                                                                                                           Disclosure; Page 180-181; 363pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "encoded by INT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW71560 standard; Protein; 630 AA.
960S-0029679.
960S-0025719.
960S-0028056.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     / Match 28.7%;
Local Similarity 39.5%;
Nes 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
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                                                   (ARCH-) ARCH DEV CORP
                                                                             , Furuta H,
Yamagata K;
                                                                                                                    WPI; 1998-271667/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            415 AA;
                                                                                                                                N-PSDB; AAV52628
30-OCT-1996;
10-SEP-1996;
02-OCT-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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                                                                              Bell GI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                    animal.
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Domain
                                                                                            oda N,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hepatocyte nuclear factor 1 alpha; HNF-1 alpha; MODY3; human; transcription factor; maturity onset diabetes of the young; diabetes; NIDDM; diagnosis; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human hepatocyte nuclear factor 1 alpha (truncated mutant).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "DNA binding domain"
281..415
/note= "truncated transactivation domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 RRAKALRWIRQKSV - - EEGEPPGQGEGPRSRPAAESTGLEA
                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 63.5; DB 21;
Pred. No. 0.9;
3; Mismatches 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "dimerisation domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ...280
Le= "DNA binding domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW71562 standard; Protein; 415 AA
                                                                                                                                                                                             990S - 0160767
990S - 0160768
990S - 0160760
990S - 0160814
990S - 01608815
990S - 0160981
990S - 0160981
990S - 0161404
990S - 0161405
990S - 0161405
                                    900S-0158232
990S-0158232
990S-0159293
990S-0159294
990S-0159329
990S-0159330
990S-0159331
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99US-0159584.
99US-0160741.
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990S-0161361.
990S-0161920.
990S-0161992.
990S-0161993.
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43.98;
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 39US-0157753
                          99US-0158029
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ses 18; Conserv
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                                                                                                                                                                                                                                                                                                                                         26-0CT-1999;
26-0CT-1999;
26-0CT-1999;
28-0CT-1999;
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Best Local S
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14-0CT-1
14-0CT-1
14-0CT-1
14-0CT-1
18-0CT-1
21-0CT-1
21-0CT-1
21-0CT-1
21-0CT-1
21-0CT-1
21-0CT-1
                                                                                                                                                                                                                                                               22-0CT-1
22-0CT-1
22-0CT-1
25-0CT-1
25-0CT-1
25-0CT-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 12
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This is the amino acid sequence of human hepatocyte nuclear factor
1 beta (HNF-1 beta), deduced from a partial gene sequence (see
2 AAV52729). HNF-1 beta is a homeodomain containing transcription
2 factor. Mutations in HNF are indicative of a propensity to diabetes
2 mellitus. The invention concerns the identification of genes
3 responsible for non-insulin dependent diabetes mellitus (NIDDM) for
3 responsible for non-insulin dependent diabetes mellitus (NIDDM) for
3 use in diagnostics and therapeutics. It demonstrates that the
3 mody3 locus is the HNF-1 alpha gene (see AAV52625), the MODY4 locus
4 is the HNF-1 beta gene (see AAV52630) and the MODY1 locus is the
5 cens can be diagnostic for diabetes. The invention also provides
5 methods of utilising HNF nuclein and puppeptides in Screens
5 centing diabetes by modulating HNF function in an animal.
                                                                                                                                                                                                                                                                                                                                                                     Isolated nucleic acid encoding hepatocyte nuclear factor i-alpha and 1-beta - useful for detecting susceptibility for non-insulin dependent diabetes, especially maturity-onset diabetes of the young
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28.7%; Score 61.5; DB 19; Length 631; 39.5%; Pred. No. 20; ive 4; Mismatches 18; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hepatocyte nuclear factor 1 alpha; HNF-1 alpha; MODY3; human; transcription factor; maturity onset diabetes of the young; diabetes; NIDDM; diagnosis; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "DNA binding domain with POU-like and homeodomain-like motifs"
                                                                                                                                                                                                                           Menzel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     271 RKKEEAFRHKLAMDTYSGPPGPGPGP-ALPAHSSPGL 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 KRRAKALRWIRQKSVEEGEPPGQGEGPRSRPAAESTGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human native hepatocyte nuclear factor 1 alpha.
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                                                                                                                                                                                                                           Horikawa Y, Kaisaki PJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "dimerisation domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 94; Page 228-230; 363pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "encoded by TNT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW71559 standard; Protein; 631 AA.
                                                                    96US-0029679.
96US-0025719.
96US-0028056.
                          97WO-US16037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 39.5 mes 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         150..280
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                                                                                                                                                                            (ARCH-) ARCH DEV CORP.
                                                                                                                                                                                                                      Bell GI, Furuta H,
Oda N, Yamagata K;
                                                                                                                                                                                                                                                                                                WPI; 1998-271667/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      631 AA;
                                                                                                                                                                                                                                                                                                                          N-PSDB; AAV52729
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                          10-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-DEC-1998
                                                                          30-0CT-1996;
                                                                                                                       02-OCT-1996;
                                                                                                    10-SEP-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Key
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This is the amino acid sequence of a mutant (R131Q) form of human hepatocyte nuclear factor I alpha (HNF-1 alpha, see also AAW7159) that arises from a missense mutation (G to A) of codon 131 of the coding region of the HNF-1 alpha gene (see AAV52626). The mutation has been detected in a patient with the MODY3 (maturity onset diabetes of the young) form of diabetes. Arg-131 is conserved in human, rat, mouse, hamster, chicken, Kenopus and salmon HNF-1 alpha, concerns the identification of genes responsible for non-insulin concerns the identification of genes responsible for non-insulin dependent diabetes mellitus (NUDW) for use in diagnostics and the MODY1 locus is the HNF-1 alpha gene (see AAV2687). Analysis of mutations in cours is the HNF-1 beta gene (see AAV278730) and the MODY1 locus is the HNF-1 day gene (see AAV27877) and the MODY1 locus is the HNF-1 day gene (see AAV27887). Analysis of mutations in contemplates methods of screening for modulators of HNF innotion also contemplates methods of screening for modulators of HNF function in an energy of the modulators being weeking the modulators being the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Isolated nucleic acid encoding hepatocyte nuclear factor 1-alpha and 1-beta - useful for detecting susceptibility for non-insulin dependent diabetes, especially maturity-onset diabetes of the young
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ·.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hepatocyte nuclear factor 1 beta; HNF-1 beta; MODY4; human; transcription factor; maturity onset diabetes of the young; diabetes; NIDDM; diagnosis; therapy.
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                                                                                                                                                                                                                                                                                                     Menzel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18;
                                                                                                                                                                                                                                                                                                   Kaisaki PJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 61.5; DB
Pred. No. 20;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 169-172; 363pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human hepatocyte nuclear factor 1 beta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW71580 standard; Protein; 631 AA
                                                                                                                                                                                                                                                                                                   Horikawa Y,
                                                                                                                                            96US-0029679.
96US-0025719.
96US-0028056.
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                                                                                                 97WO-US16037.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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Best Local Similarity 39.55
Matches 15; Conservative
                                                                                                                                                                                                                                                   ARCH-) ARCH DEV CORP.
                                                                                                                                                                                                                                                                                                                                                                       WPI; 1998-271667/24.
                                                                                                                                                                                                                                                                                                , Furuta H,
Yamagata K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                630 AA;
                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAV52626.
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WO9811254-A1
                                                                                               10-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-DEC-1998
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                                                                                                                                                 30-0CT-1996;
                                                                                                                                                                            10-SEP-1996;
                                                                                                                                                                                                   32-0CT-1996;
                                                  19-MAR-1998
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                                                                                                                                                                                                                                                                                                                             oda N,
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AAW71580
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Gaps 1;

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                                                                                                                                                                                                                                                                                                                                                              Isolated nucleic acid encoding hepatocyte nuclear factor 1-alpha and 1-beta - useful for detecting susceptibility for non-insulin dependent diabetes, especially maturity-onset diabetes of the young
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
28.7%: Score 61.5; DB 19; Length 631;
Best Local Similarity 39.5%; Pred. No. 20;
Matches 15; Conservative 4; Mismatches 18; Indels 1;
                                                                                                                                                                                                                                             , Furuta H, Horikawa Y, Kaisaki PJ, Menzel S;
Yamagata K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 KRRAKALRWTRQKSVEEGEPPGQGEGPRSRPAAESTGL, 39
                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 14; Fig 11; 363pp; English.
                                                                                                                            96US-0029679.
96US-0025719.
96US-0028056.
                                                                                            97WO-US16037.
                                                                                                                                                                                                            (ARCH-) ARCH DEV CORP.
                                                                                                                                                                                                                                                                                                    WPI; 1998-271667/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 631 AA;
                                                                                                                                                                                                                                                                                                                           N-PSDB; AAV52625
                W09811254-A1
                                                                                          10-SEP-1997;
                                                                                                                               30-OCT-1996;
10-SEP-1996;
                                                                                                                                                                     02-0CT-1996;
                                                       19-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                               Bell GI,
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οχ
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Search completed: June 6, 2003, 11:01:02 Job time: 8.60596 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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- protein search, using sw model OM protein June 6, 2003, 10:58:29; Search time 2.65674 Seconds (without alignments) 1483.588 Million cell updates/sec Run on:

Title: Perfect score:

US-09-826-581-6_COPY_51_91 214 1 GKRRAKALKWTRQKSVEEGE......PGQGEGPRSRPAAESTGLEA 41 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283224 segs, 96134422 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	hypothetical prote	_	transcription fact	transcription fact	transcription fact	(ranscription fact	synapsin I splice	pseudouridylate sy	ribosomal protein	D-alanyl-D-alanine	McrB-related prote	probable transcrip			synapsin Ia - rat	hypothetical prote	myosin heavy chain	ubiquitin thiolest	anion exchange pro	mucin - human (fra	3-ketoacyl-CoA thi	phenylalanine ammo	probable potassium	hypothetical prote	antigen (C-termina	interleukin-2 rece	C 3.4.25.1 proteas	protein C36C5.13 (homeotic protein H
D	T05105	539607	839608	A39262	A33343	A36749	A35464	AF3639	R5MXE	H87516	A75634	S36336	T34847	A25704	A30411	F96712	S54307	S68227	S21086	S55461	D69378	S06475	T31100	876108	B48441	JC1113	T51975	E88990	S16318
% Query Match Length DB								565	149	435	696	673	943	691	704	1085 2	1980	858	1240	171	396	701	1087	203	206	275	277	303	323
% Query Match	7	28.7	28.7	28.7	28.7	28.7	27.6	26.9	26.6	26.2	26.2	25.9	25.9	25.7	25.7	25.7	25.7	25.5	25.5	25.2	25.2	25.2	25.0	24.8	24.5	24.5	24.5	24.5	24.5
Score		Н	61.5	_		_		57.5	57	56		55.5	S	55	55	55	52	54.5	54.5	54	54	54	53.5	53	\sim	N	52.5	$^{\circ}$	$^{\circ}$
Result No.		5	m	4	5	9	7	œ	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

850866446044741	000 CC7 CC7 CC7 CC7 CC7 CC7 CC7 CC7 CC7		2QBE3 BHLF1 protein - hu	195995 hypothetical prote	270666 probable membrane-		S53714 probable dinitrifi	146517 hypothetical prote	A34911 band 3-related pro	A31789 band 3-related pro	A56764 band 3-related pro	T00365 hypothetical prote	S14277 NADH2 dehydrogenas	R34536 hypothetical prote)ZZQAK circumsporozoite p	34036 hypotherical prote	01393 DNA-directed RNA p
		356	099	78	369	517	612	751	1234	1237	1237	1280	200	259	363	1359	1530
	250 680 780 780 751 751 751 751 751 751 751 751 751 751		s.	4.3	4.3	24.3	24.3	24.3	24.3	24.3	24.3	24.3	24.1	24.1	24.1	24.1	24.1
	तलतम तन	24.5	24	C	(1												
24.5 24.3 24.3 24.3 24.3 24.3 24.3 24.3 24.3 24.3 24.3 24.3 24.3 24.1 200 24.1 200 24.1 259 261 270 270 270 270 270 270 270 270	2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	52.5 24.5					52	52	52	52	52	52	51.5	51.5	51.5	51.5	51.5

ALIGNMENTS

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                                                                                                                                                                                                                           Gaps
                                                                                                                                            A;Map position: 4
A;Introns: 26/3; 105/1; 146/3; 296/3; 406/3
A;Note: F28M20.160
C;Superfamily: Arabidopsis thaliana hypothetical protein F28M20.180
                                                                                                                                                                                                                           14;
                                                                                                                                                                                                    29.0%; Score 62; DB 2; Length 493; 35.6%; Pred. No. 9.1; tive 7; Mismatches 8; Indels
                                                                                                                                                                                                                                                           3 RRAKALRWT------RQKSVEEGEPPGGGEGPRSRPAAESTG 38
                                                                                                                                                                                                             Best Local Similarity 35.6
Matches 16; Conservative
                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                  qq
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Cipacipers (man) spine form in the spine form of the spine form of the spiens (man) spine form of the spine form of t transcription factor HNF-1A, splice form C - human

R; Bach, I

submitted to the EMBL Data Library, April 1993
A;Reference number: S39752
A;Accession: S39752
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 118-494 <BAL>
A;Residues: 118-494 <BAL>
A;Cross-references: EMBL:X71347

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Millernate names: hepatic nuclear factor 1-alpha; transcription factor APF; transcr (5)Species: Repatic nuclear factor 1-alpha; transcription factor APF; transcr (5)Species: hepatic nuclear factor at)
C)Species: Battus norvegicus (Norway rat)
C)Species: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C)Accession: A3333; A34580; S11568; S70435
R)Frain, M.; Swart, G.; Monaci, P.; Nicosia, A.; Staempfli, S.; Frank, R.; Cortese, SA; Friel: The liver-specific transcription factor LF-Bl contains a highly diverged how A; Accession: A3333; MUID:90003224; PMID:2571419
A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Description: transcription activator required for the expression of a number of lima; b). Note: also expressed in other tissues (kidney, stomach, intestine), where it may p. C; Superfamily: transcription factor HNF-1; homeobox homology C; Keywords: DNA binding; heterodimer; homeobox; homodimer; liver; nucleus; transcription: 12,13, Region: dimerization expression homeobox homology <HOX>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Title: A distal dimerization domain is essential for DNA-binding by the atypical Hi A;Reference number: S11568; MUID:91016926; PMID:2216777
A;Accession: S11568
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A;Residues: 1-628 cFRA>
A;Ressicues: 1-628 cFRA>
A;Cross-references: GB:J03170; NID:g205164; PIDN:AAA41524.1; PID:g205165
R;Baumhueter, S.; Mendel, D.B.; Conley, P.B.; Kuo, C.J.; Turk, C.; Graves, M.K.; Edw.
Genes Dev. 4, 372-379, 1990
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A; Residues: 'R',166-628 <BAU>
A; Cross-references: GB:X5329; NID:957867; PIDN:CAA37387.1; PID:957868
A; Cross-references: GB:X53297; NID:957867; PIDN:CAA37387.1; PID:957868
A; Note: the authors translated the codon GAG for residue 616 as Asp
R; Chouard, T.; Blumenfeld, M.; Bach, I.; Vandekerckhove, J.; Cereghini, S.; Yaniv, Nucleic Acids Res. 18, 5853-5863, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ä
                                                                                                                                                                        hepatocyte nuclear factor 1 (HNF1).
26; PMID:1354855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Note: the list of introns is incomplete C:Complex: homodimer; can also form heterodimers with, for example, HNF-1B C;Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Residues: 1-628 CCHO>
A; Cross-references: EMBL:X54423; NID:g56367; PIDN:CAA38295.1; PID:g56368
A; Cross-references: EMBL:X54423; NID:g56367; PIDN:CAA38295.1; PID:g56368
B; Bach, I:; Pontoglio, M.; Yaniv, M.
Nucleic Acids Res. 20, 4199-4204, 1992
A; Title: Structure of the gene encoding hepatocyte nuclear factor I (HNFI). A; Reference number: S70435; MUID:92375726; PMID:1354855
A; Reference number: S70435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
A,Molecule type: mRNA
A;Residues: 1-628 <KUO>
A;Residues: 1-628 <KUO>
A;Cross-references: 6700>
A;Cross-references: 6700
A;Cross-references: 6700
A; Yaniv, M.
Nucleic Acids Res. 20, 4199-4204, 1992
A;Title: Structure of the gene encoding hepatocyte nuclear factor 1 (HNP1 A;Reference number: S70435; MUID:92375726; PMID:1354855
A;Recession: S70436
A;Status: not compared with conceptual translation
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                                                                                                                                                                                                                                                                                                               A;Molecule type: DNA
A;Residues: 199-279 <BAC>
A;Note: only a part of the nucleic acid sequence is shown
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Matches 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Gene: Hnf-1
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N:Alternate names: hepatic nuclear factor 1-alpha; transcription factor 1, hepatic; tran
                                                                                                                                                                                                         A; Description: transcription activator required for the expression of a number of liver-A;Note: this form is a more potent transcriptional activator than the A form C.Superfamily: transcription factor HNF-1; homeobox homology C.Superfamily: transcription factor HNF-1; homeobox; homology C.Keywords: alternative splicing; DNA binding; homeobox; liver; nucleus; transcription principles of F;1-33/Region: dimerization
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Title: More potent transcriptional activators or a transdominant inhibitor of the HNF A; Reference number: S39607; MUID:94038905; PMID:7900999
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                                                                     A;Cross-references: GDB:125297; OMIM:142410; OMIM:600496
A;Map position: 12q24.3-12q24.3
C;Complex: homodimer; can also form heterodimers with, for example, HNF-1A form A
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C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 29-Aug-1997
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A;Cross-references: GDB:125297; OMIM:142410; OMIM:600496
A;Map position: 12q24.3-12q24.3
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4; Mismatches
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Best Local Similarity 39.5
Matches 15; Conservative
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Matches 15; Conservative
                                        A; Gene: GDB: TCF1; HNF1; LFB1
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R; Bach, I.; Yaniv, M.
EMBO J. 12, 4229-4242, 1993
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A; Molecule type: mRNA
A; Residues: 1-542 < BAC>
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                                                                                                                                       C; Complex: }
C; Function:
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pseudouridylate synthase (EC 4.2.1.70) [imported] - Brucella melitensis (strain 16M C.Specias: Brucella melitensis
C.Specias: Brucella melitensis
C.Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 19-Apr-2002
C.Accession: AF3639
E.Accession: AF3639
F.D. V. S. Kaparral, V. Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivan, Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Haglus, S.; O'Callaghan, D.; L. Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A.Tille: The genome sequence of the facultative intracellular pathogen Brucella mel A; Reference number: AD3252; PMID:11756688
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N.Alternate names: ribosomal protein E
C.Species: Methanococcus vannielii
C.Species: Methanococcus vannielii
C.Date: 31.Mar-1991 #sequence_revision 31-Mar-1991 #text_change 22-Jun-1999
C.Accession: S05622
R.Auer. J.; Spicker, G.; Boeck, A.
J. Mol. Biol. 209, 21-36, 1989
A.fille: Organization and structure of the Methanococcus transcriptional unit homolo
                                                                                                                                                                                                              A; Status: preliminary
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-659, 'KaSPAQAQP' <SU2>
A; Cross-references: GB:MS8378; GB:J05431
A; Cross-references: GB:MS8378; GB:J05431
B; Sauerwald, A.; Hoesche, C.; Oschwald, R.; Kilimann, M.W.
J. Biol. Chem. 265, 14932-14937, 1990
A; Title: The 5'-flanking region of the synapsin I gene. A G+C-rich, TATA- and CAAT-A; Reference number: A35805; MUID:90368667; PMID:2118519
A; Accession: A35805
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A;Experimental source: strain 16M
C;Genetics:
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C;Keywords: actin binding; alternative splicing; phosphoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ch 27.6%; Score 59; DB 2; Length 705; 1 Similarity 42.3%; Pred. No. 29; 11; Conservative 4; Mismatches 11; Indels
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A;Map position: II
C;Keywords: carbon-oxygen lyase; hydro-lyase
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                                                                                                                                A;Cross-references: GB:M58371; GB:J05431
A;Accession: B35363
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Best Local Similarity
Matches 11; Conserv
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A;Molecule type: DNA
A;Residues: 1-565 <KUR>
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A;Accession: A35363
A;Molecule type: DNA
A;Residues: 1-705 <SUE>
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A; Residues: 1-125 <SAU>
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                           A Molecule type: DNA

A Residues: 199-279 (BAC>
A Note: only a part of the nucleic acid sequence is shown
G Senetics:
A Introns: 238/2
A Introns: 238/2
A Note: the list of introns is incomplete
C Complex: homodimer; can also form heterodimers with, for example, HNF-1B
G Function:
C Superfamily: transcription activator required for the expression of a number of liver-A Note: also expressed in other tissues (kidney, stomach, intestine), where it may play C Superfamily: transcription factor HNF-1; homeobox homology
G Superfamily: heterodimer; homeobox; homodimer; liver; nucleus; transcription
F;1-33/Region: dimerization
F;222-277/Domain: homeobox homology < HOX>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Franscription factor HNF-IA - human
NiAlternate names: hepatic nuclear factor 1-alpha; transcription factor 1, hepatic; tran
C; paceies: Homo sapiens (man)
C; Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C; Accession: A36749
R; Bach, 1.; Aalchew-acargova, 2.; Mattei, M.G.; Simon-Chazottes, D.; Guenet, J.L.; Cereg
Genomics 8, 155-164, 1990
A; Tile: Cloning of human hepatic nuclear factor 1 (HNF1) and chromosomal localization chareference number: A36749; MUID:91184801; PMID:1707031
A; Molecule type: mRNA
A; Rocession: A36749
A; Molecule type: mRNA
A; Rocession: A36749
A; Molecule type: mRNA
A; Cross-references: 1-631 CBAC>
C; Genetics:
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A/Gene: GDB:135297; OMIM:142410; OMIM:600496
A/Gene: GDB:135297; OMIM:142410; OMIM:600496
A/Cross-references: GDB:135297; OMIM:142410; OMIM:600496
A/Cross-references: GDB:135297; OMIM:142410; OMIM:600496
C/Function: 12424.3-12424.3
A/Cross-references: GDB:135297; OMIM:142410; OMIM:600496
C/Function: A/Cross-references: GDB:12420 and GD
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C'Species: 17-Aug-1990 #text_change 01-Dec-2000
C;Date: 17-Aug-1990 #sequence_revision 17-Aug-1990 #text_change 01-Dec-2000
C;Accession: A35363; B35363; A35805
R;Suedhof, T.C. 265, 7849-7852, 1395
J. Balol. Chem. 265, 7849-7852, 1396
A;Title: The structure of the human synapsin I gene and protein.
A;Reference number: A35363; MUID:90243651; PMID:2110562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 628;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 28.7%; Score 61.5; DB 1; Length 6 Best Local Similarity 39.5%; Pred. No. 13; Matches 15; Conservative 4; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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    A; Status: not compared with conceptual translation
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A;Title: Fusion between a novel Krueppel-like zinc finger gene and the retinoic acid A;Reference number: S36336; MUID:93209216; PMID:8384553
A;Accession: S36336
A;Molecule type: mRNA
A;Residues: 1-673 < CHE>
A;CLOSS-references: EMBL: Z19002; NID:938517; PIDN:CAA79489.1; PID:938518
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sympton I - rat
C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Species: 21-May-1988 #text_change 05-Nov-1999
C;Accession: A25704
R;McCaffery, C.A.; DeGennaro, L.J.
R;McCaffery, C.A.; 1986
A;Title: Determination and analysis of the primary structure of the nerve terminal sheference number: A25704; MUID:87133474; PMID:3028773
                                                                                                                                                                                                                                                                                             probable transcription factor PLZF - human
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1993 #sext_change 05-Nov-1999
C;Accession: S36336; S31989
R;Chen, Z.; Brand, N.J.; Chen, A.; Chen, S.J.; Tong, J.H.; Wang, Z.Y.; Waxman, S.; Z
EMBO J. 12, 1161-1167, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   probable transcription regulator - Streptomyces coelicolor C; Species: Streptomyces coelicolor C; Species: Streptomyces coelicolor C; Date: 05-Nov-1999 #text_change 05-Nov-1999 C; Date: 05-Nov-1999 #text_change 05-Nov-1999 C; Datesion: T34847 P; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M. Stoliver, K.; Harris, Data Library, February 1999 A; Reference number: Z21559 A; Datesion: T34847 P; 
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A; Residues: 1-943 < COLI>
A; Cross-references: BMBL: AL035478; PIDN: CAB36601.1; GSPDB: GN00070; SCOEDB: SC265.14c
A; Experimental source: strain A3(2)
C; Genetics:
A; Gene: SCOEDB: SC265.14c
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       Gaps
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       14;
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       Indels
                                                                                                                 15 SVEEGEPPGQGEGPR---SRPAAEST------GLEA 41
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       7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7; Mismatches
       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 55.5; Pred. No. 71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 AKALRWIRQKSVEEGEPPGQ-GEGPRSRP 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Superfamily: POZ domain homology
C;Keywords: zinc finger
F;20-118/Domain: POZ domain homology <POZ>
       5;
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Best Local Similarity 37.9%;
Matches 11; Conservative
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Best Local Similarity 40.5°
Matches 15; Conservative
       15; Conservative
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       Matches
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C;Species: Deinococcus radiodurans
C;Species: Deinococcus radiodurans
C;Accession: A75634
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Na
S; Smith, H.O.; Venter, J.C.; Fraser, C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R.Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J. B.; Laub, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.S.; Gyinn, M.L.; Haft, D.H.; Kolon J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. Proc. Nall. Acad. Sci. U.S.A. 98, 4136-441, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference unwber: A87249; MUID:21173698; PMID:11259647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A.Cross-references: GB:AE001826; NID:96460827; PIDN:AAF12568.1; PID:96460864; TIGR:DRB01
A.Experimental source: strain R1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1. A:Reference number: A75250; MUID:20036896; PMID:10567266
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C:Species: Caulobacter crescentus
C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C:Accession: H87516
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                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                    A)Cross-references: EMBL:X16720; NID:944754; PIDN:CAA34698.1; PID:944766 C;Superfamily: rat ribosomal protein L19 C;Keywords: protein biosynthesis; ribosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          D-alanyl-D-alanine carboxypeptidase [imported] - Caulobacter crescentus
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                                                                                                                                                                                                                                                                                                               Score 57; DB 1; Length 149;
Pred. No. 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26.2%; Score 56; DB 2; Length 435; larity 41.2%; Pred. No. 41; Conservative 5; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                     Indels
S ribosomes.
A;Reference number: S05611; MUID:90040717; PMID:2530355
                                                                                                                                                                                                                                                                                                                                                                              9; Mismatches 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              286 KRRSRGERTITAANIYEDEP----SGPIERPSAE 315
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87;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 56;
Pred. No. 1
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36.6%;
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ilarity 35.3%;
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A, Genome: plasmid
A, Note: plasmid MP1
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A;Molecule type: DNA
A;Residues: 1-435 <STO>
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A; Residues: 1-969 <WHI>
                                                                                                  A; Molecule type: DNA
A; Residues: 1-149 <AUE>
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                                                                         A; Accession:
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Synabsin Ia - rat
Cispecies: Ratus norvegicus (Norway rat)
Risudhof, T.C.; Czernik, A.J.; Kao, H.T.; Takei, K.; Johnston, P.A.; Horiuchi, A.; Kana
Science 245, 1474-1480, 1980
Science 245, 1474-1480, 1980
A; Reference number: A30411; MUD:89388265; PMID:2506642
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A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-704 <SUE>
A;Cross references: GB:M27812; NID:9206920; PIDN:AAA42145.1; PID:9206921
A;Accession: B30411
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: mRNA
A;Residues: 1-659,'Ka',662,'PAQAQP' <SU2>
A;Cross-references: GB:MZ7924; NID:9206932; PIDN:AAA42148.1; PID:9206933
C;KEywords: actin binding; alternative splicing; phosphoprotein
A.Accession: A25704
A.Molecule type: mRNA
A.Residues: 1-691 <mcCoss-references: 1-692 <mcCoss-references: 1-692 <mcCoss-references: 1-692 <mcCoss-references: 1-692 <mcCoss-references: brain
C.Keywords: actin binding; alternative splicing; phosphoprotein
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42.3%; Pred. No. 85;
tive 4; Mismatches 11; Indels
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Pred. No. 83;
4; Mismatches 11; Indels
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Best Local Similarity 42.3%;
Matches 11; Conservative
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Best Local Similarity 42.3
Matches 11; Conservative
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Search completed: June 6, 2003, 11:03:36 Job time: 4.65674 secs

Page 1

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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

June 6, 2003, 10:57:04; Search time 1.50788 Seconds (without alignments) 1127.761 Million cell updates/sec Run on:

US-09-825-581-6_COPY_51_91 214 1 GKRRAKALRWIRQKSVEEGE......PGQGEGPRSRPAAESTGLEA 41 Title:
Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

112892 seqs, 41476328 residues Searched:

112892 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq Length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	09ug19 homo sapien p2281 mus musculu p1527 rattus norv p20823 homo sapien 009101 drosophila p5779 homo sapien p17600 homo sapien p05516 homo sapien Q05516 homo sapien Q05180 homo sapien Q05181 homo sapien p09951 rattus norv p26221 thermomonos Q05358 rattus norv p26221 thermomonos Q05358 homo sapien p4574 homo sapien p4574 homo sapien p2689 ovis aries Q23712 arabidopsis Q23712 arabidopsis Q23712 arabidopsis Q23713 mus musculu p14652 homo sapien p14652 homo sapien Q14165 homo sapien p2689 ovis aries O54751 mus musculu p24555 mycobacteri Q65385 rhizobium similal
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PPGA_HUMAN Y525_PSEAE B3A2_RAT B3A2_RAST B3A2_RAST B3A2_RAST BCA4_HUMAN RS5_SYNP6 CCAH_HUMAN RS5_SYNP6 CSP_PLAKH GSR2_HUMAN	ALIGNMENT	46 46 46 46 46 46 46 46 46 46 46 46 46 4
3A HI 25 PS 72 RA 72 H 72 H 73 SYP 74 PLA 75 SYP 75 SYP 76 PLA	ALIC	HUMAN STANDARD; PRT; 9, 09NRL1; 7-2001 (Rel. 40, Created) 17-2001 (Rel. 40, Last sequence of the control of Rel. 40, Last sequence of the control of Rel. 40, Last sequence of the control of the cont
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InterPro; IPR001356; Homeobox.
                                                                                                                                                                                                                                                                                                           51308 MW;
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Best Local Similarity 68.3
Matches 28; Conservative
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                                                                                                                                                                                                                                                                                                           464 AA;
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                                                                                                                                                                                                                                                                                                           SEQUENCE
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O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SENSITIVE LIPASE. THIS IS A REGULATORY SUBUNIT. IT MAY PLAY A ROLE IN THE REGULATION OF EMERGY METHABLISM IN SKELETAL MUSCLE.
SUBUNIT: HETEROTRINER OF AN ALPHA CATALYTIC SUBUNIT, A BETA AND A GAMMA NON-CATALYTIC REGULATORY SUBUNITS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -:- TISSUE SPECIFICITY: MUSCLE.
-:- DISEASE: DEFECTS IN PRAGA (RN-) ARE ASSOCIATED WITH EXCESS
-:- DISEASE: DEFECTS IN PRAGA (N SKELETAL MUSCLE. THIS MUTATION ORIGINATED IN THE HAMPSHIRE BREED PIGS AND HAS BENEFICIAL EFFECTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ON MEAT CONTENT BUT DETRIMENTAL EFFECTS ON PROCESSING YIELD. THUS, THIS MUTATION IS OF CONSIDERABLE ECONOMIC SIGNIFICANCE IN THE PIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Milan D., Jeon J.-T., Looft C., Amarger V., Robic A., Thelander M., Rogel-Gaillard C., Paul S., Iannuccelli N., Rask L., Ronne H., Lundstroem K., Reinsch N., Gellin J., Kalm E., Le Roy P., Chardon P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: BELONGS TO THE 5'-AMP-ACTIVATED PROTEIN KINASE, GAMMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
5'-AMP-activated protein kinase, gamma-3 subunit (AMPK gamma-3 chain)
                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SYNTHESIS BY PHOSPHORYLATION OF ACETYL-COA CARBOXYLASE. ALSO REGULATES CHOLESTEROL SYNTHESIS VIA PHOSPHORYLATION AND INACTIVATION OF HYDROXYMETHYLGLUTARYL-COA REDUCTASE AND HORMONE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -! - FUNCTION: AMPK IS RESPONSIBLE FOR THE REGULATION OF FAITY ACID
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Sus.
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MQ -> IE (IN REF. 1).
Q -> K (IN REF. 1).
ALGA -> PSGEPEKI (IN REF. 1).
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Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae,
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                                                                                                   CBS domain.
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                                                                                          Acid biosynthesis; Repeat, CBS 1. 147 201 CBS 1. N 228 282 CBS 2. N 303 356 CBS 2. N 375 428 CBS 4.
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                              InterPro: IPR000644; CBS_domain.
Pfam; PF00571; CBS; 4.
SMART; SM00116; CBS; 4.
                                                                                                                                                                                                                                                                                       51514 MW;
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Science 288:1248-1251(2000).
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HGNC:9387; PRKAG3
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PRKAG3.
                 MIM; 604976;
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modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Transcription regulation; DNR-binding; Homeobox; Nuclear protein;
Activator; Trans-acting factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.

MEDILINE-91088607; Pubmed=2263635;

Kuo C. J., Conley P.B., Hsieh C.L., Francke U., Crabtree G.R.;

Kuo C.J., Conley P.B., Hsieh C.L., Francke U., Crabtree G.R.;

Molecular cloning, functional expression, and chromosomal
localization of mouse hepatocyte nuclear factor I.";

Proc. Natl. Acad. Sci. U.S.A. 87.9838-9842(1990).

- FUNCTION: REQUIRED FOR THE EXPRESSION OF SEVERAL LIVER SPEC
GENES. BINDS ONA AS A DIMER.

- SUBGRIT: BINDS ONA AS A DIMER.

- SUBCELLULAR LOCATION: Nuclear.
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0
                                                                                                                                                                                                                                                                                          Fatty acid biosynthesis; Repeat; CBS domain; Disease mutation. DOMAIN 172 226 CBS 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 464;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Hepatocyte nuclear factor 1-alpha (HNF-1A) (Liver specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                             -> Q (IN RN-).
17638CB12A2BA9DF CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- TISSUE SPECIFICITY: LIVER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 142; DB 1;
Pred. No. 5.3e-09;
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CBS 3.
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                                                                                                                    EMBL, AF214521; AAF73989.1; -.
EMBL; AF214520; AAF73988.1; -.
InterPro; IPROUG644; CBS_domain.
Pfam; PF00571; CBS; 4.
SMART; SM00116; CBS; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCF1 OR HNF1A OR HNF-1A OR HNF-1.
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PROSITE; PS00027; HOMEOBOX_1; 1.
PROSITE; PS50071; HOMEOBOX_2; 1.
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DOMAIN
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                                                  21 AMINO ACID LOOP BETWEEN HELLX 2 AND 3. 737920D1A369B9DD CRC64;
                  INVOLVEMENT WITH TRANSCRIPTION).
NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
                                                                                                                                                                                                             01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
15-JUN-2002 (Rel. 14, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
Hepatocyte nuclear factor 1-Appa (HNF-1A) (Liver specific transcription factor LF-B1) (LFB1).
TCF1 OR HNF1A OR HNF-1A OR HNF-1.
Rattus norvegicus (Rat).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 166-628 FROM N.A.
MEDLINE-90249741; Pubmed-1970973;
Baumhueter S., Mendel D.B., Conley P.B., Kuo C.J., Turk C.,
Graves M.K., Edwards C.A., Courtols G., Crabtree G.R.,
"HNF-1 shares three sequence motifs with the POU domain proteins and
                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE-91016926; Pubmed=221677;
Chouard T., Blumenfeld M., Bach I., Vandekerckhove J., Cereghini S.,
                                                                                                                                                                                                                                                                                                                                                       Frain M., Swart G., Monaci P., Nicosia A., Staempfli S., Frank R.,
Cortese R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                homeodomain of the transcription factor LF-Bl has a 21 amino loop between helix 2 and helix 3."; 60:5-6(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-91105074; Pubmed-1988016;
Pastore A., de Francesco R., Barbato G., Castiglione Morelli M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                              "A distal dimerization domain is essential for DNA-binding by the
                                                                                                                                                                                                                                                                                                                                                                              "The liver-specific transcription factor LF-B1 contains a highly diverged homecbox DNA binding domain."; Cell 59:145-157(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-Sprague-Dawley; Tomiatti C., Lazzaro D., de Francesco R., Pozzi L., Gerster J., Cortese R.; Submitted (AUG-1992) to the EMBL/GenBank/DDBJ databases.
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          ASP/GLU-RICH (ACIDIC) (POTENTIAL
                                                                               Score 61.5; DB 1; Length 628; Pred. No. 8.9;
                                                                                          Pred. No. 8.9;
4; Mismatches 18; Indels
                                                                                                                                    271 RKKEEAFRHKLAMDTYNGPPGPGPGP-ALPAHSSPGL 307
                                                                                                                       2 KRRAKALRWTRQKSVEEGEPPGQGEGPRSRPAAESTGL 39
                                                                                                                                                                                             628 AA
 DIMERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic Acids Res. 18:5853-5863(1990).
                                         HOMEOBOX.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       is identical to LF-B1 and APF.";
Genes Dev. 4:372-379(1990).
                             205 NI
279 HG
258 21
67237 MW;
                                                                               28.7%;
39.5%;
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STRUCTURE BY NMR OF 1-32.
                                                                                                   15; Conservative
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\frac{31}{80}
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                            197
199
238
628 AA;
                                                                             Query Match
Best Local Similarity
Matches 15; Conserv
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                                                 DOMAIN
SEQUENCE
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                                         DNA_BIND
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DOMAIN
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Gasge by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
"IH resonance assignment and secondary structure determination of the dimerization domain of transcription factor LFB1."; Biochemistry 30:148-153(1991).
                                                                                                                                                                                                                              "The three-dimensional NMR-solution structure of the polypeptide fragment 195-286 of the LFBL/HNV1 transcription factor from rat liver comprises a nonclassical homeodomain."; EMBO J. 12:1797-1803(1993).
                                                                                                                                                                                                                                                                                                                                                                                 STRUCTURE BY NWR OF 195-286.
MBDLINE-9772/2000, Pubmed-912845;
SCHOLT O., Billeter M., Leiting B., Wider G., Wuethrich K.;
The NWR solution structure of the non-olassical homeodomain from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AMINO ACID LOOP BETWEEN HELIX 2 AND 3.
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rat
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PROSITE; PS00071; HOMEOBOX_2; 1.
Transcription regulation; DNN-binding; Homeobox; Nuclear protein; Activator; Trans-acting factor; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ceska T.A., Lamers M., Monacl P., Nicosia A., Cortese R., Suck "The X-ray structure of an atypical homeodomain present in the liver transcription factor LFB1/HNF1 and implications for DNA
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                                                                                                                   STRUCTURE BY NMR OF 195-286.
MEDLINE-93259120; PubMed=8491172;
Leiting B., de Francesco R., Tomei L., Cortese R., Otting G.,
Wuethrich K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 195-286.
MEDLINE-93259121; PubMed=8491173;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        t liver LFB1/HNF1 transcription factor."; Mol. Biol, 267:673-683(1997).
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EMBL, X67649; CAA47891.1; -.
EMBL, X53297; CAA37387.1; ALT_INIT.
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InterPro; IPR001356; Homeobox.
SMART; SM00389; HOX; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; J03170; AAA41524.1; -.
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PTR, A34590; A34590.
PIR, S11568, S11568.
PIR, S25465; S25465.
PDB; ILFB; 31-0CT-93.
PDB; ZLFB; 12-MAR-97.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-97100943; PubMed-8945470; Vamagata K., Oda N., Kaisaki P.J., Menzel S., Furuta H., Vamagata K., Oda N., Kaisaki P.J., Menzel S., Furuta H., Vazilalize M., Southam L., Cox R.D., Lathrop G.M., Boriraj V.V., Chen X., Cox N.J., Oda Y., Yano H., le Beau M.M., Yamada S., Nishigori H., Takeda J., Fajans S.S., Hattersley A.T., Iwasaki N., Hansen T., Pedersen O., Polonsky K.S., Turner R.C., Velho G., Cherre J.-C., Froquel P., Bell G.I., "Mutations in the hepatocyte nuclear factor-lalpha gene in maturity-onset diabetes of the young (MODY3).";
                                                                            Gaps
                                                                                                                                                                                                  P20823; Q99861;
01-FEB-1991 (Rel. 17, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Hepatocyte nuclear factor 1-alpha (HMF-1A) (Liver specific transcription factor LF-B1) (LFB1) (Transcription factor-1) (TCF-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "More potent transcriptional activators or a transdominant inhibitor of the HNF1 homeoprotein family are generated by alternative RNA
                                                                                                                                                                                                                                                                                                                                                                                          Bach I., Galcheva-Gargova Z., Mattei M.-C., Simon-Chazottes D., Guenet J.-L., Cereghini S., Yaniv M.; "Cloning of human hepatic nuclear factor I (HNFI) and chromosomal localization of its gene in man and mouse."; Genomics 8:155-164(1990).
                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-97309269; PubMed-9166684; Glucksmann M.A., Lehto M., Tayber O., Scotti S., Berkemeier L., Pulido J.C., Wu Y., Nir W.-J., Fang L., Markel P., Munnelly K.D., Gozranson J., Orho M., Young B.M., Whitacre J.L., McMenimen C., Wantman M., Tuomi T., Warram J., Porsblom C.M., Carlsson M., Rosenzweig J., Kennedy G., Duyk G.M., Krolewski A.S., Groop L.C.,
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                                                 28.7%; Score 61.5; DB 1; Length 628; 39.5%; Pred. No. 8.9;
                                                                            Indels
261 273
274 275
628 AA; 67213 MW; 8D28099308C86A52 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VARIANTS MODY3 ARG-107; TRP-131; MET-260 AND HIS-272.
                                                                                                                  33
                                                                         18;
                                                                                                  2 KRRAKALRWTRQKSVEEGEPPGQGEGPRSRPAAESTGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A., AND VARIANT MODY3 LEU-447.
                                                                                                                                                                                         631 AA.
                                                                           4; Mismatches
                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Liver;
MEDLINE=91184801; PubMed=1707031;
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MEDLINE=94038905; PubMed=7900999;
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                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nature 384:455-458(1996).
                                                                                                                                                                                         STANDARD;
                                                Query Match
Best Local Similarity
Matches 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bach I., Yaniv M.;
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"Identification of mutations in the hepatocyte nuclear factor (HNF)-1-alpha gene in Japanese subjects with IDDM.";
Diabetes 46:1643-1647(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WARIANTS MODY3 GLN-131; GLN-229; GLY-241 AND HIS-272.
MEDLINE-97184312; PubMed-9032114;
Kaisaki P.J., Menzel S., Lindner T., Oda N., Rjasanowski I., Sahm J.,
Meninck G., Schulze J., Schmechel H., Petzold C., Ledermann H.M.,
Sachse G., Borlizaj V.V., Menzel R., Kerner W., Turner R.C.,
Tamagata K., Bell G.I.;
"Mutations in the hepatcoyte nuclear factor-lalpha gene in MODY and
early-onset NIDDM: evidence for a mutational hotspot in exon 4.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VARIANTS LEU-27; VAL-98 AND ASN-487.
MEDLINE-97278987; PubMed=9133564;
Urhammer S.A., Fidberg M., Hansen T., Rasmussen S.K., Moeller A.M.,
Clausen J.O., Pedersen O.;
"A prevalent amino acid polymorphism at codon 98 in the hepatocyte
                                                                                                                                                                                                                            MEDLINE-97431550; PubMed-9287055; Yamada S., Nishigori H., Onda H., Takahashi K., Kitano N., Morikawa A., Takeuchi T., Takeda J.; "Mutations in the hepatocyte nuclear factor-lalpha gene (MODY3) are not a major cause of late-onset NIDDM in Japanese subjects."; Diabetes 46:1512-1513(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-98052398; PubMed=9392505; Boutin P., Cherre J.-C., Hanh E. H., Gomis R., Pardini V.C., Boutin P., Cherre J.-C., Hanh E. H., Gomis R., Proguel P.; (aulilausseau P.-J., Vaxillaire M., Velho G., Froguel P.; "an automated fluorescent single-strand conformation polymorphism technique for screening mutations in the hepatocyte nuclear factor lalpha gene (maturity-onset diabetes of the young)."; plabetes 46:2108-2109(1997).
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     in
"Mutations in the hepatocyte nuclear factor-lalpha/MODY3 gene Japanese subjects with early- and late-onset NIDDM."; Diabetes 46:1504-1508(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VARIANTS MODY3 THR-129; TRP-131; TRP-159; LEU-519 AND ILE-620.
                                                                                                                                                                                         AND ASN-487.
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                                                                                                                                                                                         VARIANT NIDDM MET-254, AND VARIANTS LEU-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VARIANTS IDDM HIS-272 AND GLY-583.
MEDLINE=97458988; PubMed=9313763;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chevre J.-C., Hani E.H., Boutin P., Vaxillaire M., Blanche H., Volonet W., Pardini V.C., Timsit J., Larger E., Charpentier G., Beckers D., Macs M., Bellanne-Clarelot C., Velho G., Froguel P.; Mutation screening in 18 Caucasian families suggest the existence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pedersen 0.;
"Mutations in the hepatocyte nuclear factor-lalpha gene in Caucasian families originally classified as having type I diabetes.";
Diabetologia 41:1528-1531(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-99176457; PubMed=10078571; Yamada S., Tomura H., Nishigori H., Sho K., Mabe H., Iwatani N., Yamada S., Tomura H., Moriya N., Muroya K., Ogata T., Onigata K., Morikawa A., Inoue I., Takeda J.; "Identification of mutations in the hepatocyte nuclear factor-lalpha gene in Japanese subjects with early-onset NIDDM and functional
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pedersen 0.;
"Genetic variation in the hepatocyte nuclear factor-1 alpha gene in
                                                                                                                                        Vaxillaire M., Rouard M., Yamagata K., Oda N., Kaisaki P.J.,
Boriraj V.V., Chevre J.-C., Boccio V., Cox R.D., Lathrop G.M.,
Dussoix P., Philippe J., Timsit J., Charpentier G., Veiho G.,
Bell G.I., Froquel P.,
"Identification of nine novel mutations in the hepatocyte nuclear factor I alpha gene associated with maturity-onset diabetes of the
                                                                                                                                                                                                                                                                                                                                                                                                                            uncommon
                                                                                                                                                                                                                                                                                                                                  VARIANTS LEG-27; ASN-487 AND ARG-514.

BEDLINE-98265912; Pubmed-9604876;
Behn P.S., Wasson J., Chayen S., Smolovitch I., Thomas J.D.,
Glaser B., Permutt M.A.;
Hepatocyte nuclear factor lalpha coding mutations are an uncomm contributor to early-onset type 2 diabetes in Ashkenazi Jews.";
Diabetes 47:967-969(1998).
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Takeuchi T., Takeda J.;
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mutations in the hepatocyte nuclear factor-1 alpha genuntuations in the hepatocyte nuclear factor-1 alpha genuntuator cause of early-onset non-insulin-dependent diabetes mellitus in Japanese.";
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                                                                                                       VARIANTS MODY3 CYS-122; PHE-142 AND GLN-159.
                                      Danish Caucasians with late-onset NIDDM.";
Diabetologia 40:473-475(1997).
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MEDLINE=98284534; Pubmed-9621514;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=98425814; PubMed=9754819;
                                                                                                                                                                                                                                                                                          Mol. Genet. 6:583-586(1997).
                                                                                                                           MEDLINE~97252393; PubMed=9097962;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VARÍANTS IDDM LYS-48 AND GLY-241.
MEDLINE~99083111; Pubmed=9867222;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          other MODY genes.";
Diabetologia 41:1017-1023(1998).
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                  in Drosophila, encodes a novel type of protein. 1,
Neuron 10:355-407(1993).
Neuron 10:355-407(1993).
IN LOCOMOTOR: ARA ROLE IN THE DEVELOPMENT OF CNS FUNCTIONS INVOLVED
IN LOCOMOTOR ACTIVITY.
-!- SUBCELLULAR LOCATION: Extracellular.
-!- ALTERNATIVE PRODUCTS: 4 ISOFORMS; 1, 2, 3 (SHOWN HERE) AND 4; ARE
PRODUCED BY ALTERNATIVE SPLICING.
-!- TISSUE SPECIFICITY: EXPRESSED IN PC.
-!- TISSUE SPECIFICITY: EXPRESSED IN PC.
-!- TISSUE SPECIFICITY: ALTERNATIVE PROCEPHALIC NEUROBLASTS
IN THE PROCEPHALIC NEUROGENIC REGION IN THE CENTRAL NERVOUS
                                                                                                                                                                                                                                  Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropda; Mandibulata; Pancrustacea; Hexapoda;
Insecta: Pterygota; Meoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha: Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCOMOTION-RELATED PROTEIN HIKARU GENKI.
IG-LIKE C2-TYPE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                             Hoshino M., Matsuzaki F., Nabeshima Y.-I., Hama C.;
"Hikaru genki, a CNS-specific gene identified by abnormal locomotion
in Drosophila, encodes a novel type of protein.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- DEVELOPMENTAL STAGE: MOST ABUNDANT DURING AND/OR AFTER NEURONAL DIFFERENTIATION AND DURING CELL SPECIFICATION OR AXOGENESIS.
-!- SIMILARITY: BELONGS TO THE IMMUNGLOBULIN SUPERFAMILY.
-!- SIMILARITY: CONTAINS 1 IMMUNGLOBULIN-LIKE C2-TYPE DOMAIN.
-!- SIMILARITY: CONTAINS 4 SUSHI (SCR) DOMAINS.
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01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Locomotion-related protein Hikaru genki precursor.
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CELL ATTACHMENT SITE.
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SUSHI 2.
SUSHI 3.
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InterPro; IPR000436; Sushi_SCR_CCP.
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InterPro; IPR003599; Ig.
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SMART; SM00032; CCP; 5.
SMART; SM0409; IG; 1.
                                                                                                         STANDARD;
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EMBL; M58378; AAC41930.1; -.
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   Pfam; PF00036;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IDENTIFICATION.

MEDLINE-20092898; PubMed-10625670;
Haeseleer F., Sokal I., Verlinde C.L., Erdjument-Bromage H.,
Fempst P., Pronin A.N., Benovic J.L., Fariss R.N., Palczewski K.;
Fempst P., Pronin A.N., Benovic J.L., Fariss R.N., Palczewski K.;
Five members of a novel Ca(2+)-binding protein (CABP) subfamily with
similarity to calmodulin...;
J. Biol. Chem. 275:1241-1260(2000).
-1. SIMILARITY: CONTAINS 3 EF-HAND CALCIUM-BINDING DOMAINS.
BY SIMILARITY.
N-LINKED (GLCNAC...) (POTENTIAL).
M-SSING (IN ISOFORM 2 AND ISOFORM 4).
MISSING (IN ISOFORM 1 AND ISOFORM 4).
                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID=9606;
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                                                                                                                                                                                                 DB 1; Length 958;
                                                                                                                                                                                                                    11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Smith D.R.; Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-Retina;
Haeseleer F., Palczewski K.;
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                          MW; 4161258E85ABC764 CRC64;
                                                                                                                                                                                                                                                              328 ORDRSPRWRRRSTEFKGDLGOLPPESGIGPEPEPLAD 365
                                                                                                                                                                                                                                          3 RRAKALRWTRQKSVE-EGE----PPGQGEGPRSRPAAE 35
                                                                                                                                                                                                                                                                                                                 CAB4_HUMAN STANDARD; PRT; 275 AA. P57796: Q8WWY5; 16-OCT-2001 (Rel. 40, Created) 15-JUN-2002 (Rel. 41, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Calcium-binding protein CaBP4.
                                                                                                                                                                                                           Pred. No. 13;
8; Mismatches
                                                                                                                                                                                                Score 61.5;
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InterPro; IPR003299; Calflagin.
InterPro; IPR002048; EF-hand.
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Matches 14; Conservative
   755
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SEQUENCE OF 1-125 FROM N.A.

SAUCTARAL A., Hoesche C., Oschwald R., Kilimann M.W.;

"The 5'-flanking region of the synapsin I gene. A G+C-rich, TATA- and TATA-rese, phylogenetically conserved sequence with cell

type-specific promoter function."

J. Biol. Chem. 265:14932-14937(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SUBCELLULAR LOCATION: SYNAPSE.
-!- ALTERNATURE PRODUCTS: ZISOPOMAS; SYNAPSIN IA (SHOWN HERE) AND
SYNAPSIN IB; ARE PRODUCED BY ALTERNATURE SPLICING.
-!- PTM: SUBSTRATE OF AT LEAST FOUR DIFFERENT PROTEIN KINASES. IT IS
PROBABLE THAT PHOSPHORYLATION PLAYS A ROLE IN THE REGULATION OF
SYNAPSIN I IN THE NERVE TERKINAL.
-!- SIMILARITY: BELONGS TO THE SYNAPSIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Grafham D.;
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: NEURONAL PHOSPHOPROTEIN THAT COATS SYNAPTIC VESICLES,
BINDS TO THE CYTOGKELETON, AND IS BELIEVED TO FUNCTION IN THE
REGULATION OF NEUROTRANSMITTER RELEASE.
                                                                                                                                                            EF-HAND 1 (POTENTIAL).
ANCESTRAL CALCIUM SITE 2 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                         12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           e structure of the human synapsin I gene and protein.";
Biol. Chem. 265:7849-7852(1990).
                                                                                                                                                                                                                                                                                                                                  DB 1; Length 275; 7.5;
                                                                                                                                                                                                                                                                                                                                                                                            7; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 RRAKALRWIRQKSVEEGE------PPGQGEGPRSRPAA 34
                                                                                                                                                                                                                                                    F-HAND 4 (POTENTIAL).
1AEB49C93AD67DB7 CRC64;
                                                                                                                                                                                                                      EF-HAND 3 (POTENTIAL).
EF-HAND 4 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-AUG-1990 (Rel. 15, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      705 AA.
                                                                                                                                                                                                                                                                                                                                  Score 59;
                                                                                                                                                                                                                                                                                                                                                                   õ
                                                                                                                                                                                                                                                                                                                                                                   Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-Brain;
MEDLINE-90243651; PubMed-2110562;
PRINTS; PRO1362; CALFLAGIN.
PRODOM; PD000012; ER-hand; 2.
SWART; SM00054; ER-h; 3.
PROSITE; PS00018; ER-HAND; 3.
CALCium-binding; Repeat.
CA_BIND 142 153 FFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synapsin I (Brain protein 4.1).
                                                                                                                                                                                                                                                                            30433 MW;
                                                                                                                                                                                                                                                                                                                                  27.6%;
                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 2>...
Local 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 1-258 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                            153
189
230
267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human)
                                                                                                                                                                                       178 1
219 2
256 2
275 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                         [1] SEQUENCE FROM N.A. MEDING-2530355; MEDINE-90040717; PubMed-2530355; Auer J., Spicker G., Boeck A.; "Organization and structure of the Methanococcus transcriptional unit homologous to the Escherichia coli 'spectinomycin operon'. Implications for the evolutionary relationship of 70 S and 80 S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE-96121379; PubMed-8575760;
Vyas P., Vickers M.A., Picketts D.J., Higgs D.;
"Conservation of position and sequence of a novel, widely expressed gene containing the major human alpha-globin regulatory element.";
Genomics 29:679-689(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID=9606;
                                                                                                                                                J. Mol. Biol. 209:21-36(1989).
-!- SIMILARITY: BELONGS TO THE L19E FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
                                                                                                                                                                                                                                                                                                                                                                                                       26.6%; Score 57; DB 1; Length 149; llarity 35.3%; Pred. No. 6.8; Conservative 9; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (FEB-1996) to the EMBL/GenBank/DDBJ databases.
-!- TISSUE SPECIFICITY: Widely expressed.
-!- SIMILARITY: BELONGS TO THE UPF0171 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                  Ribosomal protein.
SEQUENCE 149 AA; 17286 MW; B8868F4FD5670E0B CRC64;
 Archaea; Euryarchaeota; Methanococci; Methanococcales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           U171_HUMAN STANDARD; PRT; 569 AA. Q12880; Q92469; 16-0CT-2001 (Rel. 40, Created) 116-0CT-2001 (Rel. 40, Last sequence update) 116-0CT-2001 (Rel. 40, Last annotation update) CGTHBA protein (-14 gene protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 KRRAKALRWTRQKSVEEGEPPGQGEGPRSRPAAE
                                                                                                                                                                                                                                                                                                                       InterPro: IPR000196; Ribosomal_119e. Pfam; PF01280; Ribosomal_L19e; I. PROSITE; PS00526; RIBOSOMAL_L19E; I.
            Methanococcaceae; Methanococcus
                                                                                                                                                                                                                                                                                               EMBL; X16720; CAA34698.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 1-62 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
'-Local 12; Conserve
                                                                                                                                                                                                                                                                                                             PIR; S05622; R5MXE.
                             NCBI_TaxID=2187;
                                                                                                                                      ribosomes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Thomas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CGTHBA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (IN SYNAPSIN IB).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A.
B (LINKER).
C (ACTIN'BINDING AND SYNAPTIC-VESICLE BINDING).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PHOSPHORYLATION (BY PKA AND CAMK1). PHOSPHORYLATION (BY CAMK2).
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0
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Pfan. PP02078; Synapsin. 1.
Pfan. PP02078; Synapsin. 2.
PRINTS; PR01368; SYNAPSIN.
PROSTIE; PS00415; SYNAPSIN. 1.
PROSTIE; PS00416; SYNAPSIN. 2.
Synapse; Phosphorylation; Neurone; Repeat; Actin-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (BY CAMK2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NKSQSLTNA -> KASPAQAQP (I)
MISSING (IN SYNAPSIN IB).
G -> E (IN REF. 3).
487831123FF6882F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                D (PRO-RICH LINKER).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
50s ribosomal protein L19E (ORF E).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PHOSPHORYLATION
PHOSPHORYLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   149 AA
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                                                                                                      AAC41930.1; JOINED.
AAC41930.1; JOINED.
AAC41930.1; JOINED.
AAC41931.1; ALT_SEQ.
AAC41931.1; JOINED.
AAC41931.1; JOINED.
AAC41931.1; JOINED.
AAC41931.1; JOINED.
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AAC41931.1; JOINED.
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AAC41930.1; JOINED.
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AAC41930.1; JOINED.
AAC41930.1; JOINED.
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AAC41931.1; JOINED.
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AAC41931.1; JOINED.
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AAC41931.1; JOINED.
AAA60608.1; -.
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                                                                             AAC41930.1;
AAC41930.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11; Conservative
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Methanococcus vannielii.
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112
420
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705
9
568
605
669
705
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PIR; B35363; B35363.
HSSP; P17599; lAUX.
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138 1
705 AA;
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113
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                                      M58353; A
M58359; A
M58371; A
                                                                                                                                                                                                                                                                                              M58375;
M58376;
                                                                                                                                                                                      M58341;
M58351;
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M58359;
                            M58351;
                                                                               M58372;
                                                                                          M58373;
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MIM; 313440;
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CONFLICT
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MOD_RES
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DOMAIN
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EMBL;
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EMBL;
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SLBP_HUMAN
Q14493;
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ZN_FING
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ARE PRODUCED BY ALTERNATIVE SPLICING.
TISSUE SPECIFICITY: WITHIN THE HEMATOPDIFTIC SYSTEM, PLZE IS
EXPRESSED IN BONE MARKOW, ERALY MYELOID CELL LINES AND PERIPHERAL
BLOOD MONOUCLEAR CELLS. ALSO EXPRESSED IN THE OVARY, AND AI LOWER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chen S.-J., Zelent A., Tong J.-H., Yu H.-Q., Wang Z.-Y., Derre J., Berger R., Waxman S., Chen Z.;
"Rearrangements of the retinoic acid receptor alpha and promyelocytic leukemia zinc finger genes resulting from t(11:17)(q23:q21) in a patient with acute promyelocytic leukemia.";
J. Clin. Invest. 91:2260-2267(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Structure-function studies of the BTB/POZ transcriptional repression domain from the promyelocytic leukemia zinc finger oncoprotein."; cancer Res. 59:575-5282(1999).
-:- FUNCTION: PROBABLE TRANSCRIPTION FACTOR. MAY PLAY A ROLE IN MYELOID MATURATION AND IN THE DEVELOPMENT AND/OR MAINTENANCE OF
                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -1- SUBCELLULAR LOCATION: Nuclear.
-1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; PLFZA AND PLZFB (SHOWN HERE);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INDUCTION: BY RETINOIC ACID.
DISBASE: A FORM OF ACUTE PROMYELOCYTIC LEUKEMIA (APL) IS
CHARACTERIZED BY A CHROMOSOMAL TRANSLOCATION T(11,117) (032,021)
WHICH INVOLVES YRIA'S AND RETINOIC ACID RECEPPOR ALPHA (RRRA)
SIMILARITY: BELONGS TO THE KRUEPPEL FAMILY OF C2H2-TYPE ZINC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 7-122.
MEDITME-20065701; Pubmed-10337309;
Li X., Peng H., Schultz D.C., Lopez-Guisa J.M., Rauscher F.J. III,
Marmorstein R.;
                                                                                                                                                                                                                                                                                                                                                                                              PEQUENCE FROM N.A.
TISSUE-Heart ventricle;
MEDLINE-93209216; Pubmed-8384553;
Chen Z., Brand N.J., Chen A., Chen S.-J., Tong J.-H., Wang Z.-Y.,
Waxman S., Zelent A.;
Fusion between a novel Kruppel-like zinc finger gene and the
retinoic acid receptor-alpha locus due to a variant t(11;17)
translocation associated with acute promyelocytic leukaemia.";
EMBO J. 12:1161-1167(1993).
                                                                                                                                                                                                                                                                                                                                             DARATYCE, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                          .,
m
                                                                                                                                                                                                                                                         Score 55.5; DB 1; Length 569;
                                                                                                                        15; Indels
                                                        Pram. Pro3666, UPr0171; 1.
SEQUENCE 569 AA: 63604 MW: 44BEF42AA7F2841D CRC64;
                                                                                                                                                1 GKRRAKAL-RWIRQKSVEEGEPPGQGEGPRSRPAAESTG 38
                                                                                                                                                                        16 GSRGNKLLFRYPFQRSQE--HPASQTSKPRSRYAASNTG 52
                                                                                                                                                                                                                                      673 AA
                                                                                                           Pred. No. 38;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LEVELS, IN THE KIDNEY AND LUNG.
                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 424-455 FROM N.A. MEDLINE=93253074; PubMed=8387545;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER DIFFERENTIATED TISSUES.
                                               InterPro; IPR005365; UPF0171.
          EMBL; X90857; CAA62368.1; -. EMBL; 269666; CAA93521.1; -.
                                                                                              25.9%;
                                                                                                           46.28;
                                                                                                           Local Similarity 46.2
les 18; Conservative
                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
                                    600928;
                                                                                                                                                                                                                                   2145_HUMAN
Q05516;
                                                                                                 Query Match
                                                                                                              Best Loca
Matches
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                                    MIM;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ij
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMART; SM00225; BTB; 1.

SMART; SM00325; ZnF_C2H2; 9.

PROSITE: PSS00028; ZNR_FINGER_C2H2_1; 8.

PROSITE; PSS0157; ZINC_FINGER_C2H2_1; 8.

PROSITE; PSS0157; ZINC_FINGER_C2H2_2; 9.

Transcription regulation; DNA-binding; Zinc-finger; Metal-binding; Nuclear protein; Repeat; Chromosomal translocation; Proto-oncogene; Phosphorylation; Alternative splicing; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BREAKPOINT FOR TRANSLOCATION TO FORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1;
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16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Histone RNA hairpin-binding protein (Histone stem-loop binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 673;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PHOSPHORYLATION (BY PDPK) (PP PHOSPHORYLATION (BY PHOSPHORYLATION 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PLZF-RAR-ALPHA ONCOGENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. 45;
7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZINC FINGERS.
C2H2-TYPE.
C2H2-TYPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FINGER PROTEINS.
SIMILARITY: CONTAINS 1 BTB/POZ DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5 AKALRWTRQKSVEEGEPPGQ-GEGPRSRP 32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C2H2-TYPE.
C2H2-TYPE.
C2H2-TYPE.
C2H2-TYPE.
C2H2-TYPE.
C2H2-TYPE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PR00048; ZINCFINGER. ProDom; PD000003; Znf_C2H2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Znf_C2H2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            74332 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25.9%;
                                                                                                                                                                                                                                                                                                                                                  EMBL; 219002; CAA79489.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000210; BTB_POZ.
InterPro; IPR000822; Znf_C2H2
Pfam; PF00096; zf-C2H2; 9.
Pfam; PF00651; BTB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genew; HGNC:12930; ZNF145.
MIM; 176797; -.
                                                                                                                                                                                                                                                                                                                                                                                    S60093; AAC60590.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 37.9 ses 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            652
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197
197
256
282
628
377
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TRANSFAC; T02336; -.
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Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               256
282
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255
673 AA;
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32 KRRADGRRW-RPEDAEEAEHRGAERRPESFTTPEGPKPRSRCSDWASAVE 80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                 RESULT 13
SYN1_MOUSE
   Dp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Highlormatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ä
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -1- FUNCTION: BINDS THE STEM-LOOP STRUCTURE OF REPLICATION-DEPENDENT HISTONE PRE-WRANS, AND CONFIDENTES TO EFFECIENT 3' END PROCESSING BY STABILIZING THE COMPLEX BETWEEN HISTONE PRE-MRNA AND UT SMALL NUCLEAR RIBONUCLEOPROTEIN (SNRNP), COULD PLAY AN IMPORTANT ROLE IN TARGETHIC MATURE HISTONE MRNA FROM THE NUCLEUS OF THE CYTOPLASM AND TO THE TRANSLATION MATURENTS. STABILIZES MATURE HISTONE MRNA AND COULD BE INVOLVED IN CELL-CYCLE REGULATION OF HISTONE GENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-Lymphocytes;
MEDLINE-97201520; PubMed-9049306;
Martin F., Schaller A., Eglite S., Schuemperli D., Mueller B.;
"The gene for histone RNA hairpin binding protein is located on human chromosome 4 and encodes a novel type of RNA binding protein.";
EMBO J. 16:769-778(1997).
                                                                                                                                                                                        McCombie W.R., Martin-Gallardo A., Gocayne J.D., FitzGerald M., Dubnick M., Kelley J.M., Castilla L., Liu L.I., Wallace S., Trapp S., Tagle D., Whaley W.L., Cheng S., Gusella J., Frischauf A.-M., Poustka A., Lehrach H., Collins F.S., Kerlavage A.R., Fields C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                Expressed genes, Alu repeats and polymorphisms in cosmids sequenced
Chordata, Craniata, Vertebrata, Euteleostomi,
Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "The protein that binds the 3' end of histone mRNA: a novel RNA-binding protein required for histone pre-mRNA processing."; Genes Dev. 10:3028-3040(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CELL CYCLE: PROTEIN
G1 AND DECREASE AT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBUNIT: MONOMER.
SUBCELLULAR LOCATION: NUCLEAR AND CYTOPLASMIC (POLYRIBOSOME-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RNA-binding: mRNA processing: Nuclear protein: Phosphorylation.
MOD_RES 62 62 SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-Cervical adenocarcinoma;
MEDLINE-97115884; Pubmed-8957003;
Wang Z.-F., Whitfield M.L., Ingledue T.C. III, Dominski Z.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25.7%; Score 55; DB 1; Length 270; 34.0%; Pred. No. 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4E84E502393D1BF7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -i- TISSUE SPECIFICITY: WIDELY EXPRESSED.
-i- DEVELOPMENTAL STACE: REGULATED DURING THE
LEVELS INCREASE 10 TO 20 FOLD IN THE LATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: BELONGS TO THE SLBP FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RNA-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entities requires a license agreement (sor send an email to license@isb-sib.ch)
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EMBL; U75679; AAB97091.1; -.
EMBL; Z71188; CAA94918.1; -.
                                                                                                                             SEQUENCE FROM N.A. MEDLINE=93251024; PubMed=1338771;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31285 MW;
                                                                                                                                                                                                                                                                                                                                                                                            from chromosome 4p16.3.";
Nat. Genet. 1:348-353(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 34.0
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genew; HGNC:10904; SLBP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     198
   Eukaryota; Metazoa;
                               Mammalia; Eutheria;
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              270 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            THE S/G2 BORDER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ASSOCIATED)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EXPRESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Marzluff W.F.;
                                                                                                                                                                                                                                                                                                                                    /enter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MIM; 602422;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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--- QGEGPRSRPAAESTGLE 40

2 KRRAKALRWTRQKSVEEGEPPG---

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                                                                                                                                                                                                                                                                                                            Chin L.S., Li L., Greengard P., "Neuron-specific expression of the synapsin II gene is directed by a
                                                                                                                                                                                                         "Cloning from insulinoma cells of synapsin I associated with insulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PHOSPHORYLATION (BY PKA AND CAMK1) (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (ACTIN-BINDING AND SYNAPTIC-VESICLE
                                                                                 Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBL_TaxID=10090;
                                                                                                                                                                               Matsumoto K., Ebihara K., Yamamoto H., Tabuchi H., Fukunaga K., Yasunami M., Ohkubo H., Shichiri M., Miyamoto E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY).
PHOSPHORYLATION (BY CAMK2) (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Neurone; Repeat; Actin-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY).
PHOSPHORYLATION (BY CAMK2)
                                                                                                                                                                                                                       secretory granules.";
Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (PRO-RICH LINKER)
                                    Last sequence update)
Last annotation update)
                                                                                                                                         [1]
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
Vamamoto islets;
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                                                                                                                                                                                                                                                         SEQUENCE OF 1-125 FROM N.A.
MEDLINE=94308086; PubMed=8034599;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam: PF02078; Synapsin; 1.
Pfam: PF02750; Synapsin; 1.
PFam: PF02750; Synapsin_C; 1.
PRINTE; PR01846; SYNAPSIN.
PROSITE; PS00416; SYNAPSIN_1; 1.
PROSITE; PS00416; SYNAPSIN_2; 1.
                    30-WAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last segu
15-JUN-2002 (Rel. 41, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MGD; MGI:98460; Synl.
InterPro; IPR001359; Synapsin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AF085809; AAD09833.1; -.
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HSSP; P17599; 1AUX.
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STANDARD;
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         088935; 062279;
                                                                           SYN1 OR SYN-1.
SYN1_MOUSE
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                                                              Synapsin
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Pfam; PF02078; Synapsin; 1.
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus. NCBL_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -:- SUBCELLULAR LOCATION: SYNAPSE.
-:- ALTERNATIVE PRODUCES: 2 ISOFORMS: SYNAPSIN IA (SHOWN HERE) AND SYNAPSIN IS ARE PRODUCED BY ALTERNATIVE SPLICING.
-:- PTM: SUBSTRATE OF AT LEAST FOUR DIFFERRY PROTEIN KINASES. IT IS PROBABLE THAT PHOSPHORYLATION PLAYS A ROLE IN THE REGULATION OF SYNAPSIN I IN THE NERVE TERMINAL (BY SIMILARITY).
-:- SIMILARITY: BELONGS TO THE SYNAPSIN FAMILY.
-:- CAUTION: REF. 2 SEQUENCE WAS INCORRECT AT MANY PLACES DUE TO SEQUENCING ERRORS.
                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'Synapsins: mosaics of shared and individual domains in a family of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               McCaffery C.A., Degennaro L.J.;

"Deternination and analysis of the primary structure of the nerve terminal specific phosphoprotein, synapsin I.";

EMBO J. 5:3167-3173(1986).

-!- FUNCTION: NEURONAL PHOSPHOPROTEIN THAT COATS SYNAPTIC VESICLES, BINDS TO THE CYTOSKELETON, AND IS BELIEVED TO FUNCTION IN THE REGULATION OF NEUROTRANSMITTER RELEASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Suedhof T.C., Czernik A.J., Kao H.-T., Takei K., Johnston P.A., Horiuchi A., Kanazir S.D., Wagner M.A., Perin M.S., de Camilli P.,
                                                                                           o;
                                                             DB 1; Length 670;
                                                                                           Indels
SIMILARITY).
44 P -> L (IN REF. 2).
70035 MW; DE64BF0090A2B58E CRC64;
                                                                                           11;
                                                                                                                                                                                                                              STANDARD, PRT; 704 AA. P09951, Q9WUX7; Created) 80-MAR-1899 (Rel. 10, Created) 80-MAY-2000 (Rel. 39, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update)
                                                         25.7%; Score 55; DB 42.3%; Pred. No. 51; tive 4; Mismatches
                                                                                                                                        13 QKSVEEGEPPGQGEGPRSRPAAESTG 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         synaptic vesicle phosphoproteins.";
Science 245:1474-1480(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-Brain;
MEDLINE-87133474; PubMed=3028773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; M27924; AAA42148.1; -.
EMBL; X04655; CAA28353.1; ALT_SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=89388265; Pubmed=2506642;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR; A25704; A25704.
PIR; A30411; A30411.
PIR; B30411; B30411.
INSSP: P17599; LAUX.
InterPro; IPR001359; Synapsin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; M27812; AAA42145.1; -.
                                                                                          Conservative
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                44
670 AA;
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nes 11; Conserv
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              CONFLICT
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92221; 008167;
01-NAY-1992 (Rel. 22, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 34), Last annotation update)
Endoglucanase E-1 precursor (EC 3.2.1.4) (Endo-1,4-beta-glucanase E-4) (Cellulase E-4) (Cellulase E4).
                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                     NKSOSITUR -> KASPAOAOP (IN SYNAPSIN IB)
MISSING (IN SYNAPSIN IB).
65799FEF7CFE18B5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria, Actinobacteria; Actinobacteria (class); Actinobacteridae; Actinomycetales; Streptosporangineae; Nocardiopsaceae; Thermobifida
                                                                                                                            (ACTIN-BINDING AND SYNAPTIC-VESICLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-94028932; PubMed=8215374;
Jung B.D., Lao G., Irwin D., Barr B.K., Benjamin A., Wilson D.B.;
"DRA sequences and expression in Streptomyces lividans of an
exoglucanase gene and an endoglucanase gene from Thermomonospora
Pfam: PPC2750; Symposin_C; 1.
PRINTS; PR01368; SYNAPSIN_1: 1.
PROSITE; PS00415; SYNAPSIN_1: 1.
Synapse; Phosphorylation; Nerve; Neurone; Repeat; Actin-binding; Alternative splicing.
                                                                                                                                                                                          PHOSPHORYLATION (BY PKA AND CAMKI). PHOSPHORYLATION (BY CAMK2). PHOSPHORYLATION (BY CAMK2).
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Lao G., Ghangas G.S., Jung B.D., Wilson D.B.;
"DNA sequences of three beta-1,4-endoglucanase genes from
                                                                                                                                                                                                                                                                                                     DB 1; Length 704;
                                                                                                                                                                                                                                                                                                                                    11; Indels
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Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                             (PRO-RICH LINKER).
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MEDLINE-97475222; pubmed=9334746;
Sakon J., Irwin D., Wilson D.B., Karplus P.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Appl. Environ. Microbiol. 59:3032-3043(1993)
                                                                                                                                                                                                                                                                                                                    Pred. No. 54;
4; Mismatches
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                                                                                                                  (LINKER)
                                                                                                                                                                                                                                                                                                     Score 55;
                                                                                                                                                                                                                                                                                                                                                                 13 OKSVEEGEPPGQGEGPRSRPAAESTG 38
                                                                                                                                                BINDING)
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                                                                                                                                                                                                       566 PE
603 PE
668 NR
704 MI
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Matches 11; Conservative
                                                                                                               112
                                                                                                                                                             655
704
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660
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704 AA;
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113
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656
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VARSPLIC
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DR EMBL; M73322; AAA27397.1; ALF_SEQ.
DR PIK; BA2360; BA2360.
DR PIK; BA2360; BA2360.
DR PIK; BA2360; BA2360.
DR PIK; 104-SEP-97.
DR PDB; 17F4; 04-SEP-97.
DR PDB; 17F4; 04-SEP-97.
DR PDB; 17F4; 04-SEP-97.
DR InterPro; IPR001956; CBD_3:
DR InterPro; IPR001956; CBD_3:
DR InterPro; IPR001962; FMIII.
DR InterPro; IPR00130; Prenyl_site.
DR InterPro; IPR00130; Prenyl_site.
DR Pfam; PF00041; fn3; 1.
DR Pfam; PF00053; CBM_2; 1.
DR Pfam; PF00053; CBM_2; 1.
DR Pfam; PF00069; FMIYEIII.
DR PROSITE; PS00592; GLYCOSYL_HYDROL_F9_1; 1.
DR PROSITE; PS00592; GLYCOSYL_HYDROL_F9_2; 1.
DR PROSITE; PS00599; GLYCOSYL_HYDROL_F9_2; 1.
DR PROSITE; PS00599; GLYCOSYL_HYDROL_F9_2; 1.
DR PROSITE; PS00599; GLYCOSYL_HYDROL_F9_1; 1.
DR PROSITE; PS0059
                                                                                                                                                                                                                                                                                                       HYDROLASES).
-!- SIMILARITY: CONTAINS 1 FUNGAL-TYPE CELLULOSE-BINDING DOMAIN (CBD).
"Structure and mechanism of endo/exocellulase E4 from Thermomonospora
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Pred. No. 67;
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0; Mismatches
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Matches 10; Conservative
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Search completed: June 6, 2003, 11:01:30 Job time : 3.50788 secs

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Q8vcq7 mus musculu Q8vcq7 mus musculu Q91782 arabidopsis Q917e3 drosophila Q9v560 drosophila Q9v560 drosophila Q9bid7 arabidopsis Q9big7 arabidopsis Q9big2 homo sapien Q8s568 oryza sativ Q9ns7 leishmania Q9ns7 leishmania
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Q8us87 human immun
Q910d4 streptomyce
Q98gw6 rhizobium 1
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1589.904 Million cell updates/sec
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                                                                 ; Search time 5.31349 Seconds
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1 GKRRAKALRWTRQKSVEEGE.....POGGEGPRSRPAAESTGLEA
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Q8S5D8
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Q42174
Q8S835
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Q9L0D4
Q98GW6
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Q9VRV3
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Gapop 10.0 , Gapext 0.5
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sp_human:*
sp_invertebrate:*
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sp_mhc:*
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sp_phage:*
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                                                                                                                                                                                                                                                                                                                                                                                                                            sp_plant:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                  sp_virus:*
                                                                                                                                                                                                                                                                                                                 SPTREMBL_21:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        958
136
314
486
793
330
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Match 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28.0
28.0
28.0
28.0
27.8
27.8
27.6
27.6
27.1
27.1
                                                                  June
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Perfect score:
                                                                                                                                                        Scoring table:
                                                                                                                                                                                                                                                                                                                 Database :
                                                                                                                                                                                        Searched:
                                                                                                                                    Sedneuce:
                                                                  Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Result
                                                                                                             Title:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         No.
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Q9qy66 mus musculu Q941u8 oryza sativ Q9as24 oryza sativ Q69020 human herpe Q8sq03 canis famil	Q8yb61 brucella me Q95qa7 caenorhabdi Q95qa6 caenorhabdi Q95qa8 caenorhabdi	09rkc5 streptomyce Q9sni9 oryza sativ Q9h7/7 homo sapien Q12845 homo sapien	Q8xU84 neurospora Q91ch6 macropodid Q8y15 ralstonia s Q8xq57 ralstonia s Q90xe6 leucopsario		Q8ty7 methanopru Q91h7 streptomyce Q8tal4 homo sapien Q9zba9 streptomyce
Q9QY66 Q941U8 Q9AS24 Q69020 Q8SQ03	_08%b61 0950a7 0950a6 0950a8	Q9RKC5 Q9SNI9 Q9H7J7 Q12845	Q8X0S8 Q91CH6 Q8X1J6 Q8XQ57 Q90WE6	284X67 284X67 294X15 294X10 285Z07 285Z07	Q8TY27 Q93JH7 Q8TAL4 Q9Z5A9
11 10 10 12	19 22 22	911440	112 116 117	10110110	17 16 16 16
399 516 88 198	565 603 663 706	952 952 278 278	367 1234 246 304 326 435	4 C C C C C C C C C C C C C C C C C C C	618 673 673 943
27.1 27.1 26.9 26.9 26.9	26.9 26.9 26.9 26.9	26.6 26.6 26.4 26.4	222222 20222 40222 4022 4022 4032 40	, c,	25.9 25.9 25.9 25.9
58 58 57.5 57.5	57.5 57.5 57.5 57.5	57 56.5 56.5	o o	1 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	000000 000000 0000000
17 18 19 20 21	2222	28 28 29 88		3 3 3 4 4 4 4 9 9 9 9 9 9 9 9 9 9 9 9 9	4443

ALIGNMENTS

RESULT 1

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Gaps
                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                   .;
0
                                                                                                                                                                                                                                        30.4%; Score 65; DB 11; Length 399; 47.1%; Pred. No. 3.2;
                                                                                                                                                                       Strausberg R.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC019440; AAH19440.1; -.
SCARB8342B56932B CRC64;
                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                              081782, 01-NOV-1998 (TrEMBLrel. 08, Created) 01-NOV-1998 (TrEMBLrel. 08, Last sequence update) 01-OCT-2000 (TrEMBLrel. 15, Last annotation update) Hypothetical 56.2 kDa protein.
                                 01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Open reading frame 6.
                                                                                                                                                                                                                                                                 15;
                                                                                                                                                                                                                                                                                                           3 RRAKALRWIRQKSVEEGEPPGQGEGPRSRPAAES 36
          399 A.A.
                                                                                                                                                                                                                                                                                                                                                                                    493 AA.
                                                                                                                                                                                                                                                                 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arabidopsis thaliana (Mouse-ear cress).
          PRT;
                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                    16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
          PRELIMINARY;
                                                                                       Mus musculus (Mouse)
                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                 SEQUENCE FROM N.A. TISSUE-LIVER;
                                                                                                                            NCBI_TaxID=10090;
                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                         Local
                         Q8VCQ7;
                                                                                                                                                                                                                                                                                                                                                                                    081782
          Q8VCQ7
                                                                                                                                                                                                                                                         Best Loc
Matches
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081782
28VC07
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Q917E4
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Q917E4
            RRAPA RRAPA BRAPA 
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RA Addams M.D., Celniker S.E., Holt R.A., Hoskins R.A., Galle R.F.,
RA Addams M.D., Celniker S.E., Richards S., Ashburner M., Henderson S.N.,
Bacorge R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Button G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H.C., Blazej R.G., Champe M., Pfelffer B.D.,
RA Man K.H., Doyle C., Baxrer E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Barxendell D., Bayraktaroglu L., Beaaley E.M.,
RA Ballew R.M., Basu A., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P.,
RA Borkova D., Botcher A., Bouck J., Cadieu E., Center A., Chadra I.,
RA Burtis K.C., Busam D.A., Buller H. G. Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Gann P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Jalali M., Kalush F., Karpen G.H., Ke.J., Kenjison J.A., Ketchum K.A.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda: Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14;
                                                                                                                                                                        Rieger M., Mueller-Auer S., Zipp M., Schaefer M., Hoheisel J., Mewes H.W., Mayer K.F.X., Schueller C., Bevan M.; Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
Rieger M., Mueller-Auer S., Zipp M., Schaefer M., Mewes H.W.,
Lemcke K., Mayer K.F.X.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29.0%; Score 62; DB 10; Length 493; 35.6%; Pred. No. 9.6; Ative 7; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 RRAKALRWT------RQKSVEEGEPPGQGEGPRSRPAAESTG 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                       EU Arabidopsis sequencing project;
Submitted (WAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AL031004; CAA19758.1; -.
EMBL; AL161579; CAB79883.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein.
SEQUENCE 493 AA; 56230 MW; 0F13F7890EFEA920 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hig protein (GH23986p).
HIG OR CG2040.
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NCBL_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 29.0%
Best Local Similarity 35.65
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
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                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                 NCBI_TaxID=3702;
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Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
Melson D.R., Nelson K.A., Nixon K., Nussern D.R., Pacche J.M.,
Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
Shue B.C., Siden-Kiamos I., Simpson M., Stupski M.P., Smith T.,
Spier E., Spradling A.C., Texpleton M., Strong R., Sun E.,
Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
Wang Z.Y., Wasaarman D.A., Neinstock G.M., Weissenbach J.,
Manilams S.M., Woodage T., Worley K.C., Wu D., Yang S., Zhon Q.A.,
Milliams S.M., Woodage T., Worley K.C., Wu D., Yang S., Zhon Q.A.,
Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
Glibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
The genome sequence of Dissophila melanogaster.";
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MEDIATE-EARGEDING,
MEDIATE-EARGEDING,
MEDIATE-EARGEDING,
MEDIATE S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Mogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Stableton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
Nunco J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K.,
Yu C., Lewis S.E., Rubin G.M., Celniker S.,
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AV069188; AAG22297.1; -.
HSSP; P10998; 1VVD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28.7%; Score 61.5; DB 5; Length 866; 36.8%; Pred. No. 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART; SM0032; CCP; 4.
SMART; SM00409; IG; 1.
SEQUENCE 866 AA; 96747 MW; FOFFEGEC20608BED CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    :| :: || |::| | :| | 358 QRDRSPRWRRRRSTEFKGDLGQLPPESGIGPEPELAD 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 RRAKALRWTRQKSVE-EGE----PPGQGEGPRSRPAAE 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT; 933 AA.
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01-MAR-2001 (TrEMBLrel. 16, Last sequ
01-DEC-2001 (TrEMBLrel. 19, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Interpro; IPR003599; Ig.
Interpro; IPR003006; Ig_MHC.
Interpro; IPR002306; Selectin.
Interpro; IPR00436; Sushi_SCR_CCP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FlyBase; FBgn0010114; hig.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00047; ig; 1.
Pfam; PF00084; sushi; 4.
PRINTS; PR00343; SELECTIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2001 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
Hig protein.
HIG OR CG2040.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-BERKELEY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=BERKELEY;
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RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W., RA Posler C., Gabrariellan A.B., Gang N.S., Galbart W.M., Glasser K., Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Harvey D., Heiman T.J., Hernandez J.R., Houck J., RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J., RA Harris N.L., Havey D., Kardt C., Kravitz S., Kulp D., Lai Z., Jalai M., Kalush F., Karpen G.H., Kee Z., Kennison J.A., Ketchum K.A., Jalai M., Kalush F., Karpen G.H., Kee Z., Kennison J.A., Ketchum K.A., Jalai M., Mattei B., McIntosh T.C., Morris J., Moshrefi A., Mourt S.M., Moy M., Murphy B., Murphy B., Mpherson D., Morris J., Moshrefi A., Mourt S.M., Woy M., Murphy B., Murphy B., Morris J., Moshrefi A., Mour S.M., Nosy M., Murphy B., Muskern D.R., Pacleb J.M., Raleson D.R., Nelson K.A., Sunder K.B., Smith T., Sander Klamos I., Simpson M., Stupski M.P., Smith T., Shong R.A., Weinsenbach J., Wang X., Walsenbach J., Wang X., Wang Z.-Y., Wassarman D.A., Weinsenbach J., Wang X., Jahen G. Jane R.A., Robi R.A., Mondage T., Wonley K.C., Wu D., Yang S., Yao Q.A., R. Jaheng X.H., Zhong F.N., Robi M., Nelson W., Rabing S.M., Woodage T., Wonley K.C., Wu D., Yang S., Zhu X., Smith H.S., Reiner E., Sperdling A.C., Stapleton M., Strong S., Zhao Q., Zhao G., Zhao M., Sheng X.H., Zhong F.N., Zhong W., Zhan M., Zhu S., Zhu X., Zhu S., Zhu X., Zhu S., Zhu X., Zhu S., Zhu K., Shin H., Shin R. H., Zhong F.N., Zhong W., Weissenbach J., The Genome sequence of Drosophila melanogaster.";

R. Schence 207: 2195-2195-206:1: -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster (Fruit fly).

Ekaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophilidae;

NCBL_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .;
S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28.7%; Score 61.5; DB 5; Length 933; 36.8%; Pred. No. 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         933 AA; 104178 MW; 9C0B696854C6C9FA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      328 QRDRSPRWRRRRSTEFKGDLGQLPPESGIGPEPEPLAD 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 RRAKALRWIRQKSVE-EGE----PPGQGEGPRSRPAAE 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        958 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 22;
8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAY-2000 (TrEMBLrel. 13, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR003599; 1g. /
InterPro; IPR003005; 1g_MHC.
InterPro; IPR002306; Selectin.
InterPro; IPR000436; Sushi_SCR_CCP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=BERKELEY;
MEDI.INE=20196006; PubMed=10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FlyBase; FBgn0010114; hig.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00047; ig; 1.
Pfam; PF00084; sush1; 5.
PKINTS; PR00343; SELECTIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 36.8
nes 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART; SM00032; CCP; 5.
SMART; SM00409; IG; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HSSP; P10998; IVVD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HIG protein.
HIG OR CG2040.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Si
Matches 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      098860
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Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Button G.G., Wortman J.R., Yandell M.D., Zhang Q., Chan L.X.,
Brandon R.C., Rogers Y.-H.C., Blazel R.G., Champe M., Pfeiffer B.D.,
RA Brandon R.C., Ragers Y.-H.C., Blazel R.G., Champe M., Pfeiffer B.D.,
RA Ballew R.M., Basul A., Baxandale J., Rayraktaroglu L., Beasley E.M.,
Ballew R.M., Basul A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Beson K.Y., Benos P.V., Derman B.P., Bhandari D., Bolshakov S.M.
Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis M.L., Cawley S., Dahlke C., Davarenport L.B., Davies P.,
RA Ge Pablos B., Delcher A., Deng Z., Mays A.D., Dew I. Dietz S.M.,
Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Burtis M.L., Evangelista C.C., Ferraz C., Ferriac S., Fleischman W.,
RA Goog F., Gorrell J.H., Gu Z., Guan P., Harris M.L.,
RA Hostin D., Harvey D., Heinan T.J., Heinandez J.R., Houck J.,
RA Hostin D., Harvey D., Heinan T.J., Wei M.-H., Degwan C.,
Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
Jalali M., Mattei B., Murphy B., Murphy L., Muzzy D.M., Nelson D.L.,
Mount S.M., Moy M., Murphy B., Murphy L., Muzzy D.M., Nelson D.L.,
Rangson D.R., Pettann G.S., Pan S., Pollard J., Moshrefi A.,
Rhenert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
Spier E., Spradling A.C., Stapleton M., Stupski M.P., Santh T.,
Rhe Spier E., Spradling A.C., Stapleton M., Stupski M.P., Santh T.,
Rhe Spier E., Spradling A.C., Stapleton M., Stupski M.P., Santh T.,
Rhe Spier E., Spradling A.C., Stapleton M., Stupski M.P., Santh T.,
Rhe Spier E., Spradling A.C., Stapleton M., Stupski M.P., Santh R.,
Rhiams S.M., Woodage T., Worley K.C., Mu W., Stupski M.P., Santh H.,
Rhench S.H., Myers E.W., Robin G.W., Weiter J.C.,
Rhench S.H., Reserved J.S., Shon M., School S.H., R.P., Zaveri J.S., School S., School S., School S., School S., School S., 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5
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Arabidopsis thaliana (Mouse-ear cress).

Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.

NCBI_TaxID-3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ŝ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                107027 MW; 7B2A08477672E674 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          328 QRDRSPRWRRRSTEFKGDLGQLPPESGIGPEPELAD 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 RRAKALRWIRQKSVE-EGE----PPGQGEGPRSRPAAE 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     136 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR003599; Ig. InterPro; IPR003006; Ig.MHC. InterPro; IPR002396; Selectin. InterPro; IPR000436; Sushi_SCR_CCP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Science 287;2185-2195(2000).
EMBL; AE003834; AAF58960.1;
HSSP; P10998; 1VVD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PR00343; SELECTIN.
SMART; SM00032; CCP; 5.
SMART; SM00409; IG; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FlyBase; FBgn0010114; hig.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00047; ig; 1.
Pfam; PF00084; sushi; 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       958 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          042174;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 6
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STRAIN=COLUMBIA;
                                                                                          Nakamura Y.;
                                                                                                                                                                                                                                                                                Ecker J.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Ecker J.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9H5Z2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9H5Z2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 9
Q9H5Z2
 δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5
                                                                                                                                                                         ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-007-2000 (TrEMBLrel. 15, Created)
01-007-2000 (TrEMBLrel. 15, Last sequence update)
01-007-2000 (TrEMBLrel. 15, Last sequence update)
01-007-2002 (TrEMBLrel. 21, Last annotation update)
Genomic DNA, chromosome 3, Pl clone: WM133 (AT342640/MWI23_1).
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II: Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 McCombie W.R., Cordum H., Minx P., de la Bastide M., Spiegel L.,
Nascimento L., Zutavern T., Balija V., Bell M., Baker J., Santos L.,
Miller B., Katzenberger F., Muller S., Preston R., Kirchoff K.,
                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Pracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kuit K., King L., Yang C., O'Sahughnessy A., Palmer L., Dedhia N.,
Wilson R.;
                                    Raynal M., Grellet F., Laudie M., Meyer Y., Cooke R., Delseny M.; Submitted (NOV-1993) to the EMBL/GenBank/DDBJ databases. EMBL; 227252; CAA81765.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5;
                                                                                                                                                                         5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Genomic sequence for Oryza sativa, Nipponbare strain, clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            / Match 28.0%; Score 60; DB 10; Length 314; Local Similarity 43.9%; Pred. No. 11; Local 8; Conservative 6; Mismatches 15; Indels
                                                                                                                                             28.0%; Score 60; DB 10; Length 136; 56.5%; Pred. No. 4.5; Alswatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OSJNBa0053D03, from chromosome 10, complete sequence.";
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AC021892; AAM00958.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical protein.
SEQUENCE 314 AA: 32758 MW; 0156F123C759B2C0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  S3 RRRPSARRSSARESGEEGETEGTVHGSPRDTRTAETTNGVE 123
                                                                                                                   136 AA; 15542 MW; EA2AFD6490BE13C1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 KRRAKALRWTRQKSVEEGEPPGQGEG-PRSRPAAEST-GLE 40
                                                                                                                                                                                                                                                                                                                       01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 32.8 kDa protein.
0SJNBA0053D03.22.
                         TISSUE=DRY SEEDS OF A.THALIANA ECOTYPE COLUMBIA;
                                                                                                                                                                                                                                                                                                 314 AA.
                                                                                                                                                                                                    16 VEEGEPPGQG--EGPRSRPAAES 36
                                                                                                                                                                                                                             29 IDEFEPPQQGEQEGPRRPGGGS 51
                                                                                                                                                                                                                                                                                                 PRT;
                                                                       Interpro; IPR001113; Seedstore_7s. Pfam; PF00546; Seedstore_7s; 1. NON_TER 136 136
                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                           Oryza sativa (Rice).
                                                                                                                                                            Best Local Similarity
[1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=NIPPONBARE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=4530;
                                                                                                                                                                         13;
                                                                                                                     SEQUENCE
                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          091037;
                                                                                                                                                                                                                                                                                                 088835
                                                                                                                                                                                                                                                                                                            088835;
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                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                   RESULT 7
Q8S835
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RR RR RR RR DR DR DR DR SQ
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SEQUENCE FROM N.A.
1258DE-ILEAL MUCOSAS,
Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T., Matsumura K.,
Nakajama T., Mizuno T., Morinaga M., Tanigami A., Fujiwara T., Ono T.,
                                                                                                                                                                                                                                                                                                                                                                              Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Banh J.,
Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin-Nemnann G.,
Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M.,
Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai T.,
Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,
Pammanra Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Satou M.,
                                                                                                                                                                                                           "Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequen features of the regions of 4,504,864 bp covered by sixty Pl and TAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
Kim C.J., Chen H., Cheuk R., Meyers M.C., Shinn P., Banh J.,
Bowser L., Carninci P., Chang E., Dale J.M., Goldsmith A.D.,
Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G.,
Kawai J., Lam B., Lee J.M., Lin J., Miranda M., Narusaka M.,
Nguyen M., Onodera C.S., Palm C.J., Quach H.L., Sakurai T., Satou M.
Seki M., Southwick A., Tang C.C., Toriuni M., Wu H.C., Yamada K.,
Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID=9606;
Sato S., Nakamura Y., Kaneko T., Kato T., Asamizu E., Tabata S.;
Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28.0%; Score 60; DB 10; Length 486;
56.5%; Pred. No. 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Arabidopsis cDNA clones.";
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Arabidopsis ORF clones.";
Submitted (MAF-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; A805203; BAB01239.1; -.
EMBL; AY058085; AAL24193.1; -.
EMBL; AY058087; AAL90968.1; -.
HASSP; POABS3; 2PHL.
HASSP; POABS3; 2PHL.
InterPro; IPR001064; Crystallin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                325ECF68D9A6345B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
CDNA: FLJ22757 fis, clone KAIA0803.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 02808; Seedstore_7s_C; 1.
PS00225; CRYSTALLIN_BETAGAMMA; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16 VEEGEPPGQG -- EGPRSRPAAES 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IDEFEPPQQGEQEGPRRPGGGS 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001113; Seedstore_7s.
Pfam; PF00546; Seedstore_7s; 1.
Pfam; PF02808; Seedstore_7s_C; 1.
                                                                                                                                                   MEDLINE=20277480; PubMed=10819329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                55063 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        56.5%;
                                                                                                                                                                                                                                                                                                   DNA Res. 7:131-135(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   486 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                             SEQUENCE FROM N.A.
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A Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
Gonzalez M., Guarin H., Li P., Lio G., Miranda A., Mungall C.J.,
A Nunco J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K.,
Xu C., Lewis S.E., Rubin G.M., Celniker S.;
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
BMBL; AYOSI740; AAK931641; -
RIPARSe; FERMO0350; CG10274.
InterPro; IPRO00130; Znf_CZH2.
InterPro; IPRO00130; Znf_CZH2.
R PROSITE; PSO0045; ZINC_FINGER C2H2_1; UNKNOWN_7.
RPOSITE; PSO0145; ZINC_FINGER C2H2_2; 9.
RPOSITE; PSO0145; ZINC_FINGER C3H2_2; 9.
RPOSITE; PSO0142; ZINC_FINGER C3H2_4; 9.
RPOSITE; PSO0145; ZINC_FINGER C3H2_5; 9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Eukaryota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophilia.
NCBL_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endoptera; Endop
                                                                                                                                                                                      Length 1400;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 5; Length 514;
                                                                                                                                                                                 27.8%; Score 59.5; DB 5; Length 1 36.4%; Pred. No. 60; ive 0; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                        Myler P.J.;
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AC005836, AAF35994.1; -.
SEQUENCE 1400 AA: 149577 MW; OCDCF4E925BEAEF4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20; Indels
                                                                                                                                                                                                                                                                                        183 KRVLRAIETYRQRQVEMGETPGEQFDNPPAPPVEGISIE 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 KRRAKALRWTRQKSVEEGEPPGQGEGPRSRPAAESTGLE 40
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       514 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 863 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27.6%; Score 59; DB 35.9%; Pred. No. 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila melanogaster (Fruit fly).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36.4%;
                                                                                                                                                                                                                                           16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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Best Local Similarity
Matches 16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
       SEQUENCE FROM N.A. STRAIN=FRIEDLIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-BERKELEY;
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CG10274.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 13
Q9VRV3
                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 12
Q961A3
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Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y., Ota T., Suzuki Y., Obayashi M., Nishi T., Shibahara T., Tanaka T., Nakamura Y., Isogai T., Sugano S.;
"NEDO human cDNA sequencing project.";
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
InterPro: IPR005112; ADBN.
InterPro: IPR005112; ADBN.
                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-WIPPOWBARE;
MCCOmbie W.R., de la Bastide M., Spiegel L., Preston R., Ferraro K.,
Kuit K., Mascimento L., Zutavern T., Balija V., Ball M., Baker J.,
Santos L., Miller B., Katzenberger F., Muller S., King L., Yang C.,
Dike S., O'Shaudhnessy A., Palmer L., Dedhia N.;
"Genomic sequence for Oryza sativa, Nippombare strain, clone
SCJNBDOQTAB19, from chromosome 10, complete sequence.";
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; ACI13339; AAM08880.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Leishmania major.
Eukaryota; Buglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
NCBI_TaxID=5664;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                  4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27.8%; Score 59.5; DB 10; Length 330; 37.2%; Pred. No. 13; vative 5; Mismatches 13; Indels 9,
                                                                                                                                                                                                                                                                                                                                                          28.0%; Score 60; DB 4; Length 793; 50.0%; Pred. No. 28; tive 4; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 KRRAKALRWIRQKSVEEGEPPGQGEGPRS---RPAAESTGLEA 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       38 RRRFAALRWRR-----GGPPVTARGPQATARQPLATMRGSQA 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein.
SEOUENCE 330 AA: 37674 MW; 01AD287515E7DD43 CRC64;
                                                                                                                                                                                                                                                                                                             793 AA; 86230 MW; 3F37ACA836F24AF4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 37.7 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              504 GKNR--PLRPSRRRQLEEGTSEPPGAGTPPLS 533
                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GKRRAKALRWIRQKSVEEG--EPPGQGEGPRS 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             330 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT; 1400 AA.
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01-0CT-2000 (TrEMBLrel. 15, Last sequ
01-DEC-2001 (TrEMBLrel. 19, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ehrhartoideae; Oryzeae; Oryza
                                                                                                                                                                                                         InterPro; IPR005113; uDENN.
Pfam: PF03455; dDENN; 1.
Pfam: PF02141; DENN; 1.
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Matches 16; Conservative
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                                                                                                                                                                                                                                                                                        uDENN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oryza sativa (Rice).
                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
hes 16; Conserv
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                                                                                                                                                                                                                                                                                     Pfam; PF03456;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-2000
01-DEC-2001
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Retroid viruses; Retroviridae; Lentivirus.
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                                          NCBI_TaxID=11676;
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                                                                                                                                                               STRAIN=99CMLB33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Polyprotein.
NON_TER
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                                                                                                                                  Adding M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amantides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.E., Tandell N.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazel R.G., Champe M., Preiffer B.D.,
Wan K.H., Doyle C., Baxerer E.G., Helt G., Nelson C.R., Miklos G.L.G.,
Abril J.F., Agbayani A., An H.-J., Andrews Pfannkoch C., Baldwin D.,
Ballew R.M., Basu M. Baxendale J., Bayraktaroly L.,
Besson K.Y., Benos P.V., Berman B.P., Hhandari D., Bolshakov S.,
RA Berson K.Y., Benos P.V., Berman B.P., Hhandari D., Bolshakov S.,
RA Berson K.Y., Busam D.A., Buller H., Cadleu E., Center A., Chandra R.,
Butris K.C., Subsam D.A., Dalke C., Davenport L.B., Davies P.,
RA Cherry J.W., Cawley S., Dahlke C., Davenport L.B., Davies S.,
RA Cherry J.W., Cawley S., Dahlke C., Perraz C., Ferriera S., Platez S.M.,
RA Cherry J.W., Edyngelista C.C., Ferraz C., Ferriera S., Platez S.M.,
RA Adalim M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum X.A.,
RA Harris N.J., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Alalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum X.A.,
RA Kammel B.E., Kodira C.D., Kratt C., Kravitz S., Kulp D., Lal Z.,
RA Alasko P., Lei Y. Warpen G.H., Ke Z., Kennison D.L.,
RA Kalush F., Nelson K.A., Nixon K., Nussern D., Merkulov G., Milshina N.V. Mobartry C., Morris J., Puri N., Mallen B.M., Walberler E., Shen H.,
Ralasko P., Lei Y., Wassarman D.A., Worley C., Worris J., Puri, V. Reinert K., Remighton K., Saunders R.D., Chrod R., Siden K., Nelson D.L.,
RA Spier E., Spradling A.C., Stapleton M., Stuppski M.P., Smith T.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q., A.,
RA Mennell S. Sharman D.A., Weinstock G.M., Weissenbach J.,
RA Weinert K., Remighton R., Standers R., Verley S., Yao Q., Shen R.,
Raderner S., Shen R., Rody W., Shill G., Shen R., Shen R., Shen R., Shen R., Shen 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00096; z1-Czuz, ...; SMARY; SM0035; znF-Czuz; 12. SMARY; SM00355; znF-Czuz; 12. PROSITE; PS00028; ZINC_FINGER_CZHZ_1; 10. PROSITE; PS00142; ZINC_FINGER_CZHZ_2; 12. PROSITE; PS00142; ZINC_FINGER_CZHZ_2; 12. DNA binding; Metal-binding; Zinc-finger. Suc. 3 Section 10 Se
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01-MAR-2002 (TrEMBLrel. 20, Last Sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27.6%; Score 59; DB 5; 35.9%; Pred. No. 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human immunodeficiency virus type 1.
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InterPro; IPR000130; Zn_MTpepidse.
                                                                                                                 MEDLINE=20196006; PubMed=10731132;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
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Tebit D.M., Zekeng L., Kaptue L., Salminen M., Krausslich H.G.,
Herchenroder O.;
"Genotypic and Phenotypic Analysis of HIV Type I Primary Isolates from
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                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K., Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-A3(2) / Mi45;
Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
Harper D., Bateman A., Brown S., Chendra G., Chen C.W., Collins M.,
Crohin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,
Rabbinowitsch E., Rajandream M.A., Rutherford K., Stuter S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                 ä
                                                                                                                                                                                                                                                                                                                                   27.3%; Score 58.5; DB 15; Length 207; 42.4%; Pred. No. 11; Live 3; Mismatches 15; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cerdeno A.M., Parkhill J., Barrell B.G., Rajandream M.A., Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Saunders D.C., Harris D.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                             207 AA; 23082 MW; D99E86CA6421EE21 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                              175 BAAEWDRLHPVQAGPHPFGQLRDFRGRDIAGTT 207
                                                                                                                                                                                                                                                                                                                                                                                                                      6 KALRWTRQKSVEEG-EPPGQGEGPRSRPAAEST 37
                                                                                     Western Cameroon.";
AIDS Res. Hum. Retroviruses 18:39-48(2002).
EMBL; AF355294; AAL68724.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   277 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
MEDLINE=21663212; PubMed=11804555;
                                                                                                                                            InterPro; IPR000721; Gag_p24.
InterPro; IPR000071; Retrovir_p17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=97000351; PubMed=8843436;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30S ribosomal protein S3. RPSC OR SCO4708 OR SCD31.33.
                                                                                                                                                                                        Pfam; PF00540; Gag_p17; 1.
Pfam; PF00607; Gag_p24; 1.
                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptomyces coelicolor
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Les 14; Conserv
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June 6, 2003, 10:59:34 ; Search time 2.44133 Seconds (without alignments) 494.132 Million cell updates/sec
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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Description	Sequence 8, Appli Sequence 2, Appli Sequence 127, App Sequence 1287, App Sequence 4, Appli Sequence 4, Appli Sequence 40, Appl Sequence 40, Appl Sequence 40, Appl Sequence 40, Appl Sequence 40, Appl Sequence 40, Appl Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 7, Appli	
SUMMARIES	05-08-927-219-8 0S-08-927-219-2 0S-08-927-219-2 0S-08-927-219-12 0S-08-927-219-12 0S-08-91-95-65-4 0S-08-98-709A-50 0S-08-98-709A-50 0S-09-055-589-40 0S-09-565-588-40 0S-09-565-588-40 0S-09-565-588-40 0S-09-565-588-40 0S-09-565-588-40 0S-09-565-13-13 0S-08-139-780-3 0S-09-138-1030-7 0S-09-138-1030-7 0S-09-146-4854-7 0S-09-164-671-7	
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	8 AAPPI AAPP	NE:
00000 444 00000 4444 0000 0000 0000 00000 00000000	T 1 927-219-8 uence 8, Application US, ent No. 6187533 NERAL INFORMATION: APPLICANT: Yamagata, K, APPLICANT: Yamagata, K, APPLICANT: Yamagata, K, APPLICANT: Yamagata, K, APPLICANT: Kaisski, INTELECTONT: Wencel, Stepticant: Furuta, Hiva APPLICANT: Horikawa, Y, APPLICANT: Houston GEINVERSE OF INVENTION: GEINVERSE OF INVENTION: GEINVERSE OF INVENTION: GEINVERSE OF INVENTION: AND STREETS: P.O. BOX 443 STREET: P.O. BOX 443 STREET: P.O. BOX 443 STREET: IBM PC COMPOUTER: IB	OMMU EPHC EFAX TION
	1 927-21 ence 8 ence 8 eprica 927-21 eprica 927-21 pplica	ELEC TEL TEL ORMA
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APPLICANT: HOLIKAWA, YUKIO

APPLICANT: MEDICAL, SEPPHEN
TITLE OF INVENTION: MUTATIONS IN THE DIABETES SUSCEPTIBILITY
TITLE OF INVENTION: GENES HEPATOCYTE NUCLEAR FACTOR (HNF) I ALPHA, HNF-1BETA
TITLE OF INVENTION: AND HNF-4ALPHA
NUMBER OF SEQUENCES: 147
CORRESPONDENCE ADDRESS:
    Gaps
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    18; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDULM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: Patentin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: CONCULTENTLY HEREWITH
CLASSIFICATION NUMBER: US 60/029,679
FILING DATE: 30-OCT 1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/028,056
FILING DATE: 02-OCT -1996
PRIOR APPLICATION DATA:
FILING DATE: 10-SPP-1996
PRIOR APPLICATION NUMBER: US 60/025,719
FILING DATE: 10-SPP-1996
ATTORREY AGENT INFORMATION:
NAME: WILSON, MATER B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          271 REKEEAFRHKLAMDIYSGPPPGPGPGP-ALPAHSSPGL 307
                                            2 KRRAKALRWIRQKSVEEGEPPGQGEGPRSRPAAESIGL 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 KRRAKALRWIRQKSVEEGEPPGQGEGPRSRPAAESTGL 39
    4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: ARCD:272
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arnold, White & Durkee
                                                                                                                                                                                     Sequence 4, Application US/08927219; Patent No. 6187533; Fatent No. 618753; APPLICANT: Bell, Graeme I.; APPLICANT: Yamagata, Kazuya; APPLICANT: Oda, Naohisha; APPLICANT: Kaisaki, Pamela J.; APPLICANT: Furuta, Hiroto
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TELEFAX: 512/474-7577
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amino acid
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 39.55
Matches 15; Conservative
    15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: P.O. Box 4433
CITY: Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Wilson, Mark B. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; MOLECULE TYPE: protein US-08-927-219-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Texas
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                                                                                                                                                                        US-08-927-219-4
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    Matches
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APPLICANT: Kaisaki, Pamela J.
APPLICANT: Euruta, Hiroto
APPLICANT: Horitawa, Yukio
APPLICANT: Horitawa, Yukio
APPLICANT: Horitawa, Yukio
APPLICANT: Horitawa, Yukio
APPLICANT: Monzel, Stephen
TITLE OF INVENTION: MUTANTION: IN THE DIABETES SUSCEPTIBILITY
TITLE OF INVENTION: AND HNF-4ALPHA
TITLE OF INVENTION: AND HNF-4ALPHA
CORRESSORDENCES: 147
CORRESSORDENCES: 147
ADDRESSEE: Annold, White & Durkee
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Pred. No. 3.6;
                                                                                                                             Score 61.5; DB 4; Length 415; Pred. No. 2.2;
                                                                                                                    28.7%; Score bi...;
39.5%; Pred. No. 2.2;
39.5%; Pred. Mismatches 18; Indels
..ive 4; Mismatches 18; Indels
                                                                                                                                                                                                                                           2 KRRAKALRWIRQKSVEEGEPPGQGEGPRSRPAAESIGL 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/028,056
FILING DATE: 02-0CT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/025,719
FILING DATE: 10-SEP-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/927,219
FILING DATE: Concurrently Herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Arnold, White & Durkee STREET: P.O. Box 4433 CITY: Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/029,679
FILING DATE: 30-0CT-1996
                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/08927219
Patent No. 618753
GENERAL INFORMATION:
APPLICANT: Bell, Graeme I.
APPLICANT: Yamagata, Kazuya
APPLICANT: Oda, Naohisha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        512/418-3000
LENGTH: 415 amino acids
                                                                                                                                                 Best Local Similarity 39.59
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Wilson, Mark B.
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; MOLECULE TYPE: protein US-08-927-219-2
                                                            MOLECULE TYPE: protein
                      TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amino acid
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Best Local Similarity
                                            linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: Tea...
SCOUNTRY: USA
77210
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                                                              ; MOLECULE T1
US-08-927-219-8
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Gaps
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APPLICANT: Forton, Barbara
APPLICANT: Row, Hung-Tab.
TITLE OF INVENTION: DNA ENCODING THE HUMAN SYNAPSIN III GENE
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
STREET: 411 Hackensack Ave, Continental Plaza, 4th
STREET: Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 60, DB 4; Length 187;
Pred. No. 1.4;
6; Mismatches 16; Indels
APPLICANT: Tan, Man-Wah
APPLICANT: Cao, Hui
APPLICANT: Cao, Hui
APPLICANT: Trongalis, Eliana
APPLICANT: Trongalis, John
TITLE OF INVENTION: VIRULENCE-ASSOCIATED NUCLEIC ACID
TITLE OF INVENTION: SEQUENCES AND USES THEREOF
FILE REFERENCE: 0786/361002
CURRENT APPLICATION NUMBER: 19509/199,637A
CURRENT FILING DATE: 1998-11-25
PRIOR APPLICATION NUMBER: 60/066,517
PRIOR FILING DATE: 1997-11-25
NUMBER OF SEQ ID NOS: 437
SOFTWARE: FastSEQ for Mindows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GKRRAKALRWIRQ-----KSVEEGEPPGQGEGPRSRPAAEST 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              47 GRRANGARRWIRRLPPRPGRSLADAAPAPCAAASRARPRASSI 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 600-1-202
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/906,865 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 4, Application US/08906865; Patent No. 6040168; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Pseudomonas aeruginosa
US-09-199-637A-287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
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INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 696 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 28.0%;
Best Local Similarity 34.9%;
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
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New Jersey
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: U
                                                                                                                                                                                                                                                                                                                      SEQ ID NO 287
LENGTH: 187
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STATE:
                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
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                                                                                        DEBUGANT: Bell, Graeme I.

APPLICANT: Yamagata, Kazuya
APPLICANT: Yamagata, Kazuya
APPLICANT: Yamagata, Kazuya
APPLICANT: Kaisaki, Pamela J.
APPLICANT: Kaisaki, Pamela J.
APPLICANT: Rorikaw, Yukio
APPLICANT: Horikaw, Horikaw, Horibeta
TITLE OF INVENTION: AND HIF-4ALPHA
NUMBER OF SEQUENCES: 147
CORRESPONDERCE ADRICASS:
ADDRESSEE: Arnold, White & Durkee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ij
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CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/927,219
FILING DATE: CONCULTENTLY HETEWITH
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/029,679
FILING DATE: 30-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/028,056
FILING DATE: 10-OCT-1996
FILING DATE: 10-SEP-1996
APPLICATION NUMBER: US 60/025,719
FILING DATE: 10-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MATK B.
REGISTRATION NUMBER: ARCD:272
TELECOMMUNICATION NUMBER: ARCD:272
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          271 RKKEEAFRHKLAMDTYSGPPGPGPGP-ALPAHSSPGL 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 KRRAKALRWTRQKSVEEGEPPGQGEGPRSRPAAESTGL 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                           Sequence 127, Application US/08927219 Patent No. 6187533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rahme, Laurence G.
Mahajan-Miklos, Shalina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Ausubel, Frederick
APPLICANT: Goodman, Howard M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: 512/418-3000
TELEFAX: 512/474-7577
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3est_Local Similarity 39.5
Watches 15; Conservative
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                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: US
ZIP: 77210
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US-09-199-637A-287
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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Sequence 40, Application US/08820170A
Patent No. 5831058
GENERAL INFORMATION:
APPLICANT: Taxtomu, FUJIWARA
APPLICANT: Taxeshi, WATANABE
APPLICANT: Toyomasa, KATAGIRI
TILE OF INVENTION: HUMBE
MUMBER OF SEQUENCES: 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 536
TELECHONE: (202) 293-7060
TELEPHONE: (202) 293-7060
TELEFAX: (202) 293-7860
TELEFAX: (202) 293-7860
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
  REGISTRATION NUMBER: 33,779
                                                                                                                                                                                                                                                                                                                                                  Query Match 24.3%;
Best Local Similarity 40.0%;
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : 499 amino acids
amino acid
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                                                                                                                                                                                                                                                                           internal
                                                                                                                                                                             single
                                                                                                                                                                                                                MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: sir
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
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                                                                                                                                                                                                                                                                     ; FRAGMENT TYPE: i
; ORIGINAL SOURCE:
US-08-984-709A-50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                    HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-820-170A-40
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                                                                                                                                                                                                                                                       ANTI-SENSE:
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                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                              APPLICANT: POTCOT, BATCATA
APPLICANT: POTCOT, BATCATA
APPLICANT: RAO, HUNG-Teh
TITLE OF INVENTION: DNA ENCODING THE HUMAN SYNAPSIN III GENE AND USES
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
CURRENT APPLICATION NUMBER: US/09/129,668B
CURRENT APPLICATION NUMBER: US/09/129,668B
EARLIER FILING DATE: 1998-08-05
EARLIER FILING DATE: 1997-08-06
NUMBER OF SEQ ID NOS: 8
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Sequence 50, Application US/08984709A
Patent No. 632003.
GENERAL INFORMATION:
APPLICANT: Williams, Mark E.
APPLICANT: Stauderman, Kenneth A.
APPLICANT: Harpold, Michael M.
TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND TITLE OF INVENTION: METHODS.
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
                                                       Score 59, DB 3; Length 696;
Pred. No. 8.6;
4; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 4; Length 696;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 59; DB 4
Pred. No. 8.6;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     516 QOPASQAAPPTQGQGRQSRPVAGGPG 541
                                                                                                                                      13 OKSVEEGEPPGGGEGPRSRPAAESTG 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13 QKSVEEGEPPGQGEGPRSRPAAESTG 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/984,709A
FILING DATE: 02-DEC-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                       Sequence 4, Application US/09129668B Patent No. 6429010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fast56Q Version 1.5
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seidman, Stephanie L.
                                                         27.6%;
42.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 27.6%;
Best Local Similarity 42.3%;
Matches 11; Conservative
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IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 4
                                                           Query Match 27.69
Best Local Similarity 42.33
Matches 11; Conservative
    Homo sapiens
                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Greengard, Paul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapiens
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ORGANISM:
                                                                                                                                                                                                                                    RESULT 7
US-09-129-668-4
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        ; ORGANISM
US-08-906-865-4
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REFERENCE/DOCKET NUMBER: 24735-9815 (formerly 6362-9815)
TELECOMMUNICATION INFORMATION:
TELEPRONE: (619) 450-8400
TELEPRONE: (619) 587-550
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 2353 amino acids
                                                                                                                                                                                                                                                                                                                                                                      Length 2353;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23.8%; Score 51; DB 2; Length 499; 38.7%; Pred. No. 66;
                                                                                                                                                                                                                                                                                                                                                                      Score 52; DB 4; Length 235
Pred. No. 2.8e+02;
3; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: D.C.
COUNTRY: United States
ZIP: 20037-3202
COMPUTER READABLE FORM:
MEDIUM TYPE: FIOPPY disk
COMPUTER: IRW PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NAMBER: US/08/820,170A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Sughrue, Mion, Zinn, Macpeak & Seas
STREET: 2100 Pennsylvania Avenue, N.W.
STAIE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 KRRAKAL--RWTR--QKSVEEGEPPGQGEGPRSRPAAEST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Mismatches
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Query Match 23.8%; Score 51; DB 4 Best Local Similarity 38.7%; Pred. No. 66; Matches 12; Conservative 1; Mismatches
                                                                                                                                                                                                                                                                                                            10 WTROKSVEEGEPPGOGEGPRSRPAAESTGLE 40
                                                                                                                                                                                                                                                                                                                                       21 WEHSKEVSEAEPGGGSSGDSGPP--EESGQE 49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR FILING DATE: 1999-03-22
PRIOR APPLICATION NUMBER: 09/055,699
PRIOR PILING DATE: 1998-04-07
PRIOR FILING DATE: 1998-04-07
PRIOR FILING DATE: 1997-03-19
PRIOR FILING DATE: 1997-03-19
PRIOR FILING DATE: 1997-03-19
PRIOR APPLICATION NUMBER: JP 69163/1997
PRIOR FILING DATE: 1997-03-05
NUMBER OF SEQ ID NOS: 95
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CURRENT APPLICATION NUMBER: US/09/661,468
CURRENT FILING DATE: 2000-09-13
PRIOR FILING DATE: 1998-04-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-661-468-40
; Sequence 40, Application US/09661468
; Patent No. 6376189
                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-565-538-40
; Sequence 40, Application US/09565538
; Patent No. 6333404
EARLIER FILING DATE: 1997-03-05
NUMBER OF SEQ ID NOS: 95
SOFTWARE: PATENTIN VET. 2.1
SEQ ID NO 40
LENGTH: 499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: FUJUNARA, TSUTOMU
APPLICANT: WATANABE, TAKESHI
APPLICANT: HORIE, MASATO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 40
LENGTH: 499
                                                                                                                                        ORGANISM: Homo sapiens
US-09-273-565-40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 12; Conserv
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APPLICANT: FUJIWAR
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                                                                                                                     TYPE: PRT
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CURRENT APPLICATION NUMBER: US/09/273,565A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT ARPLICATION DATA:
APPLICATION NUMBER: US/09/055,699
                                                                                                                                                                                                                                                                                                                                       E: Sughrue, Mion, Zinn, Macpeak & Seas
2100 Pennsylvania Avenue, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21 WEHSKEVSEAPPGGGSSGDSGP--EESGQE 49
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EARLIER APPLICATION NUMBER: 09/055,699
EARLIER REPLICATION DATE: 1998-04-07
EARLIER APPLICATION DATE: 1998-04-07
EARLIER PELLING DATE: 1997-03-19
EARLIER FILING DATE: 1997-03-19
EARLIER FILING DATE: 1996-03-19
EARLIER FILING DATE: 1996-03-19
EARLIER RAPPLICATION NUMBER: JP 63410/1996
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; Sequence 40, Application US/09273565A
; Patent No. 6166190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/820,170
                                                                                            Sequence 40, Application US/09055699
Patent No. 6005088
GENERAL INFORMATION:
APPLICANT: TSULOMU, FUJIWARA
APPLICANT: Takeshi, WATANABE
                                                                                                                                                                                                               APPLICANT: Masato, HORIE
APPLICANT: TOYOMASA, KATAGIRI
TITLE OF INVENTION: HUMAN GENE
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: TELECOMMUNICATION :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (202) 293-7060
TELEFAX: (202) 293-7860
TELEX: 6491103
INFORMATION FOR SEQ ID NO: 40:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 499 amino acids TYPE: amino acid
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APPLICANT: FUJIWARA, TSUTOMU
APPLICANT: WATANABE, TAKESHI
                                                                                                                                                                                                                                                                                                                                                                                                         STATE: D.C. COUNTRY: United States ZIP: 20037-3202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; MOLECULE TYPE: protein US-09-055-699-40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: HORIE, MASATO
                                                                                                                                                                                                                                                                                                                                                      STREET: 2100 Penns
CITY: Washington
STATE: D.C.
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Best Local Similarity
Thas 12; Conserve
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
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                                                   RESULT 10
US-09-055-699-40
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TITLE OF INVENTION: SKELETAL MUSCLE-SPECIFIC UBIQUITIN-CONJUGATING ENZINE
FILE REFERENCE: 0-5559
CURRENT APPLICATION NUMBER: US/09/565,538
CURRENT FILING DATE: 2000-05-05
PRIOR APPLICATION NUMBER: 09/273,565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: FUJIWARA, TSUTOMU
APPLICANT: WATANABE, TAKESHI
APPLICANT: HORIE, MASAPI
TITLE OF INVENTION: SKELETAL MUSCLE-SPECIFIC UBIQUITIN-CONJUGATING HUMAN
TITLE OF INVENTION: SKELETAL MUSCLE-SPECIFIC UBIQUITIN-CONJUGATING ENZYME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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DB 4; Length 499;
                                                         Indels
                                                         16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: Sequence
                                                                                                                                                                                                                                                                                                         5;
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Pred. No. 67;
3; Mismatches 15; Indels
                                                                                                                                                                                                                                                                   23.8%; Score 51; DB 4; Length 499; 38.7%; Pred. No. 66; ive 1; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 62, Application US/09562737;
Fatent No. 6428967;
GENERAL INFORMATION:
APPLICANT: HORMATION:
FILE REFERENCE: US/09/562,737;
CURRENT APPLICATION NUMBER: US/09/562,737;
CURRENT FILING DATE: 2000-05-01
NUMBER OF SEO ID NOS: 132;
SOUTHARE: PatentIn Ver. 2.1;
SEQ 1D NO 6: 23
                                                                                                                                                                                                                                                                                                                                                                      21 WEHSKEVSEAEPGGGSSGDSGPP--EESGQE 49
                                                                                                                                                                                                                                                                                                                                              10 WTRQKSVEEGEPPGQGEGPRSRPAAESTGLE 40
PRIOR APPLICATION NUMBER: 08/820,170
PRIOR FILING DATE: 1997-03-19
PRIOR APLICATION NUMBER: JP 63410/1996
PRIOR FILING DATE: 1996-03-19
PRIOR FILING DATE: 1996-03-19
PRIOR FILING DATE: 1997-03-05
PRIOR FILING DATE: 1997-03-05
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: METHODS AND COMPOS TITLE OF INVENTION: CELLS NUMBER OF SEQUENCES: 18 CORRESPONDENCE ADDRESS: ADDRESSE: ATDORESSES AND STREET P.O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: Texas
COUNTRY: United States of America
ZIP: 77210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3, Application PC/TUS9502251 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 23.6
Matches 17; Conservative
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204 STATAEETGIDA 215
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 KRRAKALRWIR---
                                                                                                                                                                                                            ; ORGANISM: Homo sapiens US-09-661-468-40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PCT-US95-02251-3
                                                                                                                                                                        LENGTH: 499
TYPE: PRT
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         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPatible
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
SOFTWARE: #1.30
SOFTWARE: #1.30
                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Parker, David L.
REGISTRATION NUMBER: 32,165
REFERINCE/DOCKET NUMBER: UMIC009P--
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELERAX: (713) 789-2679
                                                                                                                                                           FILING DATE: CONCURRENTLY HEREWITH CLASSIFICATION:
PRIOR APPLICATION NUMBER: US 08/316,650
FILING DATE: 30-SEP-1994
CLASSIFICATION:
APPLICATION NUMBER: US 08/199,780
FILING DATE: 18-EB-1994
CLASSIFICATION:
                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/02251
FILING DATE: CONCURRENTLY HEREWITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         completed: June 6, 2003, 11:04:14 ne : 3.44133 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX: 79-0924
INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: LENGTH: 1251 amino acid TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           :||| |||| :: ||
172 DPPGPGEGPPAQHAA 186
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Matches 9; Conservative
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COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
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APPLICANT: Andersson, Leif
APPLICANT: Andersson, L. Holger
APPLICANT: Luthman, L. Holger
APPLICANT: Luthman, L. Holger
APPLICANT: Luthman, L. Holger
TITLE OF INVENTION: VARIANTS OF THE HUMAN AMP-ACTIVATED PROTEIN KINASE GAMMA 3 &
CURRENT APPLICATION WHERE: US/09/826,581
CURRENT APPLICATION WHERE: US 60/195,665
PRIOR APPLICATION WHERE: US 60/195,665
PRIOR PILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FASTSEQ FOR WINDOWS Version 4.0
 Sequence 108, App
Sequence 184, App
Sequence 188, App
Sequence 118, App
Sequence 41214, A
Sequence 5773, Ap
Sequence 67, Appl
Sequence 18, Appl
Sequence 12, Appl
Sequence 2, Appl
Sequence 2, Appl
Sequence 21, Appl
Sequence 21, Appl
Sequence 211, App
US-09-924-340-108
US-09-925-600A-108
US-09-746-783-184
US-10-000-489-108
US-10-000-986-108
US-09-864-761-41214
US-09-788-526-5773
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100.0%; Pred. No. 4.1e-17;
Live 0; Mismatches 0;
                                                                                                                                            0 US-09-946-175-2
0 US-09-946-175-3
0 US-09-946-175-3
US-09-796-753-156
US-09-798-295A-211
US-09-978-192A-211
US-09-978-192A-211
US-09-978-191A-211
US-09-978-191A-211
US-09-978-191A-211
US-09-978-191A-211
US-09-978-608A-211
US-09-978-608A-211
US-09-978-608A-211
US-09-978-608A-211
US-09-978-608A-211
US-09-978-608A-211
US-09-978-608A-211
US-09-978-101A-211
US-09-978-101A-211
US-09-978-101A-211
US-09-978-101A-211
US-09-978-101A-211
                                                                                                                      US-10-211-962-62
US-09-796-753-158
                                                                                                            US-09-976-165-40
                                                                                                US-10-153-668-86
                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 6, Application US/09826581 Patent No. US20020142310A1 GENERAL INFORMATION:
                          Query Match 100.

Best Local Similarity 100.
Matches 41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Homo sapiens
US-09-826-581-6
  SEQ ID NO 6
LENGTH: 489
                                                                                                                                                                                                                                                                                                                                                                                           US-09-826-581-6
  TYPE: PRT
   Sequence 6, Appli
Sequence 287, App
Sequence 132, App
Sequence 4, Appli
                                                                                                 (without alignments)
1254.259 Million cell updates/sec
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                                                                                   June 6, 2003, 11:02:59; Search time 3.37478 Seconds
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1 GKRRAKALRWTROKSVEBGF......PGQGBGPRSRPAAESTGLEA
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2: /cgn2_6/ptodata/2/pubpaa/NEV_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/NEOE_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/USOG_NEW_PUB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/USOG_NEW_PUB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/USOT_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/USOT_NEW_PUB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/USOB_PUBCOMB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/USOB_NEW_PUB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/USOB_PUBCOMB.pep:*
            GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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0 US-09-968-17-113-10

0 US-09-968-17-113-10
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                                                                                                                                                                                                                     392085 segs, 103240269 residues
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                                                                                                                                                                                                                                                                                                                                                        Published_Applications_AA:*
                                                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                            protein search, using sw model
                                                                                                                                   US-09-826-581-6_COPY_51_93
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Length 489;
                                       Indels
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                                                                                                                   91
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TITLE OF INVENTION: VIRULENCE-ASSOCIATED NUCLEIC ACID
TITLE OF INVENTION: SEQUENCES AND USES THEREOF
FILE REFRENCE: 00786/361003
CURRENT APPLICATION NUMBER: US/09/975,719
                                                                                                  51 GKRRAKALRWTRQKSVEGGEPPGQGEGPRSRPAAESTGLEA
                                                                               1 GKRRAKALRWTRQKSVEEGEPPGQGEGPRSRPAAESTGLEA
                                                                                                                                                                                                                     Sequence 287, Application US/09975719 Publication No. US20030022349A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                 APPLICANT: Ausubel, Frederick M. APPLICANT: Rahme, Laurence G.
                                                                                                                                                                               RESULT 2
US-09-975-719-287
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                                                                                                                                                                                                                                                             Sequence 47489. R. Sequence 38, Appl Sequence 134, Appl Sequence 57, Appl Sequence 1640, Appl Sequence 1131, Ap
                                                                                              Sequence 44, Appl
Sequence 109, App
Sequence 2, Appl
Sequence 4, Appli
Sequence 4, Appli
Sequence 1210, Ap
Sequence 113, App
Sequence 113, App
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US-10-091-458-38 US-09-870-759-134 US-09-842-758-57 U US-09-925-300-1640 US-09-870-758-84-1131 US-09-870-759-140

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GENERAL INFORMATION:
APPLICANT: PAGAGO, M.
TITLE OF INVENTION: PROLIFERATIVE AND DIFFERENTIATIVE DISORDERS
FILE REFERENCE: 5914-090-599
CURRENT APPLICATION NUMBER: 05/10/042,417
CURRENT FILING DATE: 2002-201-07
PRIOR APPLICATION NUMBER: 60/260,179
PRIOR APPLICATION NUMBER: 60/260,179
PRIOR FILING DATE: 2001-01-5
      TITLE OF INVENTION: THEREOF
FILE REPRENCE: 600-1-202 CIP
CURRENT APPELICATION NUMBER: US/10/122,805
CURRENT FILING DATE: 2002-04-15
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/129,668
PRIOR FILING DATE: EARLIER FILING DATE: 1998-05
PRIOR PLING DATE: EARLIER FILING DATE: 1997-08-05
NUMBER: EARLIER FILING DATE: 1997-08-06
NUMBER OF SEQ ID NOS: 8
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                                                                                                                                                                                                                                                                                                                  DB 9; Length 696;
55;
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CURRENT FILING DATE: 2001-06-26
PRIOR PPLIOR DATES: 2000-06-26
NUMBER OF SEQ ID NOS: 150
                                                                                                                                                                                                                                                                                                                                                                                                                             Score 59;
                                                                                                                                                                                                                                                                                                                                                                                                         13 QKSVEEGEPPGQGEGPRSRPAAESTG 38
                                                                                                                                                                                                                                                                                                                                                 Pred. No
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: MANNING, GERARD
APPLICANT: SUDARSANAM, SUCHA
TITLE OF INVENTION: NOVEL PROTEASES
FILE REFERENCE: 038602/1214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-042-417-44
; Sequence 44, Application US/10042417
; Patent No. US20020123082A1
                                                                                                                                                                                                                                                                                                                          27.68; 42.38;
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32.7%;
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                                                                                                                                                                                 SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 4
LENGTH: 696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 89
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 44
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APPLICANT: PLOWMAN, GREGORY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 26.4
Best Local Similarity 32.7
Matches 16; Conservative
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                                                                                                                                                                                                                                                                ; ORGANISM: Homo sapiens
US-10-122-805-4
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Query Match
Best Local Similarity
"has 11; Conserve
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TYPE: PRT
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APPLICANT: Fechtel, Kim
APPLICANT: Genetics Institute, Inc.
TITLE OF INVENTION: SERRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
FILE REFERENCE: 6055-64X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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Sequence 4, Application US/10122805
Sequence 4, Application US/10122805
Publication No. US20030082645A1
GENERAL INFORMATION:
APPLICANT: Greengard, Paul
APPLICANT: Porton, Barbara
APPLICANT: Kao, Hung-Teh
TITLE OF INVENTION: DNA ENCODING THE HÜMAN SYNAPSIN III GENE AND USES
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                                                                                                                                                                                                                                                            Score 60; DB 9; Length 187;
Pred. No. 11;
6; Mismatches 16; Indels
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                                                                                                                                                                                                                                                                                                                                           1 GKRRAKALRWTRQ-----KSVEEGEPPGQGEGPRSRPAAEST 37
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Pred. No. 16;
8; Mismatches 8
CURRENT FILING DATE: 2001-10-10
PRIOR APPLICATION NUMBER: US 09/199,637
PRIOR FILING DATE: 1998-11-25
PRIOR FILING DATE: 1997-11-25
NUMBER OF SEQ ID NOS: 437
SEQ ID NO 287
SEQ ID NO 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/729,674 CURRENT FILING DATE: 2000-12-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Merberg, David
Treacy, Maurice
Agostino, Michael J.
Steininger II, Robert J.
Spaulding, Vikki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 09/539,330 PRIOR FILING DATE: 2000-03-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 132, Application US/09729674 Patent No. US20010039335A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              McCoy, John M.
LaVallie, Edward R.
Collins-Racie, Lisa A.
                                                                                                                                                                                                ORGANISM: Pseudomonas aeruginosa
US-09-975-719-287
                                                                                                                                                                                                                                                              28.0%;
34.9%;
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36.6%;
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 132
                                                                                                                                                                                                                                                                               Best Local Similarity 34.9
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Jacobs, Kenneth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wong, Gordon G.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Homo sapiens
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Best Local Similarity
' had 15; Conserva
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US-09-729-674-132
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                                                                                                                                                                 LENGTH: 187
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APPLICANT:
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APPLICANT:
APPLICANT:
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LOCATION: (84)
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Publication No. US20030009011A1
GENERAL INFORMATION:
APPLICANT: Shi, Jinrui
APPLICANT: Shoon, Larry
APPLICANT: Rafalski, Antoni J.
APPLICANT: Cahoon, Repecce E.
TITLE OF INVENTION: No. US20030009011A1e1 Inositol Polyphosphate Kinase;
FILE REFERENCE: 1286
FILE REFERENCE: 1286
CURRENT APPLICATION NUMBER: US/10/042,894A
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                                                                                                                                              26.2%; Score 56; DB 10; Length 447; 55.0%; Pred. No. 78; tive 1; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: ANDO, SELMO
APPLICANT: ANDO, SELMO
APPLICANT: OCHIAI, KEIKO
APPLICANT: OCHIAI, KEIKO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: TATEISHI, NAOKO
APPLICANT: TEBOA, MASATO
APPLICANT: IKEDA, MASATO
APPLICANT: OZAKI, AKIO
TILLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-16
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR PELING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-08-03
NUMBER: OF SEQ ID NOS: 7059
SOFTWARE: PATENTIN VET: 3.0
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61 WSRTKEVERSPGLPEDGRPPGAAPASTASP 90
                                                                                                                                                                                                                                                                                                                                                                               Sequence 6443, Application US/09738626; Publication No. US20020197605A1; GENERAL INFORMATION: APPLICANT: MARAGAMA, SATOSHI APPLICANT: MIZOGUCHI, HIROSHI APPLICANT: ANDO, SEIKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Corynebacterium glutamicum
                                                                                                                                                                                                                                                            19 GEPPGQGEGPRSRPAAESTG 38
                                                                                                                                                                    Best Local Similarity 55.09
Matches 11; Conservative
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 109
LENGTH: 447
                                                                                   ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
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LENGTH: 107
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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                                                               TYPE: PRT
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APPLICANT: Lifton, Richard P
APPLICANT: Lifton, Richard P
APPLICANT: Lifton, Richard H
APPLICANT: Choate, Keith
APPLICANT: Choate, Kailh
APPLICANT: Choate, Kailh
APPLICANT: Choate, Kailh
APPLICANT: Choate, Kailh
APPLICANT: Nelson-Williams, Carole
TITLE OF INVENTION: COMPOSITIONS METHODS AND KITS RELATING TO TREATING AND DIAGNOS
TITLE OF INVENTION: HYPERTENSION
FILE REPERBUCE: 044574-5113
CURRENT FILING DATE: 2002-10-25
FRIOR FILING DATE: 2001-07-17
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin version 3.1
SEQ ID NO 4
LENGTH: 1243
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; Sequence 3210, Application US/09764891
; Publication No. US20030077808A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; TITLE PEFFERCE: PC006
; CURRENT APPLICATION NUMBER: US/09/764,891
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper:
NUMBER OF SEQ ID NOS: 10231
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 3210
: LENTH: 150
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                                                                                                                                                                                                                                                            Query Match 25.7%; Score 55; DB 9; Length 240; Best Local Similarity 40.6%; Pred. No. 54; Matches 13; Conservative 4; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                   1 GKRRAKALRWIRQKSVEEGEPPGQGEGPRSRP 32
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PRIOR APPLICATION NUMBER: US 60/261,465
PRIOR FILING DATE: 2001-01-12
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4, Application US/10196935A Publication No. US20030082720A1 GENERAL INFORMATION:
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ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                           TYPE: PRT
ORGANISM: Zea mays
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LOCATION: (84)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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LOCATION: (148)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
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; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-908-711-123
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Publication No. US20030096982A1
GENERAL INPORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 44 Human Secreted Proteins
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                                             PRIOR FILING DATE: 2001-01-17
PRIOR PLING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: 09/764,870
PRIOR APPLICATION NUMBER: 09/764,870
PRIOR FILING DATE: 2001-01-17
PRIOR FILING DATE: 2001-01-17
PRIOR PRILING DATE: 2001-01-17
PRIOR PRILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: 09/764,896
PRIOR FILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: 09/764,896
PRIOR FILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: 09/764,864
PRIOR FILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: 09/764,864
PRIOR PILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: 09/764,864
PRIOR PILING DATE: 2001-01-17
PRIOR PELING DATE: 2001-01-17
PRIOR PELING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: 09/764,866
PRIOR PILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: 06/179,065
PRIOR PILING DATE: 2000-01-31
PRIOR PILING DATE: 2000-01-31
PRIOR APPLICATION NUMBER: 60/179,065
PRIOR PILING DATE: 2000-01-31
PRIOR APPLICATION NUMBER: 60/179,065
PRIOR PILING DATE: 2000-01-31
PRIOR PILING DATE: 2000-06-07
NUMBER OF SEQ ID NOS: 167
SEQ ID NO 123
LENGTH: 150
R FILING DATE: 2001-01-17
R APPLICATION NUMBER: US01/01239
RR FILING DATE: 2001-01-17
R APPLICATION NUMBER: 09/764,870
R FILING DATE: 2001-01-17
RR APPLICATION NUMBER: US01/01348
RR APPLICATION NUMBER: US01/01348
RR APPLICATION NUMBER: US01/01348
RFILING DATE: 2001-01-17
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NAME/KEY: SITE
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                             NAME/KEY: SITE
LOCATION: (125)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                        NAME/KEY: SITE
LOCATION: (138)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
                                                                                                                                                                                                                LOCATION: (148)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
        OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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Patent No. US20020045230A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PA128
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CURRENT FILING DATE: 2001-07-20
PRIOR APPLICATION NUMBER: US01/01360
PRIOR FILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: 09/764,867
PRIOR FILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: 09/764,867
PRIOR FILING DATE: 2001-01-17
PRIOR FILING DATE: 2001-01-17
PRIOR FILING DATE: 2001-01-17
PRIOR FILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: US01/01345
PRIOR FILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: 09/764,889
PRIOR FILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: 09/764,888
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R PILING DATE: 2001-01-17
R APLICATION NUMBER: US01/01345
OR FILING DATE: 2001-01-17
OR APPLICATION NUMBER: 09/764,888
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R APPLICATION NUMBER: USO1/01334
R FILING DATE: 2001-01-17
PREPLICATION NUMBER: 09/764,898
R FILING DATE: 2001-01-17
R APPLICATION NUMBER: USO1/01320
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APPLICATION UNMBER: 0501/01349
FILING DATE: 2001-01-17
APPLICATION NUMBER: 09/764,902
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APPLICATION NUMBER: US01/01339
FILING DATE: 2001-01-17
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APPLICATION NUMBER: US01/01340
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FILING DATE: 2001-01-17
APPLICATION NUMBER: 09/764,891
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APPLICATION NUMBER: 09/764,853
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FILING DATE: 2001-01-17
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APPLICATION NUMBER: 09/764,874
                                                                                                                                                                                                                                                                                                                                                                                           Query Match 25.0%;
Best Local Similarity 48.4%;
Matches 15; Conservative
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APPLICANT: Rosen et al.
TITLE OF INFORMATION:
CURRENT APPLICATION NUCLEIC Acids, Proteins, and Antibodies
FILE REFERENCE: PT206C1
CURRENT APPLICATION NUMBER: US/10/091,458
CURRENT FILING DATE: 2002-03-07
PRIOR APPLICATION NUMBER: 09/764,900
PRIOR APPLICATION NUMBER: 60/179,065
PRIOR APPLICATION NUMBER: 60/179,065
PRIOR APPLICATION NUMBER: 60/180,628
PRIOR PILING DATE: 2000-01-31
PRIOR PILING DATE: 2000-02-04
PRIOR PILING DATE: 2000-06-04
PRIOR PILING DATE: 2000-06-17
PRIOR PILING DATE: 2000-06-17
PRIOR PILING DATE: 2000-06-17
PRIOR FILING DATE: 2000-06-17
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OTHER INFORMATION: EST_HUMAN HIT: AW602053.1, EVALUE 7.00e-25
OTHER INFORMATION: SWISSPROT HIT: Q16696, EVALUE 3.00e-27
US-09-864-761-47489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 24.8%; Score 53; DB 10; Length 111; Best Local Similarity 41.7%; Pred. No. 41; Matches 10; Conservative 3; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Annomax Sequence Listing Engine vers. 1.1 SEQ ID NO 47489
LENGTH: 111
                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00668
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PLICATION NUMBER: PCT/USO1/00663
PRIOR FILING DATE: 2001-01-30
PRIOR PLICATION NUMBER: PCT/USO1/00670
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 69/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 69/774,203
PRIOR APPLICATION NUMBER: US 69/774,203
PRIOR PRIOR DATE: 2000-06-30
      PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR PILING DATE: 2000-09-27
PRIOR PILING DATE: 2000-09-27
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR PILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: PCT/USO1/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00669
PRIOR FILING DATE: 2001-01-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: MAP TO AC008962.4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 49117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Homo sapiens FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 14
US-10-091-458-38
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APPLICANT: Penn, Sharron G.
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINCLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: HUMAN GENOME-DERIVED SINCLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: HUMBER: US/09/864,761
CURRENT APPLICATION NUMBER: US 60/180,312
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-36
PRIOR PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR PRIOR APPLICATION NUMBER: US 60/207,456
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; LOCATION: (175)
. OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-062-548-113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: (25)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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FILE REFERENCE: P2024P1

CURRENT APPLICATION NUMBER: US/10/062,548

CURRENT FILING DATE: 2002-02-05

PRIOR APPLICATION NUMBER: 09/569,247

PRIOR FILING DATE: 1999-08-05

PRIOR PLICATION NUMBER: 60/074,118

PRIOR PLICATION NUMBER: 60/074,118

PRIOR PLILNG DATE: 1998-02-09

PRIOR PPLICATION NUMBER: 60/074,137

PRIOR PLING DATE: 1998-02-09

PRIOR PLILNG DATE: 1998-02-09

NUMBER OF SEQ ID NOS: 172

SOFTPARRE: PATENTIN VET. 2.0
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; Patent No. US20020048763A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-864-761-47489
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LOCATION: (55)
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LOCATION: (57)
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NAME/KEY: SITE
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NUMBER: 6 2000-08- 2000-07- 2000-07- NUMBER: 6 2000-07- NUMBER: 6 2000-08- 2000-07- NUMBER: 6 2000-07- NUMBER: 6 2000-08- 0000-08- NUMBER: 6 2000-08-	2000-07-07 2000-08-14 2000-08-14 2000-08-14 2000-07-07 2000-08-14 2000-08-14 2000-08-14 2000-08-14 2000-09-27 2000-09-21 2000-09-21 2000-09-21 2000-09-21 2000-09-21 2000-09-21 2000-09-21 2000-09-21 2000-09-21 2000-08-14	NUMBER: 60/249, 299 2000-11-17 NUMBER: 60/241, 785 2000-09-29 NUMBER: 60/244, 617 2000-10-20 NUMBER: 60/244, 617 2000-11-01 NUMBER: 60/225, 268 2000-08-14 NUMBER: 60/251, 858 2000-09-29 NUMBER: 60/251, 868 2000-09-29 NUMBER: 60/251, 868 2000-09-29 NUMBER: 60/251, 868 2000-09-29 NUMBER: 60/251, 868 2000-09-29 NUMBER: 60/229, 344 2000-09-01 NUMBER: 60/229, 345 2000-09-01 NUMBER: 60/229, 343 2000-09-01 NUMBER: 60/229, 343 2000-09-05
PPLICATION DA PLICATION DA	LILING DATE. LILING DATE. LILING DATE. PPLICATION LILING DATE.	APPLICATION APPLICATION APPLICATION APPLICATION FILING DATE: APPLICATION
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: 2000-09-05 NUMBER: 60/236,367 : 2000-09-29 : 2000-09-29 : 2000-10-02 NUMBER: 60/237,038 : 2000-10-02 : 2000-10-02 : 2000-10-02 : 2000-10-02 NUMBER: 60/236,370 : 2000-10-02 NUMBER: 60/237,037 : 2000-10-02 : 2000-10-02 : 2000-10-02 : 2000-10-02	NUMBER: 60/240, 96, 2000–10-20 NUMBER: 60/239, 93, 2000–10-13 NUMBER: 60/241, 78, 2000–10-13 NUMBER: 60/246, 47, 2000–11-08 NUMBER: 60/246, 53, 2000–11-17 NUMBER: 60/249, 21, 2000–11-17 NUMBER: 60/249, 21, 2000–11-17 NUMBER: 60/249, 21, 2000–11-17 NUMBER: 60/226, 68, 2000–11-17 NUMBER: 60/226, 68, 2000–11-17 NUMBER: 60/226, 75, 2000–08-12 NUMBER: 60/225, 75, 2000–08-14	NUMBER: 60 2000-08-1 NUMBER: 60 2000-09-0 NUMBER: 60 2000-06-3 NUMBER: 60 2000-011-1 NUMBER: 60 2000-11-1
ILING DATE PPLICATION ILING DATE	PLICATION LING DATE LING DATE LING DATE LING DATE PLICATION LING DATE PLICATION LING DATE LING DATE LING DATE PLICATION LING DATE	PELICATION ILLING DATE
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GENERAL INFORMATION:
APPLICANT: TERMAN, DAVIG S
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF DISEASE
TITLE OF INVENTION: COMPOSITION NUMBER: US/09/870,759
CURRENT APPLICATION NUMBER: US/09/870,759
CURRENT APPLICATION NUMBER: US/09/870,759
FILE REPRENCE: 2000-05-30
NUMBER OF SEQ ID NOS: 166
SOFTWARE: PATENTIN VARISION 3.1
SEQ ID NO 134
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Pred. No. 3.3e+02;
2; Mismatches 12;
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                                                                                                                                                               NR FILING DATE: 2000-09-08

R APPLICATION NUMBER: 60/232,081

RR APPLICATION NUMBER: 60/232,081

RR APPLICATION NUMBER: 60/232,080

RR FILING DATE: 2000-09-08

RR FILING DATE: 2000-09-08

RR PLING DATE: 2000-09-08

RR APPLICATION NUMBER: 60/231,414

DR APPLICATION NUMBER: 60/231,244

DR APPLICATION NUMBER: 60/231,244

DR FILING DATE: 2000-09-08

R FILING DATE: 2000-09-14

PRELING DATE: 2000-09-14

PRELING DATE: 2000-09-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 60/232,397
FILING DATE: 2000-09-14
APPLICATION NUMBER: 60/232,399
FILING DATE: 2000-09-14
APPLICATION NUMBER: 60/232,401
APPLICATION NUMBER: 60/249,297
FILING DATE: 2000-11.17
APPLICATION NUMBER: 60/232,400
FILING DATE: 2000-09-14
APPLICATION NUMBER: 60/231,242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 2000-09-14
APPLICATION NUMBER: 60/241,808
FILING DATE: 2000-10-20
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FILING DATE: 2000-11-08
APPLICATION NUMBER: 60/231,243
FILING DATE: 2000-09-08
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; Patent No. US20020177551A1
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Best Local Similarity 44.0%;
Matches 11; Conservative ;
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; ORGANISM: Homo sapiens
US-09-870-759-134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-870-759-134
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Matches
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Search completed: June 6, 2003, 11:16:42 Job time : 4.37478 secs

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213
1 HILTHKRLLKFLHIFGSLLP......PSFLYRIQDLGIGTFRDLA 41
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Human AMP-activate	Human AMPK gamma s	Human Prkad3 R410	Human Prkad3 V401	Human AMPK gamma s	PRKAG3, Homo sapi	Pig AMPK gamma sub	Sus scrofa AMPK da	Sus scrofa AMPK qa	Pig AMPK gamma sub
1D	ABB11241	AAE00221	AAE00328	AAE00329	AAE00223	AAB47679	AAE00220	AAE00225	AAE00226	AAE00222
DB	22	22	22	22	22	22	22	22	22	22
Length	181	305	305	305	464	489	305	305	305	464
% Query Match Length DB ID	100.0	100.0	100.0	100.0	100.0	100.0	98.6	98.6	98.6	98.6
Score	213	213	213	213	213	213	210	210	210	210
Result No.	1	7	e	4	Ŋ	Q	7	80	6	10

AAE22984 AAE22985 AAE22987 AAE22988 AAE22988 AAE220384 AAB93432 AAB93432 AAB20078 AAW2817 AAB54009 ABB06101 ABB66245	23 ABB89679	ABB11241 standard; peptide; 181 AA. ABB11241 standard; peptide; 181 AA. ABB11241; 11-JAN-2002 (first entry) Human AMP-activated protein kinase subunit homologue, SEQ ID NO:1611. Human AMP-activated protein kinase subunit homologue, SEQ ID NO:1611. Human AMP-activated protein kinase subunit homologue, SEQ ID NO:1611. Human AMP-activated proliferation; issue growth; immunomodulator; activin; inhibin; chemotaxis; chemokinesis; thrombolysis, onoogenesis, hamatopoiesis cancer; tumour; hamatopoietic disorder; chronic inflammatory condition; proliferative retinopathy; atherosclerosis; oronomary heart disease; arterial ischaemia; chronic inflammatory wound healing; infection; immune disorder; tissue regeneration; wound healing; infection; immune disorder; cell culture; drug screening; gene therapy; antiinflammatory; antisthmatic; antiatreriosclerotic; cycostatic; osteopathic; baemostatic; antiinflammatory; antifungal; vulnerary; antiulcer. WO200157188-A2. 09-AUG-2001; 2001WO-US03800.
	L a	standard; peptide; 18; 20 (first entry) activated protein kin tokine; cell prolifers tesis regulation; tiss chemotaxis; chemokine thon; metastasis; can thon; metastasis; can ell disorder; lumpholi filon; metastasis; can filon; metastasis; can filon; metastasis; can trois coronary hear tracis; coteoporosis; va generation; vation hear tric; antiarthritic; l tric; valnerary; antiuloc ens. 88-A2.
യയയയയയെ സെ സ സ സ ന എ ന റ	5.5 5.5 5.5 5.5 5.5 5.5 5.5 5.5	ABB11241 standard; pe ABB11241 standard; pe ABB11241; 11-JAN-2002 (first e Human, AMP-activated F F F F F F F F F F F F F F F F F F F
11111111111111111111111111111111111111	7	RESULT 1 ABB11241 LD ABB1124 XX ABB112 XX ABB112 XX DT 11-JAN DT 11-JAN DE HUMAN; KW HUMAN; KW PICOLIF KW PICOLIF KW ATHERO KW CELLO KW ATHERO KW AND CON KW AND CO

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preferably a carbohydrate metabolism disorder. Primers that can detect a genetic polymorphic marker linked to a sequence encoding PRRAG3, are useful for detecting a dysfunction of carbohydrate metabolism resulting from the expression of a functionally altered allele of PRRAG3.

Transgenic animal and host cell transformed with PRRAG3 or a heterotrimeric AMPK consisting of PRRAG3 or its mutant, are useful for encoding PRRAG3 is useful for detecting mutations in a Prkag3 gene, or in a sequence encoding the first cystathione beta synthase (CBS) domain
                                         PRKAG3; diabetes; obesity; myopathy; cardiovascular disease; anorectic; genetic testing; carbohydrate metabolism disorder; skeletal muscle; cystathione beta synthase; CBS; cardiant; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New variants of the gamma subunit of vertebrate adenosine monophosphate-activated kinase for diagnosis or treatment of disorders associated with energy metabolism such as diabetes, obesity, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Robic A, Rogel-Gaillard C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence is human adenosine monophosphate (AMP)-activated kinase (AMPK) gamma subunit muscle-specific isoform, PRRAG3. Mutation in Prkag3 results in an altered regulation of carbohydrate metabolism, particularly in skeletal muscle. PRRAG3 is useful as therapeutic for treating carbohydrate metabolism disorders sasociated with muscle metabolism such as myopathy and disorders associated with muscle metabolism ectivity, and for restoring a normal AMPK function. PRRAG3 sequence and its functionally altered mutatis are useful for the diagnostic
                            gamma subunit; adenosine monophosphate-activated kinase; AMPK;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Looft C, Kalm E, Milan D, Robic Gellin J, Le Roy P, Chardon P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 213; DB 22; 100.0%; Pred. No. 2.8e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of PRKAG3 and is useful in gene therapy.
                                                                                                                                                                                                                                                                                                                                                               NAT RECH AGRONOMIQUE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 4; Page 55-57; 71pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAE00328 standard; Protein; 305 AA.
                                                                                                                                                                                                                                                        11-SEP-2000; 2000WO-EP09896.
                                                                                                                                                                                                                                                                                               10-SEP-1999; 99EP-0402236.
18-MAY-2000; 2000EP-0401388.
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(/) ANDERSSON I
(/) LOOFT C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAD03296,
                                                                                                                                                                                                                                                                                                                                                                                                                            (KALM/) KALM E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Iannuccelli N,
                                                                                                                                                                       WO200120003-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Andersson L,
                                                                                                                                Homo sapiens
                                                                                                                                                                                                             22-MAR-2001
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Best Local Si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             myopathy
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                                                                                                                                                                                                                                                                                                      Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and sequences ABA08225-ABA09574 represent nucleic acids encoding them. The invention also relates to vectors and recombinant host cells comprising a nucleotide of the invention, methods of producing the novel polypeptides, antibodies against the polypeptides, methods of detecting the nucleotides. C nucleotides against the polypeptides, methods of identifying compounds which bind to polypeptides of the invention. Although novel, many of the polypeptides of the invention and recombination activities, and hence potypeptides of the invention have homology to known proteins, thereby giving an insight into their probable biological activities, and hence potential therapeutic applications. The polypeptides of the invention may compare the activities activity activity; tassue growth activity.

Individual partial activities; stem cell growth factor activities, haematopolesis regulatory activity; tissue growth activities; chemotactic or chemokinetic activities; haemacotic or chemokinetic activities; polypeptides and nucleotides of the invention are useful for preventing, tracting or amelicating medical conditions, e.g., by protein or gene therapy. Such conditions include cancers, haemacopolatic disorders (e.g., myeloid or lymphoid cell disorders), chronic inflammatory conditions (e.g., asthma or arthritis), cracers, haemacopolatic acids encoding them) may be used to promote wound repair (or nucleic acids encoding them) may be used to promote wound crepair (or nucleic acids encoding them) may be used to promote wound crepair part provent factors and ulcers), while those with immunomodulatory activities and be used in the treatment of viral, and fungal infections in addition to immune disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ·;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         that can be used to augment or replace cells damaged by illness, autoimmune disease or accidental damage. The polypeptides and nucleotides may also be used in the diagnosis of the above conditions, and in drug
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Polypeptides with growth factor activity may be used in cell cultures to promote cell growth. For example, such polypeptides may be used to manipulate stem cells in culture to give rise to neuroepithelial cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        techniques. The present sequence represents a novel human \ensuremath{\mathsf{le}} of the invention.
                                                                                                                                                                                     Human proteins and DNA encoding sequences useful for preventing, treating or ameliorating a medical condition in a mammalian subject
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ·;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 181;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human AMPK gamma subunit muscle-specific isoform, PRKAG3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 HILTHKRILKFLHIFGSLLPRPSFLYRTIQDLGIGTFRDLA 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 213; DB 22; 100.0%; Pred. No. 1.6e-23;
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                                                                                                                                                                                                                                                                          Claim 20; Page 159-160; 1963pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAE00221 standard; Protein; 305 AA
                                                                                  Liu C, Drmanac RT;
27-APR-2000; 2000US-0560875.
                                                                                                                                                                                                                              e.g. arthritis and cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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                                                                                                                     WPI; 2001-457740/49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
Matches 41; Conserv
                                         (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 AA;
                                                                                                                                               N-PSDB; ABA08485
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                                                                                Tang YT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Seguence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      evaluation, genetic testing and prognosis of a metabolic disorder, preferably a carbohydrate metabolism disorder. Primers that can detect a genetic polymorphic marker linked to a sequence encoding PRRAG3, are useful for detecting a dysfunction of carbohydrate metabolism resulting from the expression of a functionally altered allele of PRRAG3.
                                                                                                                                             Human; gamma subunit; adenosine monophosphate-activated kinase; AMPK; PRKAG3; diabetes; obesity; myopathy; cardiovascular disease; anorectic; genetic testing; carbohydrate metabolism disorder; skeletal muscle; cystathione beta synthase, CBS; cardiant; gene therapy; mutant; mutein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               in a sequence encoding the first cystathione beta synthase (CBS) domain of PRKAG3 and is useful in gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence is a R410 mutant of human muscle-specific isoform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New variants of the gamma subunit of vertebrate adenosine monophosphate-activated kinase for diagnosis or treatment of disorders associated with energy metabolism such as diabetes, obesity, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Transgenic animal and host cell transformed with PRKAG3 or a
heterotrimeric AMPK consisting of PRKAG3 or its mutant, are useful for
screening compounds able to modulate AMPK activity. Nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rogel-Gaillard C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            encoding PRKAG3 is useful for detecting mutations in a Prkag3 gene, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     activity, and for restoring a normal AMPK function. PRKAG3 sequence and its functionally altered mutants are useful for the diagnostic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mutation in Prkag3 results in an altered regulation of carbohydrate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of gamma subunit of adenosine monophosphate (AMP)-activated kinase (AMPK) Prkag3. This mutant sequence results in increased glycogen content in human skeletal muscle.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            metabolism, particularly in skeletal muscle. PRRAG3 is useful as therapeutic for treating carbohydrate metabolism disorders such as diabetes, obesity, and disorders associated with muscle metabolism such as myopathy and cardiovascular diseases, to modulate AMPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Note: The present sequence is not shown in the specification, but
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "Wild-type Arg substituted with Gln"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        D, Robic A,
Chardon P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kalm E, Milan D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (INRG ) INRA INST NAT RECH AGRONOMIQUE.
(ANDE/) ANDERSSON L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Le Roy P,
                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page -; 71pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of sequence listing (AAE00221).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11-SEP-2000; 2000WO-EP09896.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99EP-0402236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18-MAY-2000; 2000EP-0401388
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gellin J,
                                                                            Human Prkag3 R41Q mutant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Looft C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-244810/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Misc-difference 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        305 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOOFT C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KALM E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           [annuccelli N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200120003-A2.
                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-SEP-1999;
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13-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seguence
                                                                                                                                                                                                                                                                                                      variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (KALM/)
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; 0

Gaps

; 0

Indels

Length 305;

100.0%; Score 213; DB 22; 100.0%; Pred. No. 2.8e-23; ive 0; Mismatches 0;

41; Conservative

Matches

Query Match Best Local Similarity

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Human; gamma subunit; adenosine monophosphate-activated kinase; AMPK; PRKAG3; diabetes; obesity; myopathy; cardiovascular disease; anorectic; genetic testing; carbohydrate metabolism disorder; skeletal muscle; cystathione beta synthase; CBS; cardiant; gene therapy; mutant; mutein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             a genetic polymorphic marker linked to a sequence encoding PRRAG3, are useful for detecting a dysfunction of carbohydrate metabolism resulting from the expression of a functionally altered allele of PRRAG3. Transgenic animal and host cell transformed with PRRAG3 or a heterotrimeric AMPK consisting of PRRAG3 or its mutant, are useful for screening compounds able to modulate AMPK activity. Nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence is a V40I mutant of human muscle-specific isoform of gamma subunit of adenosine monophosphate (AMP)-activated kinase (AMPK) Prkag3. This mutant sequence results in decreased glycogen content in human skeletal muscle.

Wutation in Prkag3 results in an altered regulation of carbohydrate metabolism, particularly in skeletal muscle. PRKAG3 is useful as therapeutic for treating carbohydrate metabolism disorders such as diabetes, obesity, and disorders associated with muscle metabolism such as myopathy and cardiovascular diseases, to modulate AMPK activity, and for restoring a normal AMPK function. PRKAG3 sequence and its functionally altered mutants are useful for the diagnostic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New variants of the gamma subunit of vertebrate adenosine monophosphate-activated kinase for diagnosis or treatment of disorders associated with energy metabolism such as diabetes, obesity, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Andersson L, Looft C, Kalm E, Milan D, Robic A, Rogel-Gaillard C;
Tannuccelli N, Gellin J, Le Roy P, Chardon P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          evaluation, genetic testing and prognosis of a metabolic disorder, preferably a carbohydrate metabolism disorder. Primers that can detect
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "Wild-type Val substituted with Ile"
                    1 HILTHKRILKFLHIFGSLLPRPSFLYRTIQDLGIGTFRDLA 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (INRG ) INRA INST NAT RECH AGRONOMIQUE.
(ANDE/) ANDERSSON L.
(LOOF/) LOOFT C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                      AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page -; 71pp; English.
                                                                                                                                  AAE00329 standard; Protein; 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11-SEP-2000; 2000WO-EP09896.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10-SEP-1999; 99EP-0402236.
18-MAY-2000; 2000EP-0401388.
                                                                                                                                                                                                              13-JUN-2001 (first entry)
                                                                                                                                                                                                                                                       Human Prkag3 V40I mutant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-244810/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Misc-difference 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (KALM/) KALM E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200120003-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Andersson L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-MAR-2001.
                                                                                                                                                                           AAE00329;
                                                                                                                                                                                                                                                                                                                                                                             variant.
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                                                                                                                  AAE0032
                                                                                                RESULT
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associated with energy metabolism such as diabetes, obesity, and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                        AA.
                                                                                                                                                                                                                                                                                                                                                                                                      AAB47679 standard; Protein; 489
                                Claim 5; Fig 3; 71pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-APR-2001; 2001WO-SE00765.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-APR-2000; 2000US-195665P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
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                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Andersson L, Luthman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-657170/75.
                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                     464 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (AREX-) AREXIS AB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAH43685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200177305-A2
                                                                                                                                                                                                                                                                                          Mac.
Local Slur.
41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                               21-JAN-2002
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                                                                                                                                                                                                                                                                       Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                            AAB47679;
                                                                                                                                                                                                                                                                                                                                                     295
                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRKAG3.
                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                    RESULT 6
                                                                                                                                                                                                                                                                                                                                                                                               AAB47679
                                                                                                                                                                                                                                                                                                                                                    qq
                                                                                                                                                                                                                                                                                                                                                                                                                            .;
0
encoding PRKAG3 is useful for detecting mutations in a Prkag3 gene, or in a sequence encoding the first cystathione beta synthase (CBS) domain of PRKAG3 and is useful in gene therapy.

Note: The present sequence is not shown in the specification, but is derived from the human Prkag3 sequence SEQ.ID.NO.4 shown in page 57-58
                                                                                                                                                                                                                                                                                       Human; gamma subunit; adenosine monophosphate-activated kinase; AMPK; presses; abstactivated blabetes; obesity; myopathy; cardiovascular disease; anorectic; genetic testing; carbohydrate metabolism disorder; skeletal muscle; cystathione beta synthase; CBS; cardiant; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New variants of the gamma subunit of vertebrate adenosine monophosphate-activated kinase for diagnosis or treatment of disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Andersson L, Looft C, Kalm E, Milan D, Robic A, Rogel-Gaillard C;
Iannuccelli N, Gellin J, Le Roy P, Chardon P;
                                                                                                                 Gaps
                                                                                                                                                                                                                                                                     Human AMPK gamma subunit muscle-specific isoform, complete PRKAG3.
                                                                                                                 ;
0
                                                                                           Length 305;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label= CBS
/note= "Cystathione beta synthase domain"
/doc.45
/label= CBS
/note= "Cystathione beta synthase domain"
                                                                                                                                                                                                                                                                                                                                                                                                                           /label= CBS
/note= "Cystathione beta synthase domain"
329..382
                                                                                                                                                                                                                                                                                                                                                                                             /note= "Cystathione beta synthase domain"
                                                                                                                 Indels
                                                                                                                                               41
                                                                                                                                    1 HILTHKRLLKFLHIFGSLLPRPSFLYRTIQDLGIGTFRDLA
                                                                                                                  ..
                                                                                            Score 213; DB 22;
Pred. No. 2.8e-23;
                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                 'note= "RN- mutation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (INRG ) INRA INST NAT RECH AGRONOMIQUE (ANDE/) ANDERSSON L.
                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
172..225
                                                                                                                                                                                                         AAE00223 standard; Protein; 464 AA
                                                                                                                ;
                                                   sequence listing (AAE00221).
                                                                                           100.0%;
100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10-SEP-1999; 99EP-0402236.
18-MAY-2000; 2000EP-0401388.
                                                                                                                                                                                                                                                                                                                                                                                   /label= CBS
                                                                                                                                                                                                                                                  (first entry)
                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-244810/25.
                                                                                            Query Match
Best Local Similarity
                                                                        305 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAD03320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOOFT C.
                                                                                                                                                                                                                                                                                                                                                                                                        Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KALM E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200120003-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Andersson L,
                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                13-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-MAR-2001
                                                                                                                41;
                                                                         Sednence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOOF
                                                                                                                                                                                                                                                                                                                                                                         Domain
                                                                                                                                                                                                                                                                                                                                                                                                                            Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Domain
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                                                                                                      Best Loca
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The present sequence is human adenosine monophosphate

(AMP)-activated kinase (AMPK) gamma subunit muscle-specific isoform,
complete PRKAG3 whitation in Prkag3 results in an altered regulation of
carbohydrate metabolism, particularly in skeletal muscle. PRKAG3 is
useful as therapeutic for treating carbohydrate metabolism disorders such
as diabetes, obesity, and disorders associated with muscle metabolism
such as myopathy and cardiovascular diseases, to modulate AMPK
activity, and for restoring a normal AMPK function. PRKAG3 sequence
and its functionally altered mutants are useful for the diagnostic
evaluation, genetic testing and prognosis of a metabolic disorder,
preferably a carbohydrate metabolism disorder. Primers that can detect
a genetic polymorphic marker linked to a sequence encoding PKRAG3, are
useful for detecting a dysfunction of carbohydrate metabolism resulting
from the expression of a functionally altered aliele of PRKAG3 or
ransgenic animal and host cell transformed with PRKAG3 or a resolute can beterotrimeric AMPK consisting of PRKAG3 or its mutant, are useful for
screening compounds able to modulate AMPK activity. Nucleic acid
encoding PRKAG3 and is useful for detecting mutations in a Prkag3 gene, or
in a sequence encoding the first cystethione beta synthase (CBS) domain
of PRKAG3 and is useful in gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human, AMP-activated protein kinase gamma 3 subunit; PRKAG3; variant; metabolic disease; diabetes; obesity; substitution; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 464;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Possible variation point R340W"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HILTHKRULKFLHIFGSLLPRPSFLYRTIQDLGIGTFRDLA 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "Possible variation point P71A"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 HILTHKRLLKFLHIFGSLLPRPSFLYRTIQDLGIGTFRDLA 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 213; DB 22; 100.0%; Pred. No. 4.5e-23;
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Sus scrofa.
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAE00225;
                                                                                                                                                      myopathy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Domain
                           LOOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
New variants of human AMP-activated protein kinase gamma3 subunit associated with a metabolic disease e.g. diabetes or obesity and method for determining a risk estimate of diseases in subject by detecting the
                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRKAG3; diabetes; obesity; myopathy; cardiovascular disease; anorectic; genetic testing; carbohydrate metabolism disorder; skeletal muscle; cystathione beta synthase; CBS; cardiant; gene therapy; RN locus;
                                                                                  AMP-activated protein kinase gamma 3 subunit (PRKAG3). Detecting the presence of the PRKAG3 DNA, or a variant, is useful in determining a risk estimate of a metabolic disease, such as diabetes or obesity, in a subject. The variation may occur in exons 3, 4 or 10. In exon 3 variation may be a substitution of a G for a C at nucleotide 320, resulting in the amino acid substitution P71A; in exon 4 variation may be a substitution of a T for a C at nucleotide 1037, resulting in the amino acid substitution of a T for a C at nucleotide 1037, resulting in the amino acid substitution R340W. There may also be
                                                                                                                                                                                                                                                                        Gaps
                                                                          This sequence is encoded by the full length cDNA encoding the human
                                                                                                                                                                     nucleotide variation in intron 6. The numbering of these variations is based on the full length CDNA, rather than on position 1 of the open reading frame.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pig; gamma subunit; adenosine monophosphate-activated kinase; AMPK;
                                                                                                                                                                                                                                                                       ;
0
                                                                                                                                                                                                                                                   Length 489;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Cystathione beta synthase domain"
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/note= "Cystathione beta synthase domain"
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                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note≃ "Cystathione beta synthase domain"
                                                                                                                                                                                                                                                                                                                                                                                                                               Pig AMPK gamma subunit muscle-specific isoform, PRKAG3,
                                                                                                                                                                                                                                                                                                    1 HILTHKRLLKFLHIFGSLLPRPSFLYRTIQDLGIGTFRDLA 41
                                                                                                                                                                                                                                                 Score 213; DB 22;
Pred. No. 4.8e-23;
                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                  A.
                                                     Disclosure; Fig 5; 25pp; English.
                                                                                                                                                                                                                                                                                                                                                                AAE00220 standard; Protein; 305
                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                 100.08;
                                                                                                                                                                                                                                                           100.08;
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/label= CBS
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/label= CBS
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2000EP-0401388.
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/label= CBS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11-SEP-2000; 2000WO-EP09896
                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                      41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                . 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note=
                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                            489 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200120003-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               chromosome 15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10-SEP-1999;
18-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                           13-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sus scrofa
                                                                                                                                                                                                                             Sednence
                                                                                                                                                                                                                                                                                                              320
                                                                                                                                                                                                                                                                                                                                                                                     AAE00220;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Domain
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                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                        AAE00220
                                                                                                                                                                                                                                                                                                                                             RESULT
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AMP) activated kinase (AMPK) gamma subunit muscle-specific professions. PRRAG3. Prkag3 gene is located in the RN locus of chromosome 15.

Mutation in Prkag3 results in an altered regulation of carbohydrate metabolism, particularly in skeletal muscle. PRRAG3 is useful as therapeutic for treating carbohydrate metabolism disorders such as diabetes, obesity, and disorders associated with muscle metabolism such as myopathy and cardiovascular diseases, to modulate AMPK activity, and for restoring a normal AMPK function. PRRAG3 sequence and its functionally altered mutants are useful for the diagnostic evaluation, genetic testing and prognosis of a metabolic disorder, preferably a carbohydrate metabolism disorder. Primers that can detect a genetic polymorphic marker linked to a sequence encoding PRRAG3 are useful for detecting a dysfunction of carbohydrate metabolism resulting from the expression of a functionally altered allele of PRRAG3 or a present carinal and host cell transformed with PRRAG3 or a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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                                                                                                                                                                                                                                                                                                                                                                                                 New variants of the gamma subunit of vertebrate adenosine monophosphate-activated kinase for diagnosis or treatment of disorders associated with energy metabolism such as diabetes, obesity, and
                                                                                                                                                                                        Robic A, Rogel-Gaillard C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pig; gamma subunit; adenosine monophosphate-activated kinase; AMPK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present amino acid sequence is pig adenosine monophosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 305;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sus scrofa AMPK gamma chain isoform Prkag3 mutant (R41Q).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 210; DB 22;
Pred. No. 7.8e-23;
1; Mismatches 0;
                                                                                                                                                                                                                       Le Roy P, Chardon P;
                                                                                                                                                                                        Milan D,
(INRG ) INRA INST NAT RECH AGRONOMIQUE. (ANDE/) ANDERSSON L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 4; Fig 2; 71pp; English.
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                                                                                                                                                                                                                   Gellin J,
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                                                                                                                                                                                     Looft C,
                                                                                                                                                                                                                                                                                              WPI; 2001-244810/25.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                N-PSDB; AAD03295
                                                                                                         (KALM/) KALM E.
                                                                                                                                                                                                                       Iannuccelli N,
                                                                                                                                                                                     Andersson L,
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Pig; gamma subunit; adenosine monophosphate-activated kinase; AMPK; preskA3; diabetes; obesity; myopathy; cardiovascular disease; anorectic; genetic testing; carbolydrate metabolism disorder; skeletal muscle; cystathione beta synthase; CBS; cardiant; gene therapy; mutant; mutein;
                                                                                                                                                                    Sus scrofa AMPK gamma chain isoform Prkag3 mutant (R41Q).
                                                       AAE00226 standard; Protein; 305 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Misc-difference
                                                                                                                                13-JUN-2001
                                                                                                                                                                                                                                                                                                                        Sus scrofa.
                                                                                             AAE00226;
                                                                                                                                                                                                                                                                                     variant.
                                                                                                                                                                                                                                                                                                                                                            Key
Domain
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Jomain
                   RESULT 9
                                       AAE00226
                                                                                             metabolism, particularly in skeletal muscle. PRRAGS is useful as therapeutic for treating carbohydrate metabolism disorders such as diabetes, obesity, and disorders associated with muscle metabolism such as myopathy and cardiovascular diseases, to modulate AMPK activity, and for restoring a normal AMPK function. PRRAG3 sequence and its functionally altered mutants are useful for the diagnostic evaluation, genetic testing and prognosis of a metabolic disorder, preferably a carbohydrate metabolism disorder. Primers that can detect a genetic polymorphic marker linked to a sequence encoding PRRAG3, are useful for detecting a dysfunction of carbohydrate metabolism resulting from the expression of a functionally altered allele of PRRAG3 or a heterotrimeric AMPK consisting of PRRAG3 or its mutant, are useful for screening compounds able to modulate AMPK activity, Nucleic acid encoding PRRAG3 is useful for detecting mutations in a Prkag3 gene, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      in a sequence encoding the first cystathione beta synthase (CBS) domain of PRK63 and is useful in gene therapy.

Note: The present sequence is not in the specification, but is derived from the porcine Prkeq3 sequence shown in Fig 2 (AAE00220).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New variants of the gamma subunit of vertebrate adenosine monophosphate-activated kinase for diagnosis or treatment of disorders associated with energy metabolism such as diabetes, obesity, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Robic A, Rogel-Gaillard C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence is a R41Q mutant of muscle-specific isoform of gamma subunit of adenosine monophosphate (AMP)-activated kinase (AMPK) Prkag3 from Sus scrofa. This mutant sequence results in increased 41ycogen content in pig skeletal muscle.

Mutation in Prkag3 results in an altered regulation of carbohydrate
                 "Wild-type Arg substituted with Gln"
                                                                                                                                          241.294
/label= CBS
/note= "Cystathione beta synthase domain"
                                                                                                          /label= CBS
/note= "Cystathione beta synthase domain"
                                                                       /note= "Cystathione beta synthase domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kalm E, Milan D, Robic
I, Le Roy P, Chardon P;
                                                                                                                                                                                                                                                                                                                                                                                              (INRG ) INRA INST NAT RECH AGRONOMIQUE. (ANDE/) ANDERSSON L. (LOOF/) LOOFT C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 9; Page -; 71pp; English.
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18-MAY-2000; 2000EP-0401388.
                                                   /label= CBS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gellin J,
                                                                                           . 223
                                   .148
                   /note=
94..148
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Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 myopathy
                                                                                                                                                  Domain
                                   Domain
                                                                                           Domain
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/note= "Wild-type Val substituted with Ile" /note= "Cystathione beta synthase domain"

cocation/Qualifiers

(first entry)

13..66 /label= CBS

/note= "Cystathione beta synthase domain" /label= CBS /note= "Cystathione beta synthase domain"

/label= CBS

148

223

/label= CBS

..294

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New variants of the gamma subunit of vertebrate adenosine monophosphate-activated kinase for diagnosis or treatment of disorders associated with energy metabolism such as diabetes, obesity, and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence is a V401 mutant of muscle-specific isoform of gamma subunit of adenosine monophosphate (AMP)-activated kinase (AMF) Prkag3 from Sus Scrofa. This mutant sequence results in decreased glycogen content in pig skeletal muscle.

Mutation in Prkag3 results in an altered regulation of carbohydrate metabolism, particularly in skeletal muscle. PRKAG3 is useful as therapeutic for treating carbohydrate metabolism disorders such as diabetes, obesity, and disorders associated with muscle metabolism such as myopathy and cardiovascular diseases, to modulate AMPK activity, and for restoring a normal AMPK function. PRKAG3 sequence and its functionally altered mutants are useful for the diagnostic evaluation, genetic testing and prognosis of a metabolic disorder,
/note= "Cystathione beta synthase domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kalm E, Milan D, Robic A,
J, Le Roy P, Chardon P;
                                                                                                                                                                                                                                                                                                                                                                                                                    (INRG ) INRA INST NAT RECH AGRONOMIQUE. (ANDE/) ANDERSSON L.
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                                                                                                                                                                                                                           11-SEP-2000; 2000WO-EP09896
                                                                                                                                                                                                                                                                                                          99EP-0402236
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Iannuccelli N, Gellin J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-244810/25.
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                                                                              WO200120003-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KALM E.
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0;

Gaps

; 0

Indels

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Mismatches

Conservative

Best Local Similarity Matches 40; Conserve

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Query Match

1 HILTHKRLLKFLHIFGSLLPRPSFLYRTIQDLGIGTFRDLA 41

Score 210; DB 22; Length 305; Pred. No. 7.8e-23;

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fannuccelli N, Gellin J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sus scrofa.
                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAE22984;
                                                                                         myopathy
                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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                                                  heterotrimeric AMPK consisting of PRKAG3 or its mutant, are useful for screening compounds able to modulate AMPK activity. Nucleic acid encoding PRKAG3 is useful for detecting mutations in a Prkag3 gene, or in a sequence encoding the first cystathione beta synthase (CBS) domain of PRKAG3 and is useful in gene therapy.

Note: The present sequence is not shown in the specification, but is derived from the porcine Prkag3 sequence shown in Fig 2 (AABO0220).
preferably a carbohydrate metabolism disorder. Primers that can detect a genetic polymorphic marker linked to a sequence encoding PRRAG3, are useful for detecting a dysfunction of carbohydrate metabolism resulting from the expression of a functionally altered allele of PRRAG3. Transgenic animal and host cell transformed with PRRAG3 or a
                                                                                                                                                                                                                                                                                                                                                                                PRKAG3; diabetes; obesity; myopathy; cardiovascular disease; anorectic; genetic testing; carbohydrate metabolism disorder; skeletal muscle; cystathione beta synthase; CBS; cardiant; gene therapy; RN locus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Andersson L, Looft C, Kalm E, Milan D, Robic A, Rogel-Gaillard C;
                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                       Pig; gamma subunit; adenosine monophosphate-activated kinase; AMPK;
                                                                                                                                                                                                                                                                                                                                                Pig AMPK gamma subunit muscle-specific isoform, complete PRKAG3.
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0
                                                                                                                                                                Length 305;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label= CBS
/note= "Cystathione beta synthase domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "Cystathione beta synthase domain" 400..453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note= "Cystathione beta synthase domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "Cystathione beta synthase domain"
                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                   136 HILTHKRLLKFLHIFGTLLPRPSFLYRTIQDLGIGTFRDLA 176
                                                                                                                                                                                                     1 HILTHKRLLKFLHIFGSLLPRPSFLYRTIQDLGIGTFRDLA 41
                                                                                                                                                               Score 210; DB 22;
Pred. No. 7.8e-23;
                                                                                                                                                                                    1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "RN- mutation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (INRG ) INRA INST NAT RECH AGRONOMIQUE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Socation/Qualifiers
                                                                                                                                                                                                                                                                                   AA.
                                                                                                                                                                                                                                                                                 AAE00222 standard; Protein; 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     172..225
/label= CBS
                                                                                                                                                               98.68;
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                                                                                                                                                                                                                                                                                                                           13-JUN-2001 (first entry)
                                                                                                                                                           Query Match
Best Local Similarity 97.6
Matches 40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .382
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                                                                                                                                          305 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                 chromosome 15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOOFT
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Sus scrofa
                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                      AAE00222;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (KALM/)
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Paralaction, general restricts and proposis of a metabolic disorder, preferably a carbohydrate metabolism disorder. Primers that can detect a genetic polymorphic marker linked to a sequence encoding PRRAG3, are useful for detecting a dysfunction of carbohydrate metabolism resulting from the expression of a functionally altered allele of PRRAG3. Transgenic animal and host cell transformed with PRRAG3 or a heterotrimeric AMPK consisting of PRRAG3 or its mutant, are useful for screening compounds able to modulate AMPK activity. Nucleic acid encoding PRRAG3 is useful for detecting mutations in a Prkag3 gene, or in a sequence encoding the first cystathione beta synthase (CBS) domain of PRRAG3 and is useful in gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence is pig adenosine monophosphate (AMP) activated kinese (AMPK) gamma subunit muscle-specific isoform, complete PRKAG3. Prkag3 gene is located in the RN locus of chromosome 15. Mutation in Prkag3 results in an altered regulation of carbohydrate metabolism, particularly in skeletal muscle. PKRKAG3 is useful as therapeutic for treating carbohydrate metabolism disorders such as diabetes, obesity, and disorders associated with muscle metabolism such as myopathy and cardiovascular diseases, to modulate AMPK and civity, and for restoring a normal AMPK function. PKKAG3 sequence and its functionally altered mutants are useful for the diagnostic
                                                                                                                                                                     New variants of the gamma subunit of vertebrate adenosine monophosphate-activated kinase for diagnosis or treatment of disorders associated with energy metabolism such as diabetes, obesity, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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<u>й</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 210; DB 22;
Pred. No. 1.3e-22;
1; Mismatches 0;
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Le Roy
                                                                                                                                                                                                                                                                                                                                                      Claim 5; Fig 3; 71pp; English.
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97.6%;
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                                                            WPI; 2001-244810/25.
N-PSDB; AAD03319.
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mes 40; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  464 AA;
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us-09-826-581-6_copy_320_360.rag

Plastow G;

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Screening animals to determine those likely to produce larger litters and improved meat quality traits involves assaying for the presence of polymorphisms in the AMP activated protein kinase regulatory gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a method for screening animals to determine those more likely to produce large litters and improved meat quality traits. The method involves assaying for the presence of a genotype in the sample of genetic material obtained from animal. The genotype is characterised by polymorphism(s) in the AMP activated protein kinase regulatory gamma subunit (PRRAG3) gene. The method is used for screening animals e.g., pigs to determine those most likely to exhibit improved meat quality traits and to produce larger litters. The present sequence is pig PRRAG3 polymorphic variant (PRRAG3-30).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AMP activated protein kinase regulatory gamma subunit; PRKAG3 gene; screening; meat quality; single nucleotide polymorphism; SNP; pig;
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Pred. No. 1.3e-22;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             295 HILTHKRLLKFLHIFGTLLPRPSFLYRTIQDLGIGTFRDLA 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 HILTHKRLLKFLHIFGSLLPRPSFLYRTIQDLGIGTFRDLA 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pig PRKAG3 polymorphic variant (PRKAG3-52).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 91-93; 109pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Malek M,
                                                                                                                                                                         Malek M,
                                                                                                                (IOWA ) UNIV IOWA STATE RES FOUND INC.
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97.6%;
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                        08-JAN-2001; 2001US-260239P.
18-JUN-2001; 2001US-299111P.
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2001US-260239P.
                                                                                                                                                                         Ciobanu DC,
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                                                                                                                                                                                                                                   WPI; 2002-393850/42.
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es 40; Conserva
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                                                                                                                                                                                                                                                                  N-PSDB; AAD36457
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08-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a method for screening animals to determine those more likely to produce large litters and improved meat quality traits. The method involves assaying for the presence of a genotype in the sample of genetic material obtained from animal. The genotype is characterised by polymorphism(s) in the AMP activated protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AMP activated protein kinase regulatory gamma subunit; PRKAG3 gene; screening; meat quality; single nucleotide polymorphism; SNP; pig;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        kinase regulatory gamma subunit (PRKAG3) gene. The method is used for screening animals e.g., pigs to determine those most likely to exhibit improved meat quality traits and to produce larger litters. The present sequence is pig wild-type PRKAG3 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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                                                                                                                                                                                                                                                                                                                     (IOWA ) UNIV IOWA STATE RES FOUND INC
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                                                                                                                                                                                                                                                                                                                                                                               Rothschild MF, Ciobanu DC,
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2001US-299111P
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Best Local Similarity
""" 40; Conserva
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18-JUN-2001;
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Gaps

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AA.

Plastow G;

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Gaps

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Screening animals to determine those likely to produce larger litters and improved meat quality traits involves assaying for the presence of polymorphisms in the AMP activated protein kinase regulatory gamma
                                                                                                 those more likely to produce large litters and improved meat quality traits. The method involves assaying for the presence of a genotype in the sample of genetic material obtained from animal. The genotype is characterised by polymorphism(s) in the AMP activated protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a method for screening animals to determine those more likely to produce large litters and improved meat quality traits. The method involves assaying for the presence of a genotype
                                                                             The invention relates to a method for screening animals to determine
                                                                                                                                                                                 kinase regulatory gamma subunit (PRKAG3) gene. The method is used for screening animals e.g., pigs to determine those most likely to exhibit improved meat quality traits and to produce larger litters. The present sequence is pig PRKAG3 polymorphic variant (PRKAG3-199).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AMP activated protein kinase regulatory gamma subunit; PRKAG3 gene; screening; meat quality; single nucleotide polymorphism; SNP; pig;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "Wild type Arg is substituted with Gln due to single nucleotide polymorphism (SNP)"
                                                                                                                                                                                                                                                                                                                                                                            ;
0
                                                                                                                                                                                                                                                                                                                                 Length 464;
                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                       295 HILTHKRLLKFLHIFGTLLPRPSFLYRTIODLGIGTFRDLA 335
                                                                                                                                                                                                                                                                                                                                                                                                                 41
                                                                                                                                                                                                                                                                                                                                                                                                               1 HILTHKRLLKFLHIFGSLLPRPSFLYRTIQDLGIGTFRDLA
                                                                                                                                                                                                                                                                                                                                                                        0
                                                                                                                                                                                                                                                                                                                               Score 210; DB 23;
Pred. No. 1.3e-22;
1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Malek M, Plastow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pig PRKAG3 polymorphic variant (PRKAG3-200).
                                      Disclosure; Page 100-102; 109pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 105-107; 109pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (IOWA ) UNIV IOWA STATE RES FOUND INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAE22988 standard; Protein; 464
                                                                                                                                                                                                                                                                                                                               98.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10-SEP-2001; 2001WO-US28283.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ciobanu DC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2000US-231045P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08-JAN-2001; 2001US-260239P. 18-JUN-2001; 2001US-299111P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-393850/42.
                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                        464 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAD36460.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rothschild MF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200220850-A2
subunit gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        subunit gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                        40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sus scrofa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAE22988;
                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        variant.
                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 15
ó
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                         Screening animals to determine those likely to produce larger litters and improved meat quality traits involves assaying for the presence of polymorphisms in the AMP activated protein kinase regulatory gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Screening animals to determine those likely to produce larger litters and improved meat quality traits involves assaying for the presence of polymorphisms in the AMP activated protein kinase regulatory gamma
                                                                                                                                                                                                                     The invention relates to a method for screening animals to determine those more likely to produce large litters and improved meat quality traits. The method involves assaying for the presence of a genotype in the sample of genetic material obtained from animal. The genotype is characterised by polymorphism(s) in the AMP activated protein Kinase requiatory gamma subunit (PRRAG3) gene. The method is used for screening animals e.g., pigs to determine those most likely to exhibit improved meat quality traits and to produce larger litters. The present sequence is pig PRRAG3 polymorphic variant (PRRAG3-52).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AMP activated protein kinase regulatory gamma subunit, PRKAG3 gene, screening; meat quality, single nucleotide polymorphism; SNP; pig;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "Wild type Val is substituted with Ile due
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 210; DB 23; Length 464;
Pred. No. 1.3e-22;
1; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 to single nucleotide polymorphism (SNP)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 HILTHKRLLKFLHIFGSLLPRPSFLYRTIQDIGIGTFRDLA 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Malek M, Plastow G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pig PRKAG3 polymorphic variant (PRKAG3-199).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (IOWA ) UNIV IOWA STATE RES FOUND INC
                                                                                                                                                                              Claim 36; Page 96-97; 109pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAE22987 standard; Protein; 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98.68;
97.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rothschild MF, Ciobanu DC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10-SEP-2001; 2001WO-US28283.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-SEP-2000; 2000US-231045P.
08-JAN-2001; 2001US-260239P.
18-JUN-2001; 2001US-299111P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2002-393850/42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                  464 AA;
                                  N-PSDB; AAD36458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAD36459
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                                                                                                                                          subunit gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                40;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAE22987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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CC in the sample of genetic material obtained from animal. The genotype is characterised by polymorphism(s) in the AMP activated protein CC kinase requiatory gamma subunit (PRRG3) gene. The method is used CC for screening animals e.g., pigs to determine those most likely to CC exhibit improved meat quality traits and to produce larger litters. CC The present sequence is pig PRRAG3 polymorphic variant (PRRAG3-200). XX

SQ Sequence 464 AA;

Query Match
Best Local Similarity 97.6%; Pred. No. 1.3e-22;
Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY I HILTHKRLLKFLHIFGSLLPRFSFLYRTIQDLGIGTFRDLA 41

Db 295 HILTHKRLLKFLHIFGTLLPRFSFLYRTIQDLGIGTFRDLA 335

Search completed: June 6, 2003, 11:01:03

Job time: 7.60595 secs
```

```
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
```

OM protein - protein search, using sw model

(without alignments) 1483.588 Million cell updates/sec June 6, 2003, 10:58:29; Search time 2.65674 Seconds ou:

US-09-826-581-6_COPY_320_360

1 HILTHKRLLKFLHIFGSLLP......PSFLYRTIQDLGIGTFRDLA 41 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283224 segs, 96134422 residues Searched:

283224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

pirl:* pir2:* pir3:* PIR_73:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result

No.	Score	Match	Match Length	BB :	QI	Description
-	112	52.6	330	2	T10759	AMP-activated prot
7	97	45.5	478	2	T25899	hetical F
3	63	29.6	379	7	T10971	~
4	56	26.3	1270	7	T26720	hypothetical prote
S	55.5	26.1	516	2	H82145	conserved hypothet
9	54.5	25.6	491	~	ITHUA2	alpha-2-antiplasmi
7	54		269	~	T39029	hypothetical prote
80	53		305	_	S52924	coproporphyrinogen
6	53		619	7	S67067	probable membrane
10	52.5	24.6	492	7	S43977	alpha-2-antiplasmi
11	52		557	7	S61980	histone acetyltran
12	51.5		371	7	E87536	ABC transporter, p
13	51.5		527	7	S46088	hypothetical prote
14	51.5		629	7	T18227	hypothetical prote
15	51		205	7	C64677	conserved hypothet
16	51		234	7	A71838	hypothetical prote
17	51		309	7	AG0368	coproporphyrinogen
18	51		373	?	D90032	hypothetical prote
19	51		564	7	F97601	afub (AE006182) [i
20	51		564	7	AG2823	ABC transporter, m
21	51		583	7	D82634	acetolactate synth
22	50.5		205	7	AB1903	hypothetical prote
23	50.5		295	7	H82600	w
24	50.5		412	N	876239	hypothetical prote
25	50.5		470	7	F82302	ശ
26	20		160	~	B81132	conserved hypothet
27	20	23.5	160	7	D81892	hypothetical prote
28	50		181	~	T36787	probable NTP pyrop
58	20		1402	7	S75938	chemotaxis protein

transporter [impor	hypothetical prote	hypothetical prote	one of two inverse	hypothetical prote	interleukin-1 rece	hypothetical prote	hypothetical prote	3-isopropylmalate	F9L1.2 protein - A	single-strand-DNA-					
G90496	T23142	A05037	H90483	H72603	AC1527	C61213	G64175	T02620	T24334	G02512	A85096	S47285	H75373	E86284	A70485
a	7	~	~	7	7	N	7	7	ď	~	7	7	7	~	7
487	1579	2136	109	150	206	224	304	442	486	712	1039	146	177	290	538
3.2	23.2	23.2	23.0	23.0	23.0	23.0	23.0	23.0	23.0	23.0	23.0	22.8	22.8	22.8	22.8
N				_	~	6	6	6	49	49	6	٦.	'n	'n	r.
49.5	49.5	49.5	49	4	49	4	4	7	•		~	48	48	48.5	48.

ALIGNMENTS

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AMP-activated protein kinase (EC 2.7.1.-) gamma chain - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 21-Jul-2000
C;Accession: 110759
R;Woods, A.; Cheung P, C.F.; Smith, F.C.; Davison, M.D.; Scott, J.; Beri, R.K.; Car.
J. Biol. Chem. 271, 10282-10290, 1996
A;Title: Characterization of AMP-activated protein kinase beta and gamma subunits: A
A;Reference number: 220738; Mu10:96215327; PMID:8626596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Description: is responsible for the regulation of fatty acid synthesis by phospho:
C;Superfamily: CAT3 protein
C;Keywords: fatty acid biosynthesis; phosphotransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ÷
                                                                                                                                                                                                                                                                                                                                                                       A,Molecule type: mRNA
A,Residues: 1-330 <MOO>
A,Residues: 1-330 <MOO>
A,Cross-references: BMBL:X95578; NID:91185270; PIDN:CAA64831.1; PID:91185271
A;Experimental source: strain Wistar
C;Complex: heterotrimer; alpha, beta and gamma chains
C;Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 330;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               :||||||:|||| :| : |:| |: :::| |||: ::| ||| 164 YILTHKRILKFLKLFITEFPRPEFMSKSLEELQIGTYANIA 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 HILTHKRLLKFLHIFGSLLPRPSFLYRTIQDLGIGTFRDLA 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 52.6%; Score 112; DB 2; Best Local Similarity 46.3%; Pred. No. 5.7e-08; Matches 19; Conservative 14; Mismatches 8.
                                                                                                                                                                                                                                                                                                                                          A; Status: translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δ
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hypothetical protein T20F7.6 - Caenorhabditis elegans
C; Species: Caenorhabditis elegans
C; Species: Caenorhabditis elegans
C; Species: Caenorhabditis elegans
C; Species: T26899
R; Miller, N.; Gattung, S.
submitted to the EMBL Data Library, April 1997
A; Description: The sequence of C. elegans cosmid T20F7,
A; Reference number: Z20107
A; Accession: T25899
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 14.78
A; MLL>
A; Residues: L478
A; Cross-references: EMBL: U997550; PIDN: AAB52856.1; GSPDB: GN00028; CESP: T20F7.6
A; Experimental source: strain Bristol N2; clone T20F7

C; Genetics

A; Gene: CESP:T20F7.6

A;Map position: X A;Introns: 33/3; 112/2; 144/1; 205/3; 263/2; 300/3; 380/3; 402/2; 451/1

Tue Jun 17 12:17:39 2003

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conserved hypothetical protein VC1874 [imported] - Vibrio cholerae (strain N16961 se C; Species: Vibrio cholerae
C; Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C; Accession: R82145
B; Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, F. Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Seller J. R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Altitle: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae. A; Reference number: A82035; WUID:20406833; PMID:10952301
                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-516 <HEI>
A;Cross-references: GB.AE004263; GB.AE003852; NID:99656399; PIDN:AAF95022.1; GSPDB:C
A;Experimental source: serogroup 01; strain N16961; biotype El Tor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Title: Structure of human alpha-2-plasmin inhibitor deduced from the cDNA sequence A;Reference number: A41504; MUID:88139254; PMID:2830248
A;Accession: A41504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A,Molecule type: mRNA
A,Residues: 1-32, W, 34-491 <TON>
A,Cross-references: GB:D00174; NID:g219409; PIDN:BAA00124.1; PID:g219410
B;HOlmes, W.E.; Nelles, L.; Lijnen, H.R.; Collen, D.
J. Biol. Chem. 262, 1659-1664, 1987
A;Title: Primary structure of human alpha-2-antiplasmin, a serine protease inhibitor
A;Reference number: A26684; MUID:87109313; PMID:2433286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alpha-2-antiplasmin precursor [validated] - human
N;Alternate names: alpha-2-PI; alpha-2-plasmin inhibitor precursor
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 31-Jul-1989 *sequence_revision 12-Apr-1996 *text_change 08-Dec-2000
C;Accession: A31402; A32163; A41504; A26684; A24708; PC2129; S00068; S32524; S32529
R;Hirosawa, S.; Nakamura, Y.; Miura, O.; Sumi, Y.; Aoki, N.
Proc. Natl. Acad. Sci. U.S.A. 85, 6836-6840, 1988
A;Title: Organization of the human alpha-2-plasmin inhibitor gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-491 <HIR1>
A; Residues: 1-491 <HIR1>
A; Cross-references: 08: May 2078 (GB: J03830; NID: 9177884; PIDN: AAA51554.1; PID: 9177886
A; Lrosswa, S.; Makamura, Y.; Miura, O.; Sumi, Y.; Aoki, N.
Proc. Natl. Acad. Sci. U.S.A. 86, 1612-1613, 1989
A; Reference number: A32163
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A; Cross-references: GB: J02654; NID: 9178750; PIDN: AAA35543 1; PID: 9178751
A; Orde: the authors translated the codon GAT for residue 289 as His
A; Note: the authors translated the codon GAT for residue 289 as His
B; Suni, Y: Nakamura, Y: Aoki, N.; Sakai, M.; Muramatsu, M.
J. Biochem. 100, 1399-1402, 1986
A; Title: Structure of the carboxyl-terminal half of human alpha-2-plasmin inhibitor
A; Reference number: A24708; MUID: 87137400; PMID: 3818581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 516;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 ILTHKRLLKFLHIFGSLLPRPSFLYRTIQD-----LGIGTFRDL 40
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A; Residues: 1-491 <HIR2>
K; Tone, M.; Kikuno, B.; Kume-Iwaki, A.; Hashimoto-Gotoh, T.
J. Biochem. 102, 1033-1041, 1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A, Accession: A32163
A, Status: not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26.1%;
31.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 26.1
Best Local Similarity 31.8
Matches 14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Map position: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Genetics:
A;Gene: VC1874
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A;Introns: 122/1; 154/1; 183/1; 227/3; 276/2; 324/2; 368/3; 450/3; 701/3; 783/3; 852/3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary; translated from CB/EMBL/DDBJ
A;Molecule type: DMA
A;Residues: 1-1270 <WIL>
A;Residues: 1-1270 <WIL>
A;Cross-references: EMBL:AL021483; PIDN:CAA16349.1; GSPDB:GN00022; CESP:Y45F10A.6
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A;Residues: 1-1270 <WI2>
A;Cross-references: EMBL:AL021488; PIDN:CAA16368.1; GSPDB:GN00022; CESP:Y45Fl0A.6
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C.Species: Caenorhabditis elegans
C.Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                    C:Species: Phaseolus vulgaris (kidney bean)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
C:Accession: T10971
                                                                                Gaps
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         Score 97; DB 2; Length 478;
Pred. No. 1.1e-05;
9; Mismatches 8; Indels
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A:Accession: T10971
A:Status: preliminary: translated from GB/EMBL/DDBJ
A:Molecule type: mRM=
A:Residues: 1-379 cABE>
A:Cross-references: EMBL:U40713; NID:g1113940; PID:g1113941
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                                                                                                                                                                 11;
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43.6%; Pred. No. 20;
Live 3; Mismatches 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         submitted to the EMBL Data Library, January 1998
A;Reference number: 220285
A;Accession: T26911
A;Status: preliminary; translated from GB/EMBL/DDBJ
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Pred. No. 0.54;
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    submitted to the EMBL Data Library, November 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted to the EMBL Data Library, January 1998 A; Reference number: 220256 A; Accession: 126720
                                                                          9; Mismatches
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            45.5%;
52.8%;
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48.6%;
                                                                       19; Conservative
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Matches 17; Conservative
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                                           Best Local Similarity
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            Query Match
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Gaps ŝ

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N'Alternate names: coproporphyrinogen III Oxidase, aerobic
C;Species: Pseudomonas aeruginosa
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 31-Dec-2000
C;Accession: 552924; F83641
R;Hungerer, C.; Troup, B.; Jahn, D.
submitted to the EMBL Data Library, Pebruary 1995
A;Bescription: Cloning and regulation of the Pseudomonas aeruginosa hemF gene encod:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic I
A;Reference number: A42950; MUID:20437337; PMID:10984043
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A;Experimental source: strain 972h-; cosmid c6C3
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A;Status: preliminary
A;Status: preliminary
A;Status: DNA
A;Residues: 1-305 <HUNA
A;Residues: 1-305 <HUNA
A;Residues: 1-305 <HUNA
A;Cross-references: EMBL:X85015; NID:9747872; PIDN:CAA59376.1; PID:9695693
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, Nature 406, 959-964, 2000
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                                                                                                                                                                                                                                                                                                                                                                                                            C, Species: Schizosaccharomyces pombe
C, Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein SPAC6C3.05 - fission yeast (Schizosaccharomyces pombe)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C, Accession: T39029
R; Devlin, K.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V. submitted to the EMBL Data Library, February 1996
A; Reference number: 221750
A; Accession: T39029
                                                        Gaps
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                                                                                                                                                                  2 ILTHKRLLKFLHIFGSLLPRPSFLYRTIQDLGIGTFRDL
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A;Molecule type: DNA
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Pred. No. 6.9;
5; Mismatches 2
                                                                                                                        4 THKRLLKFLHIFGSLLPRPSFLYRTIQDLGIGTFR
                  ed. No. 11;
Mismatches
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                  Pred. No.
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C;Superfamily: coproporphyrinogen oxidase
                                                 2;
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A;Experimental source: strain PAO1
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                  48.68;
               Best Local Similarity 48.6
Matches 17; Conservative
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A; Residues: 1-269 <DEV>
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A; Residues: 1-305 <STO>
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A;Gene: SPDB:SPAC6C3.05
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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A; Wolecule type: mRNA
A; Residues: 218-491 < SUM>
A; Cross-references: DDBJ:D000116; NID:g219407; PIDN:BAA00070.1; PID:g219408
A; Cross-references: DDBJ:D000116; NID:g219407; F:; Suzuki, N.; Aoki, N.
Biochem. Biophys. Res. Commun. 200, 417-422, 1994
A; Title: Different NH2-terminal form with 12 additional residues of alpha2-plasmin inhib
A; Reference number: PC2129; MUID:94220119; PMID:8166714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3. Biol. Chem. 261, 15591-15595, 1986
A;Title: Cross-linking site in fibrinogen for alpha-2-plasmin inhibitor.
A;Reference number: A92565; WIDIS/87057190; PMID:2877981
A;Contents: annotation; cross-linking site for fibrin
C;Comment: After synthesis in the liver, 30-50% of alpha-2-antiplasmin circulates in pla inhibit activated coagulation factor XIII from forming an isopeptide cross-link with fi
                                                                                                                                                                                                                                                                                                                                                                  A, Experimental source: Hep G2 cells cultured in serum-free medium
A,Note: In the presence of serum, this material loses the first twelve residues and beco
Rilijnen, H.R.; Holmes, W.E.; Van Hoef, B.; Wiman, B.; Rodriguez, H.; Collen, D.
Bur. J. Biochem. 166, 565-574, 1987
A,Title: Amino-acid sequence of human alpha-2-antiplasmin.
A;Reference number: S00008; MUID:87275946; PMID:2440681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: protein
A;Residues: 40.48, (26, 50-104, D',106-114, X',116-327, X',329-340, XXXXX',345-407, 'G',409-
A;Note: 49-Gly and 408-Gly may represent heterogeneity; 2 disulfide bonds were determine
R;Bangert, K; Johnsen, A.H.; Christensen, U; Thorsen, S.
Blochen, J. 291, 623-3625, 1993
A;Title: Different N terminal forms of alpha(2)-plasmin inhibitor in human plasma.
A;Reference number: S32524; MUID:93249387; PMID:8484741
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C.Superfamily: antithrombin III
C.Keywords: extracellular protein; fibrinolysis; glycoprotein; plasma; serine proteinase
C.Z.O.T/Domain: signal sequence #status predicted <SIG>
F.28-39/Domain: propeptide #status experimental <PRO>
F.40-491/Product: alpha-2-antiplasmin #status experimental <AMT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: protein
A;Residues: 28-58 -84-8ANN
A;Residues: 28-58 -84-8ANN
B;Bophild, J.J.: Valnickova, Z.; Thogersen, I.B.; Pizzo, S.V.; Salvesen, G.
Biochem. J. 291, 933-938, 1993
A;Tile: An examination of the inhibitory mechanism of serpins by analysing the interact
A;Reference number: S32529; MUID:93256910; PMID:7683878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F.41/Cross-link: isopeptide (Gln) (interchain to Lys-322 of fibrin alpha chain) #status F.70-152.103-143/Disulfide bonds: #status experimental F.126.295, 309, 316/Disulfide bonds: #status experimental F.126.295, 309, 316/Disulfide bonds: #status experimental F.401-402/Cleavage site: Wet-Ser (chymotrypsin) (partial) #status experimental F.403-404/Cleavage site: Met-Ser (chymotrypsin) (partial) #status experimental F.403-404/Cleavage site: Met-Ser (chymotrypsin) (partial) #status experimental F.404-405/Cleavage site: Met-Ser (chymotrypsin) (partial) #status experimental F.404/Inhibitory site: Met (chymotrypsin) #status predicted F.404/Inhibitory site: Met (chymotrypsin) (covalent) #status absent
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F:39-40/Cleavage site: Pro-Asn (unidentified plasma proteinase) #status experimental
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K;Suni, Y.; Ichikawa, Y.; Nakamura, Y.; Miura, O.; Aoki, N.
J. Biochem. 106, 703-707, 1984
A;Title: Expression and characterization of Pro alpha-2-plasmin inhibitor.
A;Reference number: A57869; MuID:90110073; PMID:2606916
A;Contents: annotation; role of propebtide
R;Kimura, S.; Aoki, N.
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A;Introns: 21/3; 34/3; 55/3; 123/1; 171/1; 239/1; 286/3; 355/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 54.5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: protein
A; Residues: 28-43;64-69;405-409 <ENG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25.6%;
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A;Gene: GDB:PLI

C; Function:

Query Match

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24.48;
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25.6%;
   24.6%;
47.2%;
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A;Map position: 16L
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   Query Match
Best Local Similarity 47.23
Matches 17; Conservative
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nes 11; Conservative
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A; Residues: 1-557 < WAN>
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A; Residues: 1-371 <STO>
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C.Species: Saccharomyces cerevisiae
C.Species: 12-Jul-1996 #sequence_revision 12-Jul-1996 #text_change 19-Apr-2002
C.Species: 257067; S67063
R.Hughes, B.; Pohl, T.M.
Submitted to the Protein Sequence Database, July 1996
A.Recession: S67067
A.Molecule type: DNA
A.Residues: 1-619 - 4NGG
A.Residues: 1-619 - 4NGG
A.Residues: 1-619 - 4NGG
A.Residues: 1-619 - 4NGG
A.Residues: S7063
A.Residues: A.Resid
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C:Species: Bos primigenius taurus (cattle)
C:Date: 20-oct-1994 #sequence_revision 19-May-1995 #text_change 16-Jul-1999
C:Date: 20-oct-37226
C:Date: 20-oct-3737; S27260
R:Christensen, S.; Berglund, L.; Sottrup-Jensen, L.
FEBS Lett. 343, 223-228, 1994
A:Title: Primary structure of bovine alpha-2-antiplasmin.
A:Febreace number: S43977; MUID:94229242; PMID:7513654
A:Accession: S43977
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FEBS Lett. 312, 100-104, 1992
A:Title: Bovine alpha(2)-antiplasmin. N-terminal and reactive site sequence.
A;Reference number: S27260; MUID:93050153; PMID:1385210
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A; Residues: 1-492 < CHR>
A; Cross-references: GB:X78436; NID:9498821; PIDN:CAA55200.1; PID:9498822
A; Experimental source: liver
                                                                                                                                                                                                                                           probable membrane protein YOR175c - yeast (Saccharomyces cerevisiae)
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A:Residues: 23-27, '0', 29-39,'P', 41-42,'E', 44-45;374-415 <CH2>
S:Superfamily: antithrombin III
C:Reywords: glycoprotein
F:1-22/Domain: signal sequence #status predicted <SIG>F:23-492/Product: alpha-2-antiplasmin #status predicted <MAT>F:11-144/Disulfide bonds: #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 HKRLLKFL---HIFGSLLPRPSFLYRTIQD-LGIGTFRDL 40
                                    LTHKRLLKFLHIFGSLLP-----RPSFLYRTIQDLGI 34
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Pred. No.
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42.58;
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Best Local Similarity
Matches 17; Conserv
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C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C;Accession: E87536
B; Accession: E87536
B; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kn n, J.; Ermolaeva, M.; White, O.; Salzaberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, Proc. Natl. Acad. Sci. U.S.A. 99, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173699; PMID:11259647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R.Rang, Y.; Ahmed, A.; Bussey, H.; Fortin, N.; Friesen, J.D.; Hall, J.; Storms, R.K. submitted to the EMBL Data Library, December 1995
A;Description: The sequence of Saccharomyces cerevisiae chromosome XVI left arm. A;Reference number: S61959
A;Accession: S61980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Cross-references: EMBL: U43281; NID: 91151218; PIDN: AAB68213.1; PID: 91151240; GSPDB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABC transporter, permease protein, probable CC2318 [imported] - Caulobacter crescent
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                                                                                                                                                                                                                                                                                                                                            histone acetyltransferase (EC 2.3.1.48), RNA polymerase II-associated [validated]
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                                                                                                                                                                                                                                                                                                                                                                  N;Alternate names: protein LPG22c; protein YpL086c
C;Species: Saccharomyces cerevisiae
C;Date: 10-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 19-Apr-2002
C;Accession: S61980
                                                                   Gaps
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   Length 492;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Superfamily: hypothetical protein YPL086c
C;Keywords: acyltransferase; coenzyme A; transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11;
                                                                                                                                                               14;
   DB 2;
                                                                                                                         4 THKRLLKFLHI-FGSLLPRPSFLYRTIQDLGIGTFR 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 52; DB 2;
Pred. No. 29;
7; Mismatches 11
                                                            2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                k; Score 51.5; DE
k; Pred. No. 22;
11; Mismatches
Score 52.5; Pred. No. 22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Gene: SGD: ELP3; ELP3; MIPS: YPL086c
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2;

Gaps . 8

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A; Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Frase A; Title: The complete genome sequence of the gastric pathogen Helicobacter pylori. A; Reference number: A64520; MUID:97394467; PMID:9252185
A; Accession: C64677
A; Status: preliminary; nucleic acid sequence not shown: translation not shown A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-205 < GTOM>A; Cross-references: GB:ABC00631; GB:ABC00511; NID:92314421; PIDN:AAD08305.1; PID:92
C; Superfamily: conserved hypothetical protein bl120
                                                                                                                                                                                                                                                                                                                                              Query Match 23.9%; Score 51; DB 2; Length 205; Best Local Similarity 37.8%; Pred. No. 13; Matches 14; Conservative 6; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10 KFLHIFGSLL-----PRPSFLYRTIQDLGIGTFRDLA 41
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Job time: 4.65674 secs
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C;Species: Helicobacter pylori
C;Species: Helicobacter pylori
C;Accession: C64677
R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D. Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenne Son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L. Nature 388, 539-547, 1997
                                                                                                                                                                                                                                                                                                                                                                          A,Molecule type: DNA
A,Residues: 1-527 <RIE>
A;Cross-references: EMBL:236083; NID:9536599; PIDN:CAA85178.1; PID:9536600; MIPS:YBR214w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Experimental source: strain $288C
R;Dubois, E.; El Bakkoury, M.; Glansdorff, N.; Messenguy, F.; Pierard, A.; Scherens, B.;
submitted to the Protein Sequence Database, August 1994
A;Reference number: $45782
A;Accession: $46090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5
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                                                                                                                                       C;Species: Saccharomyces cerevisiae
C;Date: 26-Aug-1994 #sequence_revision 09-Sep-1994 #text_change 19-Apr-2002
C;Accession: S46088; S46090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein - yeast (Candida albicans)
C;Species: Candida albicans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
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                                                                   hypothetical protein YBR214w - yeast (Saccharomyces cerevisiae) N;Alternate names: hypothetical protein YBR1501
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                                                                                                                                                                                                                                          R;Rieger, M. submitted to the Protein Sequence Database, August 1994 submitted to the Protein S45734 A;Reference number: S45734 A;Accession: S46088
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A;Molecule type: DNA
A;Residues: 1-629 <BAR>
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R;Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, November 1998
A;Accession: ¶18227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A:Cross-references: EMBL:236083; MIPS:YBR214w A:Experimental source: strain S288C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 114-527 < DUB>
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June 6, 2003, 10:57:04; Search time 1.50788 Seconds (without alignments) 1127.761 Million cell updates/sec
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1 HILTHKRLLKFLHIFGSLLP......PSFLYRTIQDLGIGTFRDLA 41
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Q9ugi9 homo sapien Q9ugi9 homo sapien Q9ugi0 homo sapien P58108 bos taurus O54950 mus musculu P80385 rattus nory P54619 homo sapien Q10308 sethizosacch P08697 homo sapien Q10308 sethizosacch P18880 bos taurus Q9byh1 homo sapien P2880 bos taurus Q9byh1 homo sapien P2880 perdomonas P38314 saccharomyc Q82cf9 yersinia pe Q60677 mus musculu Q89016 mus musculu Q89016 mus musculu Q83713 rattus nory Q58196 methanococc Q57320 hamophilus P28808 perainia pe P23739 rattus nory Q58196 methanococc Q57320 hamophilus Q48211 hamophilus P28808 perainia pe P3739 rattus nory Q58196 rattus nory Q59557 homo sapien P04694 rattus nory Q99557 homo sapien P04694 rattus nory Q91500 trichechus P02500 trichechus
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606 1 ABD4_HUMAN 184 1 RR4_PATER 196 1 RR4_PATSQ 307 1 YC23_SYNY3 346 1 TH13_SCHPO 471 1 SDEF_MYCLE 471 1 YODO_BACSU 692 1 EFG_MYCPU 847 1 SYA_HELPY 923 1 PH87_YEAST 1036 1 X414_MYCGE	ULT 1 LHUMAN ALTHUMAN ALTHUMAN O9UGI9; Q9NRLI; 16-OCT-2001 (Rel. 40, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) 17-OCT-2001 (Rel. 40, Last annotation update) 18-OCT-2001 (Rel. 40,	Cheung P.C., Salt I.P., Davies S.P., Hardie D.G., Carling D.; "Characterization of AMP-activated protein kinase gamma-subuni "Soforms and their role in AMP binding."; Biochem. J. 346:659-669(2000). [2] SEQUENCE FROM N.A. TISSUE-Skeletal muscle; MEDINRE-20280150; PubMed-10818001; MIDINRE-20280150; PubMed-10818001; Milan D., Jeon JT., Looft C., Amarger V., Robic A., Thelande. Rogel-Gaillard C., Paul S., Iannuccelli N., Rask L., Ronne H., Lundstroem K., Reinsch N., Gellin J., Kalm E., Le Roy P., Charr Andersson L.; "A mutation in PRRAG3 associated with excess glycogen content."	skeletal muscle."; Schonec 288 11248-1151(2000).	രള്ള നെവ്വ്
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modified and this statement is not removed.
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40; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                      AAKH_HUMAN
                                                                                                                                                                                       SEQUENCE
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AAKH_HUMAN
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C. -! FUNCTION: AMPK IS RESPONSIBLE FOR THE REGULATION OF FATTY ACID STRUTES. BY EHOSPHORYLATION OF ACETYL-COA CARBOXYLASE. ALSO REGULATES CHOLESTEROL SYNTHESIS VIA PHOSPHORYLATION AND INACTIVATION OF HYDROXYMETHYLGLUTARYL-COA REDUCTASE AND HORMONE-STRUTIVE LIPASE. THIS IS A REGULATORY SUBUNIT. IT MAY PLAY A ROLE IN THE REGULATION OF ENERGY METABOLISM IN SKELETAL MUSCLE.

-! SUBUNIT: HETEROTRIMER OF EN ALPHA CATALYTIC SUBUNIT, A BETA AND A GAMMA NON-CATALYTIC REGULATORY SUBUNITS.

-! TISSUE SPECIFICITY: MUSCLE.

-! DISBASE: DEFECTS IN PRKAG3 (RN-) ARE ASSOCIATED WITH EXCESS GLYCOGEN COMPIENT (ABOUT 70%) IN SKELETAL MUSCLE. THIS MUTATION OF COLUMN AND HAS BENEFICIAL EFFECTS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the SWiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        THUS,
                                                                                                                                                                                                                                                                                                                                                                           16-OCT-2001 (Rel. 40, Last Sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
5'-AMP-activated protein kinase, gamma-3 subunit (AMPK gamma-3 chain)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A., AND VARIANT RN(-) GLN-200.
TISSUE-SKeletal muscle;
MEDLINE-20280150; PubMed-10818001;
Milan D., Jeon J.-T., Looft C., Amarger V., Robic A., Thelander M.,
Rogel-Gaillard C., Paul S., Iannuccelli N., Rask L., Ronne H.,
Lundstroem K., Reinsch N., Gellin J., Kalm E., Le Roy P., Chardon P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 THIS MUTATION IS OF CONSIDERABLE ECONOMIC SIGNIFICANCE IN THE PIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: BELONGS TO THE 5'-AMP-ACTIVATED PROTEIN KINASE, GAMMA SUBUNIT FAMILY.
                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "A mutation in PRKAG3 associated with excess glycogen content in pig
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ON MEAT CONTENT BUT DETRIMENTAL EFFECTS ON PROCESSING YIELD.
                                                                                                                                                                                                                            0;
                                                                                                                                                                                                 100.0%; Score 213; DB 1; Length 464; 100.0%; Pred. No. 2.1e-21; ive 0; Mismatches 0; Indels (
                                                                                                                        T -> A (IN REF. 1).
MQ -> IE (IN REF. 1).
Q -> K (IN REF. 1).
ALGA -> PSGPEKI (IN REF. 1).
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                                                                                                                                                                           53985C2C77003A63 CRC64;
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                                                              Repeat; CBS domain.
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                                                                                    CBS 2.
CBS 3.
CBS 4.
                     InterPro; IPR000644; CBS_domain.
Pfam; PF00571; CBS; 4.
SMART; SM00116; CBS; 4.
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303 356
303 356
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164
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51514 MW;
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16-0CT-2001 (Rel. 40, Last sequ
16-0CT-2001 (Rel. 40, Last anno
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Conservative (
                                                              Fatty acid biosynthesis;
HGNC:9387; PRKAG3
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                                                                                                                                                                           464 AA;
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Matches 41; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                            Sus scrofa (Pig).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          skeletal muscle.
                                                                                                                                                                                                                                                                                                                                                                                                                   (AMPK gamma3).
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          MIM; 604976;
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                                                                                                                          CONFLICT
                                                                                                                                                                           SEQUENCE
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                                                                                                                                       CONFLICT
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                                                                                                                                                                                                                                                                                                                                                    O9MYP4;
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  Genew;
                                                                          DOMAIN
                                                                                       DOMAIN
                                                                                                   DOMAIN
                                                                                                            DOMAIN
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                                                                                                                                                                                                                                                                                                                              AAKI_PIG
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and for commercial
                   (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. (ISOFORM B).
MEDLINE-20564210; PubMed-11112354;
Lang T., Yu L., Giang T., Jiang J., Chen Z., Xin Y., Liu G., Zhao S.;
"Molecular cloning, genomic organization, and mapping of PRKAG2, a
heart abundant gamma-2 subunit of 5'-AMP-activated protein kinase, to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9UGGO; Q9UDN8; Q9ULX8; Cort-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-UN-2002 (Rel. 41, Last annotation update)
5'-AMP-activated protein kinase, gamma-2 subunit (AMPK gamma-2 chain)
(AMPK gamma2) (H91620p).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (ISOFORM A).
MEDLINE-20164049; PubMed=10698692;
Cheung P.C.F., Salt I.P., Davies S.P., Hardie D.G., Carling D.;
Characterization of AMP-activated protein kinase gamma-subunit
Isoforms and their role in AMP binding.";
Biochem. J. 346:659-669(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                 Fatty acid biosynthesis; Repeat; CBS domain; Disease mutation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 464;
                                                                                                                                                                                                                                                                                       CBS 1.
CBS 3.
CBS 3.
CBS 4.
R -> Q (IN RN-).
W, 17638CB12A2BA9DF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
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Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  295 HILTHKRILKFLHIFGTILPRPSFLYRTIQDLGIGTFRDLA 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 HILTHKRLLKFLHIFGSLLPRPSFLYRTIQDLGIGTFRDLA 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 210; DB 1;
Pred. No. 5.4e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              569 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Mismatches
                         entities requires a license agreement ( or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                        EMBL; AF214521; AAF73989.1; -.
EMBL; AF214520; AAF73988.1; -.
InterPror; IFR000644; CBS_domain.
Pfam; PF00571; CBS; 4.
SMART; SM00116; CBS; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD; P1
Q9NUZ9; Q9ULX8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. (ISOFORM B).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   51308 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98.6%;
97.6%;
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Genomics 70:258-263(2000).
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SIMILARITY: CONTAINS 4 CBS DOMAINS.
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                                                                                                                                                                                                                                                                                                                                                                                                              Genew;
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J. Clin. Invest. 109:357-362(2002)

-! FUNCTION: AMEN IS RESPONSIBLE FOR THE REGULATION OF FATTY ACID SYNTHESIS BY PHOSPHORYLATION OF ACETYL.-COA CARBOXYLASE. ALSO REGULATES CHOLESTEROL SYNTHESIS VIA PHOSPHORYLATION AND INACTIVATION OF HYDROXYMETHYLGLUTARYL.-COA REDUCTASE AND HORMONE-SENSITIVE LIPASE. THIS IS A REGULARORY SUBUNIT.
-!- SUBUNIT: HETEROTRIMER OF AN ALPHA CATALYTIC SUBUNIT.
-!- ALTERNATIVE PRODUCTS: 2 ISOFORMS: A (SHOWN HERE) AND B; ARE PRODUCED BY ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- TISSUE SPECIFICITY: ISOFORM B IS UBIQUITOUSLY EXPRESSED EXCEPT IN LIVER AND THYMUS. THE HIGHEST LEVEL IS DETECTED IN HEART WITH ABUNDANT EXPRESSION IN PLACENTA AND TESTIS.
-!- DISEASE: Defects in PRRAC3 are the cause of Wolff-Parkinson-White syndrome (WPWS or preexcitation syndrome). It is the second most
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  common cause of paroxysmal supraventricular tachycardia. WPWS can be associated with a form of hypertrophic cardiomypathy (HCM), which is probably due to polysaccharide storage in the heart. Defects in PRKAG2 may not be a frequent cause of HCM where no features of pre-excitation are found in affected individuals. SIMILARIY: BELONGS TO THE 5'-AMP-ACTIVATED PROTEIN KINASE, GAMMA SUBUNIT FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                             Blair E., Redwood C., Ashrafian H., Oliveira M., Broxholme J., Kerr B., Salmon A., Oestman-Smith I., Watkins H.; "Mutations in the gamma(2) subunit of AMP-activated protein kinase cause familial hypertrophic cardiomyopathy: evidence for the central role of energy comprendse in disease pathogenesis."; Hum. Mol. Genet. 10:1215-1220(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arad M., Benson D.W., Perez-Atayde A.R., McKenna W.J., Sparks E.A., Kanter R.J., McGarry K., Seidman J.G., Seidman C.E.; "Constitutively active AMP kinase mutations cause glycogen storage
                                                                                                                                                                       MEDLINE-21614537; Pubmed=11748095;
Gollob M.H., Seger J.J., Gollob T.N., Tapscott T., Gonzales O.,
Bachinski L., Roberts R.;
"Novel PRKAG2 mutation responsible for the genetic syndrome of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gollob M.H., Green M.S., Tang A.S.-L., Gollob T., Karibe A., Almada F., Almada F., Lozado R., Shah G., Fananapazir L., Bachinski L.L., Roberts R., Shak G., Fananapazir L., New Engl. J. Med. 346:300-300(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-21279949; PubMed=11407343; Gollob H., Green M.S., Tang A.S.-L., Gollob T., Karibe A., Al Sayegh A.H., Ahmad F., Lozado R., Shah G., Fananapazir L., Bachinski L.L., Roberts R.; Bachinski L.L., Roberts R.; Midentification of a gene responsible for familial Wolff-Parkinson Wild a gene responsible for familial New Engl. J. Nec. 344:1823-1831(2001).
                                                                                                                                                                                                                                                                              ventricular preexcitation and conduction system disease with childhood onset and absence of cardiac hypertrophy.";
Circulation 104:3030-3033(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gollob M.H., Green M.S., Tang A.S.-L., Gollob T., Karibe A., Al Sayegih A.H., Ahmad F., Lozado R., Shah G., Fananapazir L., Bachinski L.L., Roberts R., G., New Engl. J. Med. 345:552-552(2001).
                                             SEQUENCE OF 254-569 FROM N.A.
Walker C., Scott K., Bauer C., Harkins R.;
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
  Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VARIANTS WPWS GLN-302; ASN-400 AND ILE-488.
                                                                                                                                                                                                                                                                                                                                                                                   VARIANTS HCM/WPWS LEU-350 INS AND ARG-383.
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                                                                                                                                                       VARIANT WPWS GLY-531.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VARIANT WPWS GLN-302,
                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=21264334;
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16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
5'-AMP-activated protein kinase, gamma-1 subunit (AMPK gamma-1 chain)
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                        biosynthesis; Repeat; CBS domain; Alternative splicing;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ALFEANORI).

R -> G (IN WPWS; ABSENCE OF CARDIAC HYPERTROPHY; ONSET IN CHILDHOOD).

/FTId=VAR_013269.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -> RL (IN FAMILIAL HCM WITH WPWS;
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H -> R (IN FAMILIAL HCM WITH WPWS;
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/FTId=VAR_013267.
N -> I (IN WPWS WITH CARDIAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 124; C. Pred. No. 3.1e-09; Pred. No. 3.1e-09;
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397 YILTHKRILKFLQLFMSDMPKPAFMKQNLDELGIGTYHNIA 437
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                                                                                                                                                                 EMBL; AJ249976; CAB65116.1; --
EMBL; AF087875; AAK00413.1; --
EMBL; AK001887; BAA91962.1; --
EMBL; BC020540; AAH20540.1; --
EMBL; AB025580; BAA84695.1; --
EMBL; AC006966; AAF03528.1; --
                                                                                                                                                                                                                                                                                                                                                             interPro; IPR000644; CBS_domain.
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Best Local Similarity 51.2%
Matches 21; Conservative
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409
483
555
302
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SMART; SM00116; CBS; 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bos taurus (Bovine).
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AAKG_BONT
ACC P58108.
DT 16-0CT
DT 16-0CT
DF 5'-AMP
DE (AMPKG
GN BOS La
OC BUNARY
OC BUNARY
OC BONTGAR
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Score 112; DB 1;
Pred. No. 7.3e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fatty acid biosynthesis; Repeat; CBS domain.
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                                                                                                       SIMILARITY: CONTAINS 4 CBS DOMAINS.
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STRAIN-Sprague-Dawley; TISSUE-Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CBS 1.
CBS 2.
CBS 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                MGD; MGI:108411; Prkaq1.
InterPro: JRR000644; CBS_domain.
Pfam: PF00571; CBS; 4.
SMART; SM00116; CBS; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-FEB-1995 (Rel. 31, Created)
01-NOV-1997 (Rel. 35, Last sequ
16-OCT-2001 (Rel. 40, Last anno
                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF036535; AAB95475.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      37554 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              52.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 Similarity 48.8%
20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Beri R.K., Carling D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      330 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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196
270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
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Best Local
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11D AAKG

AAKG

P8031

D1 01-F

P8031

D1 01-F

D1 01-F

D1 01-F

D1 01-F

D2 01-F

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D4 01-F

D5 01-F

D6 01-F

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δλ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the SWiss Institute of Bioinformatics and the EMBL outstation—the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                          SUBDILITED (DEC. 2000) TO THE PRED, GENERAL ADDED GATABASES.
-!- FUNCTION: AMPK IS RESPONSIBLE FOR THE REGULATION OF FATTY ACID
SYNTHESIS BY PHOSPHORVIATION OF ACTYL.-COA CARBOXYLASE. ALSO
REGULATES CHOLESTEROL SYNTHESIS WITH PROSPHORYLATION AND
INACTIVATION OF HYDROXYMETHYLGIUTARYL-COA REDUCTASE AND HORMONE-
SENSITIVE LIPASE. THIS IS A REGULATORY SUBUNIT.
-!- SUBUNIT: HETEROTRIMER OF AN ALPHA CATALYTIC SUBUNIT, A BETA AND A
GAMMA NON-CATALYTIC REGULATORY SUBUNITS.
-!- SIMILARITY: BELONGS TO THE 5'-AMP-ACTIVATED PROTEIN KINASE, GAMMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-DEC-1998 (Rel. 37, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
5'-AMP-activated protein kinase, gamma-1 subunit (AMPK gamma-1 chain)
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Shamsadin R., Jantsan K., Adham I., Engel W.;
Shamsadin R., Jantsan K., Adham I., Engel W.;
"Cloning, organisation, chromosomal localization and expression analysis of the mouse Prkaq1 gene.";
Cytogenet. Cell Genet. 92:134-138(2001).
-!- FUNCTION: AMPK IS RESPONSIBLE FOR THE REGULATION OF FATTY ACID SYNTHESIS BY PHOSPHORYLATION OF ACEPTYL-COA CARBOXILAGE. ALSO REGULATES CHOLESTEROL SYNTHESIS VIA PHOSPHORYLATION AND INACTIVATION OF HYPROXYMSTHYLGLUTARYL-COA REDUCTASE AND HORMONE-SENSITIVE LIPASE. THIS IS A REGULATORY SUBJUIT.
                                                                       Benkel B., Kollers S., Fries R., Sazanov A., Yoshida E., Davoren J.,
Hickey D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F130AC8EE2BFEB89 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 HILTHKRLLKFLHIFGSLLPRPSFLYRTIQDLGIGTFRDLA 41
                                                                                                                                     "Characterization of the bovine AMPK gamma-1 gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CBS domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           330 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                   SUBUNIT FAMILY.
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CBS 3.
CBS 4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fatty acid biosynthesis; Repeat;
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15-DEC-1998 (Rel. 37, Last sequ
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19; Conserv
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                                                     SEQUENCE FROM N.A.
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PRKAGI OR PRKAAC.
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054950;
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Best Local S
Matches 19
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SUBUNIT: HETEROTRIMER OF AN ALPHA CATALYTIC SUBUNIT, A BETA AND A GAMMA NON-CATALYTIC REGULATORY SUBUNITS.
SIMILARITY: BELONGS TO THE 5'-AMP-ACTIVATED PROTEIN KINASE, GAMMA SUBUNIT FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
5'-AMP-activated protein kinase, gamma-1 subunit (AMPK gamma-1 chain)
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinee, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
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BEDLINE-26050763; PubMed-7961907;
Stapleton D., Gao G., Witchell B.J., Widmer J., Mitchelhill K.,
Teh T., House C.M., Witters L.A., Kemp B.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-Wistar;
MEDLINE-96215327; PubMed-8626596;
Woods A., Cheung P.C.F., Smith F.C., Davison M.D., Scott J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           subunits. Assembly of the heterotrimeric complex in Vitro."; J. Biol. Chem. 271:10282-10290(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 330;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=Sprague-Dawley; TISSUE=Liver;
MEDLINE-96224074; PubMed=8621499;
Gao G., Rernandez C.S., Stapleton D., Auster A.S., Widmer
Dyck J.R.B., Kemp B.E., Witters L.A.;
"Non-cetalytic beta- and gamma-subunit isoforms of the
5'-AMP-activated protein kinase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9; Indels
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; D504707B83512DDC CRC64;
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DOMAIN
SEQUENCE
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Q09138;
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Best Local (
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                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the SWISS Institute of Bioinformatics and the EMBL outstation. the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-96224074; PubMed-8621499; Gao G., Fernandez C.S., Stapleton D., Auster A.S., Widmer J., Dyck J.R.B., Kemp B.E., Witters L.A.; "Non-catalytic beta-and gamma-subunit isoforms of the 5'-AMP-activated
                                                                                       HYDROXYMETHYLGLUTARYL-COA REDUCTASE. APPEARS TO ACT AS A METABOLIC STRESS-SENSING PROTEIN KIRASE SWITCHING OFF BIOSYNTHETIC PATHWAYS WHEN CELLULAR ATP LEVEUS. ARE DEPLETED AND WHEN 5'-AMP RISES IN RESPONSE TO FUEL LIMITATION AND/OR HYPOXIA. THIS IS A REGULATORY
                                                                                                                                                                    GAMMA NON-CATALYTIC REGULATORY SUBUNITS.
TISSUE SPECIFICITY: HIGHLY EXPRESSED IN HEART AND BRAIN, ALSO
FOUND IN KIDNEY, WHITE ADIPOSE TISSUE, LUNG AND SPLEEN.
SIMILARITY: BELONGS TO THE 5'-AMP-ACTIVATED PROTEIN KINASE, GAMMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
5'-AMP-activated protein kinase, gamma-1 subunit (AMPK gamma-1 chain)
"Mammalian 5'-AMP-activated protein kinase non-catalytic subunits are
                                                                                                                                                       SUBUNIT: HETEROTRIMER OF AN ALPHA CATALYTIC SUBUNIT; A BETA AND A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
             homologs of proteins that interact with yeast Snf1 protein kinase.";
J. Biol. Chem. 269:29343-29346(1994).
                     J. BIOL. Chem. 269:29343-29346(1994).
-!- FUNCTION: AMPK IS RESPONSIBLE FOR THE REGULATION OF FATTY ACID SYNTHESIS BY PHOSPHORYLATYON OF ACETYL-COA CARBOXYLASE. IT ALSO REGULATES CHOLESTEROL SYNTHESIS VIA PHOSPHORYLATION AND INACTIVATION OF PORRONE-SENSITIVE LIPASE AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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CBS 1.

CBS 2.

CBS 4.

E > Q (IN REF. 3).

A -> P (IN REF. 3).

86 MW; 36031E526C1F1E97 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 HILTHKRLLKFLHIFGSLLPRPSFLYRTIQDLGIGTFRDLA 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   52.6%; Score 112; DB 1; L
46.3%; Pred. No. 7.3e-08;
Live 14; Mismatches 8;
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                                                                                                                                                                                                                                    SIMILARITY: CONTAINS 4 CBS DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                          InterPro: IPR000644; CBS_domain.
Pfam; PF00571; CBS; 4.
SWART: SW00116; CBS; 4.
Fatty acid biosynthesis; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            37386 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           330 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                         SUBUNIT FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein kinase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
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P54619;
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                                                                                                                                                                                                                                                                                                 SENSITIVE LIPASE. THIS IS A REGULATORY SUBUNIT.
SUBUNIT: HETEROTRIMER OF AN ALPHA CATALITIC SUBUNIT, A BETA AND A
                                                                                                                                                                                                                                                                                                                                                             GAMMA NON-CATALYTIC REGULATORY SUBUNITS.
SIMILARITY: BELONGS TO THE 5'-AMP-ACTIVATED PROTEIN KINASE, GAMMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Stapleton D., Gao G., Michell B.J., Widmer J., Mitchelhill K., Teh T., House C.M., Witters L.A., Kemp B.E.; "Mammalian 5'-AMP-activated protein kinase non-catalytic subunits are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-FEB-1995 (Rel. 31, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
5'-AMP-activated protein Kinase, gamma-1 subunit (AMPK gamma-1 chain)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          homologs of proteins that interact with yeast Snf1 protein kinase."; J. Biol. Chem. 269:29343-29346 (1994).
-! FUNCTION: AMPK IS RESPONDEDE POR THE REGULATION OF FATTY ACID SYNTHESIS BY PHOSPHORYLATION OF ACETYL-COA CARBOXYLASE. ALSO
                                                                                                                                                                                                                                                                           INACTIVATION OF HYDROXYMETHYLGLUTARYL-COA REDUCTASE AND HORMONE-
                                                                                                               Eukaryota; Metázoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
NCBL_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 331;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OF22B9CAlDBD87AE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     165 YILTHKRILKFLKLFITEPPKPEFMSKSLEELOIGTYANIA 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 HILTHKRLLKFLHIFGSLLPRPSFLYRTIQDLGIGTFRDLA 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            52.6%; Score 112; DB 1; 46.3%; Pred. No. 7.3e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Repeat; CBS domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       133 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 Similarity 46.3%; Pred. No. 7.3e
19; Conservative 14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                       -! - SIMILARITY: CONTAINS 4 CBS DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (AMPKg) (38 kDa subunit) (Fragments).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CBS 2.
CBS 3.
CBS 4.
Biol. Chem. 271:8675-8681(1996).
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MEDLINE=95050763; PubMed=7961907;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000644; CBS_domain.
Pfam; PF00571; CBS; 4.
SWART; SM00116; CBS; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   123 177 CB
197 250 CB
271 323 CB
331 AA; 37579 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U42412; AAC50495.1; -. EMBL; BC000358; AAH00358.1; -
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DOMAIN 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                             SUBUNIT FAMILY
                                                         SEQUENCE FROM N.A.
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15-JUN-2002 (Rel. 41, Last annotation update)
Alpha-2-antiplasmin precursor (Alpha-2-plasmin inhibitor) (Alpha-2-PI)
REGULATES CHOLESTEROL SYNTHESIS VIA PHOSPHORYLATION AND INACTIVATION OF HYDROXYRETHYLGLUTARYL-COA REDUCTASE AND HORMONESENSITIVE LIPASE. PHIS IS A REGULATORY SUBJUIT. A BETA AND A SUBJUILLY. HETEROTRIMER OF AN ALPHA CATALYTIC SUBJUIT, A BETA AND A
                                                                                                                     GAMMA NON-CATALYTIC REGULATORY SUBUNITS.
SIMILARITY: BELONGS TO THE 5'-AMP-ACTIVATED PROTEIN KINASE, GAMMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Holmes W.E., Nelles E., Lijnen H.R., Collen D.; "Primary structure of human alpha 2-antiplasmin, a serine protease inhibitor (serpin).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Match 30.3%; Score 64.5; DB 1; Length 133; Local Similarity 31.7%; Pred. No. 0.076; es 13; Conservative 13; Mismatches 8; Indels 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14763 MW; 84C0C3D41E845CEF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 HILTHKRLLKFLHIFGSLLPRPSFLYRTIQDLGIGTFRDLA 41
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Proc. Natl. Acad. Sci. U.S.A. 86:1612-1613(1989).
                                                                                                                                                                                                                                                                                                                         Fatty acid biosynthesis; Repeat; CBS domain.
NON_TER 1
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                                                                                                                                                                                                    -:- SIMILARITY: CONTAINS 4 CBS DOMAINS.
Interpro; IPRO0644; CBS_domain.
PFan: PPO0571, CBS; 1.
SMART; SM00116; CBS; 1.
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MEDLINE~88139254; PubMed=2830248;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=87109313; PubMed=2433286;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biochem. 102:1033-1041(1987).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Alpha-2-AP).
SERPINF2 OR PLI OR AAP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     133 AA;
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                                                                                                                                                                            SUBUNIT FAMILY
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P08697;
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NON_CONS
NON_CONS
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DT 01-JAN

DT 01-JAN

DE A1pha

GN SERPIN

OS BERPIN

RR TONE R

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Christensen S., Sottrup-Jensen L.; *Bovine alpha 2-antiplasmin. N-terminal and reactive site sequence."; FEBS Lett. 312:100-104(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VARIANT ALPHA-2-PLASMIN INHIBITOR DEFICIENCY M-411, AND VARIANTS V-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Miura O., Sugahara Y., Aoki N.;
Hereditary alpha 2-plasmin inhibitor deficiency caused by a
transport-deficient mutation (alpha 2-PI-Okinawa). Deletion of Glu137
by a trinucleotide deletion blocks intracellular transport.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (alpha2-antiplasmin) gene associated with a bleeding tendency.";
Br. J. Haematol. 107:317-322(1999).
-!- FUNCTION: THE MAJOR TARGETS OF THIS INHIBITOR ARE PLASMIN AND TRRPSIN, BUT IT ALSO INACTIVATES CHYMOTRYPSIN.
-!- DISRASE: Defects in SERPINE2 are the cause of alpha-2-plasmin inhibitor deficiency, a disease resulting in severe hemorrhagic
                                                                         Sumi Y., Nakamura Y., Aoki N., Sakai M., Muramatsu M.; "Structure of the carboxyl-terminal half of human alpha 2-plasmin inhibitor deduced from that of CDNA."; J. Biochem. 100:1399-1402(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hortin G., Fok K.F., Toren P.C., Strauss A.W.; "Sulfation of a tyrosine residue in the plasmin-binding domain of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Potempa J., Shieh B.-H., Travis J.; "Alpha-2-antiplasmin: a serpin with two separate but overlapping
                                                                                                                                                                                                                                                                                                                                                         Wiman B., Collen D.; "Purification and characterization of human antiplasmin, the
                                                                                                                                                                                                                 Lijnen H.R., Holmes W.E., van Hoef B., Wiman B., Rodriguez
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lind B., Thorsen S.; *A novel missense mutation in the human plasmin inhibitor
                                                                                                                                                                                                                                                      "Amino-acid sequence of human alpha 2-antiplasmin.";
Eur. J. Biochem. 166:565-574(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                             fast-acting plasmin inhibitor in plasma.";
Eur. J. Biochem. 78:19-26(1977).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      by a trinucleotide uerecass J. Biol. Chem. 264:18213-18219(1989)
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Biol. Chem. 262:1659-1664(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Biol. Chem. 262:3082-3085(1987).
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MEDLINE=20051147; PubMed=10583218;
                                                           MEDLINE=87137400; PubMed=3818581;
                                                                                                                                                                            SEQUENCE OF 40-491.
MEDLINE=87275946; PubMed=2440681;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Plasma;
MEDLINE=93050153; PubMed=1385210;
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                                       SEQUENCE OF 218-491 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Science 241:699-700(1988).
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                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 40-43.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             reactive sites.
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SEQUENCE FROM N.A.
                                                                               NCBI_TaxID=4896;
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Matches
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PLASMIN INHIBITOR DEFICIENCY; PROBABLY
BLOCKS INTRACELLUIAR TRANSPORT OF ALPHA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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V -> M (IN ALPHA-2-PLASMIN INHIBITOR
                                                                                                                                                                                                                                                                                                       Figure PF00079; Serpin; 1.
SMART; SM00093; SERPIN; 1.
PROSITE; PS00284; SERPIN; 1.
Serpin; Serine protease inhibitor; Glycoprotein; Plasma; Signal; Sulfation; Polymorphism; Disease mutation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                     REACTIVE BOND (FOR PLASMIN).
REACTIVE BOND (FOR CHYMOTRYPSIN).
SULFATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25.6%; Score 54.5; DB 1; Length 491; 48.6%; Pred. No. 7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                L -> G (IN REF. 6).
N -> D (IN REF. 6).
F -> D (IN REF. 4).
S -> G (IN REF. 6).
D -> N (IN REF. 6).
The state of the state
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2-PLASMIN INHIBITOR).
                                                                                                                                                                                                                                                                                                                                                                                                                      ALPHA-2-ANTIPLASMIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            128 TLQRLQQVLHA-GSGPCLPHLLSRLCQDLGPGAFR 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 THKRLLKFLHIFGSLLPRPSFLYRTIQDLGIGTFR 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /FTId=VAR_013255.
R -> K.
/FTId=VAR_013256.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /FTId=VAR_013252.
R -> W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /FTId-VAR_013253.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Hypothetical protein C6C3.05 in chromosome I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     269 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 7;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DEFICIENCY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A -> V.
         EMBL; D00116; BAA00070.1; -.
EMBL; D00174; BAA0124.1; -.
EMBL; M20786; AAA51554.1; -.
EMBL; M20783; AAA51554.1; JOINED.
EMBL; M20783; AAA51554.1; JOINED.
EMBL; M20784; AAA51554.1; JOINED.
EMBL; M20785; AAA51554.1; JOINED.
EMBL; M20785; AAA51554.1; JOINED.
EMBL; A24708; AAA35543.1; -.
PIR; A24684; A24708.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              49 L
105 N
289 H
408 S
455 D
54565 MW;
                                                                                                                                                                   PIR; A31402; A31402.
PIR; A42163; A32163.
PIR; A41504; A41504.
PIR; S00068; S00068.
PISSP: O35684; JJJO.
SWISS-2DPAGE; P08697; HUMAN.
                                                                                                                                                                                                                                                                                             InterPro; IPR000215; Serpin.
                                                                                                                                                                                                                                                              Genew; HGNC:9075; SERPINF2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
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404
404
405
405
126
295
309
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289
408
455
491 AA;
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nes 17; Conserv
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404
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Q10308;
01-0CT-1996 (
01-0CT-1996 (
15-JUN-2002 (
                                                                                                                                                                                                                                                                                MIM; 262850;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACT_SITE
MOD_RES
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YD55_SCHPO
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Pseudomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25.4%; Score 54; DB 1; Length 269; 35.9%; Pred. No. 4.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    l protein.
269 AA; 31234 MW; 0C3DF87A138CA5BE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Coproporphyrinogen III oxidase, aerobic (EC 1.3.3.3)
(Coproporphyrinogenase) (Coprogen oxidase).
                    Eukaryota, Fungi, Ascomycota, Schizosaccharomycetes,
Schizosaccharomycetales, Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 ILTHKRLLKFLHIFGSLLPRPSFLYRTIQDLGIGTFRDL 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5; Mismatches
Schizosaccharomyces pombe (Fission yeast).
                                                                                                                                      STRAIN=972;
MEDLINE-21848401; PubMed=11859360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; 269731; CAB40280.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 35.9 nes 14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pseudomonas aeruginosa.
                                                       Schizosaccharomyces
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yokota J.; "Identification of a 428-kb homozygously deleted region disrupting the
                                                                                                                                                                                                                                           -!- CATALYTIC ACTIVITY: Coproporphyrinogen-III + O(2) = protoporphyrinogen-IX + 2 CO(2).
-!- COFACTOR: IRON (BY SIMILARITY).
-!- COFACTOR: IRON (BY SIMILARITY).
-!- PATHWAY: POTPHYRIN LOCATION: Cytoplasmic (By similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
                                                                                    SEQUENCE FROM N.A.
STRAIN-ATCC 15622 / PAO1:
MFDLINE-20437377; PubMed-10984043;
Stover C.K., Pham X.-O.T., Erwin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M. Garber K.L., Golltry L., Tooleftino B., Westbrock-Wadman S., Yuan Y., Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., "Complete genome sequence of Pseudomonas aeruginosa PAO1, an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nishioka M., Kohno T., Takahashi M., Niki T., Yamada T., Sone S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Prim: PF01218; Coprogen_oxidas; 1.
PRINTS; PR00073; COPRGNOXDASE.
PROSITE; PS01021; COPRGEN_OXIDASE; 1.
PORPHYIN biosynthesis; Oxidoreductase; Iron; Complete proteome.
SEQUENCE 305 AA; 34806 WW; 240BD06FEA37EAE3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
                        Hungerer C., Troup B., Jahn D.;
"Cloning and regulation of the Pseudomonas aeruginosa hemF encoding oxygen-dependent coproporphyrinogen III oxidase.",
Submitted (FEB-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24.9%; Score 53; DB 1; Length 305; 36.8%; Pred. No. 6.7; ive 3; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SZ6L_HUMAN STANDARD; PRT; 1024 AA.
Q9BYH1, Q9Y2EL; Q9NUI3; Q9NUI4; Q9NUI5; 095917; Q9Y3J6;
15-JUN-2002 (REL 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 LTHKRLLKFLHIFGSLLP-----RPSFLYRTIQDLGI 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AE004442; AAG03414.1; -
InterPro; IPR001260; Coprogen_oxidas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seizure 6-like protein precursor.
SE26L OR KIAA0927.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; X85015; CAA59376.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 36.00,
-00 14; Conservative
SEQUENCE FROM N.A.
STRAIN=ATCC 15692 / PAO1;
                                                                                                                                                                                                                     opportunistic pathogen."; Nature 406:959-964(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PubMed=11175339;
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REAL SEQUENCE FROM N.A.

REAL SEQUENCE FROM N.A.

REAL SEQUENCE FROM N.A.

REAL SEGUENCE FROM N.A.

REAL SEGUENCE FROM N.A.

REAL SEGUENCE FROM T.A. Alnoscough R., Almeida J.P., Babbage A.K.,

RA Bagguley C., Balkey S.E., Bridgeman A.M., Buck D., Burgess J.,

Blad C.P., Blakey S.E., Bridgeman A.M., Buck D., Burgess J.,

RA CORTON R., Cobley V.E. Collic G.G., Collier R.E., Connor R.,

Clegg S.M., Cobley W.E., Corlile G.J., COX A.V., Davis J., Dawson E.,

RA CORTON D., Corby N.R., Corlile G.J., COX A.V., Davis J., Dawson E.,

RA GILBERT J.G.R., Goward M.E., Carfern N.E., Garner A.B.,

RA GILBERT J.G.R., Goward M.E., Carfifths M.N.D., Hall C.,

RA HURL S.E., Jones M.C., Kershaw J., Kimberley A.M., King A.,

RA HURL S.E., Jones M.C., Kershaw J., Kimberley A.M., King A.,

RA HURL S.E., Jones M.C., Kershaw J., Kimberley A.M., King A.,

RA MISSEL, Jones M.C., Kershaw J., Kimberley A.M., King A.,

RA COLL C., Sehra H.W., Ramsay H., Ramsay Y., Roden O.T.,

RA MILL S.S., Sehra H.W., Skuce C.D., Smalley S.A., MORTIMOSE B.J.C.,

RA MORDINA M., Pavilt R., Skuce C.D., Smalley S.A., MORTIMOSE B.J.C.,

RA Soderlund C., Spragon L., Steward C.A., Sulston J.E., Swann R.M.,

RA Wilght C.L., Hulbbard T., Bentley D.E., Swann R.M.,

WIlliams L., Williams S.A., Williams C.D., Smalley S., Smith M.L.,

RA Shintani A., Shibuya K., Yoshizaki Y., Aoki N., Mitsuyama S.,

RA Dorman A., Fang F., Pu U. J., Hulb A., Kenton S., Lai H., Lao H.I.,

RA CORES M., Chen F., Chu L., Crabtree J., Deschamps S., Do A., 
                                                                                                                                                                                                                                                            Nagase T., Ishikawa K.-I., Suyama M., Kikuno R., Hirosawa M., Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O., "Prediction of the coding sequences of unidentified human genes. XIII. The complete sequences of 100 new cDNA clones from brain which code
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Suzuki H., Gabrielson E., Chen W., Anbazhagan R., Van Engeland M., Weijenberg M.P., Herman J.G., Baylin S.B.;
"A genomic screen for genes upregulated by demethylation and histone deacetylase inhibition in human colorectal cancer.";
Nat. Genet. 31:141-149(2002).
-i- FUNCTION: Candidate tumor suppressor gene.
-i- ALTERNATIVE PRODUCTS: 4 isoforms; 1, 2, 3 and 4 (shown here);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bodenteich A., Hartman K., Hu X., Khan A.S., Lane L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Collins J.E., Huckle E.J.;
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
SEZ6L gene at 22q12.1 in a lung cancer cell line."; Oncogene 19:6251-6260(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                human chromosome 22.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. (ISOFORMS 1 AND 2)
                                                                                                                                                                                                                  MEDLINE=99246063; PubMed=10231032;
                                                                                                                                  SEQUENCE FROM N.A. (ISOFORM 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                  large proteins in vitro.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENE EXPRESSION REGULATION.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA Res. 6:63-70(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wilkinson P., Bodenteid
Tilahun Y., Wright H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "The DNA sequence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-Fetal brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PubMed=11992124;
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VARSPLIC
VARSPLIC
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                                                                                                                                                                                         RESULT 13
 SOFFFFF
                                                                                                                                   δλ
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                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
      SUBCELLUIAR LOCATION: Type I membrane protein (Probable).
TISSUE SPECIFICITY: Widely expressed, including adult and fetal
Prains and lungs. Not expressed in all lung cancer cell lines.
DISEASE: SEZEL is located in a 22q region, which is frequently
deleted in small cell lung carcinomas (SCLCs) and advanced non-
small cell lung carcinomas.
SIMILARITY: CONTAINS 3 CUB DOMAINS.
SIMILARITY: CONTAINS 5 SUSHI (SCR) DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (GLCNAC. . .) (POTENTIAL).
(GLCNAC. . .) (POTENTIAL).
(IN ISOFORM 1 AND ISOFORM 2).
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(POTENTIAL).
(POTENTIAL).
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(POTENTIAL).
(POTENTIAL).
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                                                                                                                                                                                                                                                                                                          InterPro: IPR000859; CUB_domain.
InterPro: IRR000436; Sushi_SCR_CCP.
InterPro: IRR000436; Sushi_SCR_CCP.
Pfam: PP00084; sushi; 5.
SWART: SW00042; CCP; 5.
SWART: SW00042; CUB; 3.
PROSITE: PS01180; CUB; 3.
Signal; Transmembrane; Sushi; Repeat; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                              SEIZURE 6-LIKE PROTEIN.
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GLCNAC. . .)
(GLCNAC. . .)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (GLCNAC. . .)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (IN ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BY SIMILARITY.
N-LINKED (GLCNAC...)
N-LINKED (GLCNAC...)
N-LINKED (GLCNAC...)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (GLCNAC.
 be produced by alternative splicing.
                                                                                                                                                                                              EMBL; AB041736; BAB40970.1; -.
EMBL; AB023144; BAA76771.2; ALT_INIT.
EMBL; AL035545; CAB37431.1; ALT_INIT.
EMBL; AL035513; CAB43355.1; ALT_INIT.
EMBL; AL023513; CAB72345.1; -.
EMBL; AL023513; CAB72346.1; -.
EMBL; AL023513; CAB72347.1; ALT_SEQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-LINKED (
                                                                                                                                                                                                                                                                                                                                                                                                                                                          CUB 1.
SUSHI 1.
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SUSHI 2.
CUB 3.
SUSHI 3.
SUSHI 4.
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MISSING (
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806
834
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350
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618
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                                                                                                                                                              ä
                                             IMYCTDPGEVDHSTRLISDPVLLVGTTIQYTCNPGFVLEGS
SLLTCYSRETGTPIWTSRLPHCVS -> T (IN ISOFORM
                                                                                                                                                                                                                                                                                                                                         01-DEC-1992 (Rel. 24, Created)
UNOV-1995 (Rel. 32, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Alpha-2-antiplasmin precursor (Alpha-2-plasmin inhibitor) (Alpha-2-PI)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Christensen S., Sottrup-Jensen L.; "Bovine alpha 2-antiplasmin. N-terminal and reactive site sequence.";
                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                        Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEBS Lett. 312:100-104(1992).
--- FUNCTION: THE MAJOR TARGETS OF THIS INHIBITOR ARE PLASMIN AND TRYPSIN, BUT IT ALSO INACTIVATES CHYMOTRYPSIN.
--- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
             -> GTOKV (IN ISOFORM 1 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Serpin; Serine protease inhibitor; Glycoprotein; Plasma; Signal; Sulfation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REACTIVE BOND (FOR PLASMIN).
REACTIVE BOND (FOR CHYMOTRYPSIN).
SULFATION (BY SHILLARITY).
N-LINKED (GLCNAC. . ) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                              8;
                                                                                                                             Score 53; DB 1; Length 1024;
Pred. No. 24;
9; Mismatches 10; Indels
                                                                                              1024 AA; 111781 MW; CBC0679E22C23B6E CRC64;
                                                                                                                                                                                                                 347 VLANQTLL----VEGQVIRSPINTISVYFRIFQDDGLGTFQ 383
                                                                                                                                                                                             2 ILTHKRLLKFLHIFGSLLPRP----SFLYRTIQDLGIGTFR 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Christensen S., Berglund L., Sottrup-Jensen L.;
"Primary structure of bovine alpha 2-antiplasmin.";
FEBS Lett. 343:223-228(1994).
 MISSING (IN ISOFORM 2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ALPHA-2-ANTIPLASMIN.
                                 ISOFORM 2).
                  ETREYEVSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE-94229242; PubMed=7513654;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=93050153; PubMed=1385210;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 23-45 AND 374-410.
                                                                                                                             24.9%;
34.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR000215; Serpin.
Pfam; PF00079; serpin; 1.
SMART; SM00093; SERPIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; X78436; CAA55200.1; -. PIR; S27260; S27260. HSSP; P01008; IANT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00284; SERPIN;
                                                                                                                                            Best Local Similarity 34.1
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                             STANDARD;
943
1024
                                               867
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4 9 2
4 9 2
4 0 5
4 0 6
1 1 2 7
2 4 9
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                                                                                                                                                                                                                                                                                                                                                                                                          (Alpha-2-AP).
SERPINF2 OR PLI.
943
1016
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                                               803
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404
405
405
1127
249
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                                                                                                                                                                                                                                                                                                           A2AP_BOVIN
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MOD_RES
CARBOHYD
                                                                                              SEQUENCE
                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bovidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACT_SITE
                                               VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CARBOHYD
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                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dubois E., el Bakkoury M., Glansdorff N., Messenguy F., Pierard A., Scherens B., Vierendeels F.; Elmischerens Elmischerens Demokratie Elmi
  N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                             33
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                                                                                                                                                                                                                                                                                                                                                                                                                                01-0CT-1994 (Rel. 30, Created)
01-0CT-1994 (Rel. 30, Last sequence update)
15-0UL-1998 (Rel. 36, Last annotation update)
Hypothetical 57.2 kba protein in MET8-HPC2 intergenic region.
VBR214W OR YBR2501.
                                                                                                                                                                      Length 492;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 527;
                                                                                                                                            Similarity 47.2%; Score 52.5; Similarity 47.2%; Pred. No. 13; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rieger M.;
Submitted (AUG-1994) to the EMBL/GenBank/DDBJ databases.
                                                          T -> Q (IN REF. 2).
Q -> P (IN REF. 2).
Q -> E (IN REF. 2).
; 0755D6FC89B2DF5D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DC2741550A69C154 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            240 ILSQRRLIKYLWDNARSFTSLEP---LLNSSLQDLHIG 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 ILTHKRLLKFL----HIFGSLLPRPSFLYRTIQDLGIG 35
                                                                                                                                                                                                                                                                         4 THKRLLKFLHI-FGSLLPRPSFLYRTIQDLGIGTFR 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24.2%; Score 51.5; DB 1; 42.1%; Pred. No. 19; artive 6; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                527 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR; $46088; $46088.
$GD; $8000418; $5854.
InterPro; IPR000644; CBS_domain.
Pfam; PF00571; CBS; 4.
$MART; $800116; CBS; 4.
Hypothetical protein; Repeat; CBS domain.
DOMAIN 196 251 CBS 1.
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527 AA; 57187 MW;
                                                                                                                        54710 MW;
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                                                                                                                                                                                                             17; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                          28
40
43
492 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-S288c;
                                                                                                                                                                                                                                                                                                                                                                                              YB64_YEAST
                                                            CONFLICT
                                                                                                                      SEQUENCE
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  CARBOHYD
                     CARBOHYD
                                                                                                                                                                    Query Match
                                           CARBOHYD
                                                                                                       CONFLICT
                                                                                                                                                                                         Best Local
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RESULT 15

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=CO-92 / Biovar Orientalis;
Barkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,
Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,
Prentice M.B., Sebainha M., James K.D., Churcher C., Mungall K.L.,
Prentice M.B., Sebainha M., Dantley S.D., Brooks K., Cerdeno-Tarraga A.M.,
Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
Feltwell T., Hamiln N., Holroyd S., Jagels K., Karlyshev A.V.,
Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,
"Genome sequence of Yersinia pestis, the causative agent of plague.",
Nature 413:523-527(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -i- CATALYTIC ACTIVITY: Coproporphyrinogen-III + 0(2) = proteporphyrinogen-IX + 2 Co(2).
-i- COPACTOR: Irron (By similarity).
-i- PATHWAY: Porphyrin biosynthesis.
-i- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-i- SIMILARITY: BELONGS TO THE AEROBIC COPROPORPHYRINOGEN III OXIDASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfan, PF0/1218; Coprogen_oxidas; 1.
PRINTS; PR00073; COPRGNOXDASE.
PROSTITE; PS01021; COPROGEN_OXIDASE; 1.
SEQUENCE: 309 AA, 35004 MW; A3DE259C4C3714D9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6
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                                                                                                       15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Coproporphyrinogen III oxidase, aerobic (EC 1.3.3.3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9 LKFLHIFGSLLP-----RPSFLYRTIQDLGI 34
   309 AA
                                                                                                                                                                                                                 (Coproporphyrinogenase) (Coprogen oxidase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AJ414155; CAC92274.1; -. InterPro; IPR001260; Coprogen_oxidas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Search completed: June 6, 2003, 11:01:31
Job time : 2.50788 secs
                                                                        15-JUN-2002 (Rel. 41, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                              Yersinia pestis
                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=632;
HEM6_YERPE
Q8ZCF9;
                                                                                                                                                                                                                                                                                                                                                                              rersinia
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Q9Y3D1 Q9BTT2 Q9AFG1 Q08548 Q95917 Q9V3UG Q9DWE3

Q976w2 sulfolobus Q98161 streptomyce Q08548 saccharomyc Q98113 homo sapien Q97316 homo sapien Q97316 homo sapien Q972el homo sapien Q8749 mus musculu Q8749 mus musculu Q8749 mus musculu Q8729 homo sapien Q9729 homo sapien Q9729 homo sapien Q97290 saccharomyc Q97290 saccharomyc Q9730 saccharomyc Q9730 saccharomyc Q9730 saccharomyc Q9730 saccharomyc Q9731 candida alb Q9731 candida alb Q9731 candida alb Q9731 candida alb Q9731 candida alb

> 09Y2E1 099KH1 094KK4 094D56 096D33 086K451 087E4P9 08P4P2 08P4P2 08VUG2 09NUG2 09NUG2

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June 6, 2003, 10:58:04 ; Search time 5.31349 Seconds (without alignments) 1589.904 Million cell updates/sec
                                                                                                                                                           1 HILTHKRLLKFLHIFGSLLP......PSFLYRTIQDLGIGTFRDLA
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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213
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Maximum Match 100%
Listing first 45 summaries
                                                    using sw model
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                      sp_human:*
sp_invertebrate:*
sp_mammal:*
sp_mhc:*
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sp_vertebrate:*
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Perfect score:
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ALIGNMENTS

Q96V31 Q9LUV3 Q8RWB8

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.

Query Query Concemple of Match Length DB ID Description 124 58.2 566 11 091WG5 091wg5 mus musculu 105 49.3 647 5 094DBL 0994pbl Genoorhabdi 105 49.3 647 5 096613 0950blla 105 49.3 647 5 096613 0950blla 105 49.3 1400 5 088XFB 096613 drosophila 105 49.3 1400 5 088XFB 096613 drosophila 105 49.3 1400 5 088XFB 096613 drosophila 97 45.5 423 5 002168 caenorhabdi 6 31.0 105 2 002168 caenorhabdi 65.5 30.8 577 5 08SX7 095x8 095x8 65.5 30.8 577 5 095x8 095x8 095x8 56 6.3 10</

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091WG5 AC 021WG5 D (021WG5) D (021WG5) D (021WG5) D (021WG5) D (021WG5) D (01-DEC-2001 (TrEMBLrel. 19, Created) DT (01-DEC-2001 (TrEMBLrel. 19, Last sequence update) DT (01-DEC-2001 (TrEMBLrel. 19, Last sequence update) DE Hypothetical 63.0 kDa protein. OS Mus musculus (Mouse). OC ENKaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC ENKaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus NS LTAUDHENE FROM N.A. RP SEQUENCE FROM N.A. RC TISSUE-KIDNEY; RA STRAUSDERG R.; RL Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases. DR EMBL, BC015283; AAH15283.1; DR InterPro; IPR000644; GBS_domain. DR Pfam; PF00571; CBS; 4. KW Hypothetical protein. SQ SEQUENCE 566 AA; 62997 WW; 754DE4D696102C7D CRC64; QUELY MATCH BOST LOCAL SIMilarity 51.2%; Pred. NO. 5.7e-09; MATCHES 21; Conservative 13; Mismatches 7; Indels 0; G	RESULT 2 Q9BHL6 ID Q9BHL6 AC Q9BHL6; DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update) DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update) DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)

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Amount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
Nelson D.R., Parled J., Puri, P., Robertob J.M.,
Palazzolo M., Pittuan G.S., Pan S., Pollard J., Puri V., Rese. M.G.,
Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
Shue B.C., Siden Kiamos I., Simpson M., Skupski M.P., Smith T.,
Spier E., Spradling A.C., Stapleton M., Stupski M.P., Snith T.,
Spier E., Spradling A.C., Stapleton M., Stupski M.P., Snith T.,
Spier E., Spradling A.C., Stapleton M., Stupski M.P., Snith T.,
Spier E., Spradling A.C., Stapleton M., Stupski S.N. Sun E.,
Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
Williams S.M., Woodage T., Worley K.C., Wu D., Yang G., Zhao Q., Zheng L.,
A. Leng X.H., Zhong F.N., Zhon M., Zhou X., Zhu X., Smith H.O.,
A. Long Y.H., Zhong F.N., Zhong W., Zhou X., Zhu S.,
The genome sequence of Drosophila melanogaster.",
Science 287:1285-2195[2000].
B. EMBL; AE003733; ARF55864.1; -.
B. Riberton IFR000644; CBS_domain.
P. Flyasas: FB90025803; SNF4-gamma.
P. Riberton IFR00644; CBS_domain.
P. Riberton IFR00116; CBS; 4.
SMART; SW00116; CBS; 4.
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Eukaryota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophilia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 634;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             :||||||:|:|| :: ||:|::: ||||: :: || |||: :: 293 YILTHKRILRFLELYINELPKPAYMQKSLRELKIGTYNNI 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           306 YILTHKRILRFLFLYINELPKPAYMOKSLRELKIGTYNNI 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 HILTHKRLLKFLHIFGSLLPRPSFLYRTIQDLGIGTFRDL 40
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
SNR4/AMP-activated protein kinase gamma subunit.
SNR4A-GAMMA OR CG17299.
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     49.3%; Score 105; DB 5; L
40.0%; Pred. No. 2.9e-06;
tive 18; Mismatches 6;
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InterPro: PR000644; CBS_domain.
Pfam: PF00571; CBS; 4.
SMART; SM00116; CBS; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 40.0 Matches 16; Conservative
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Q8SXT8;
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Q8SXT8
ID Q8SXT
AC Q8SXT
DT 01-JU
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096613
                 DDT TO DD
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Adams M.D., Celniker S.E., Holt R.A., Ashburner M., Henderson S.N.,
Adams M.D., Celniker S.E., Richards S., Ashburner M., Henderson S.N.,
A George R.A., Lewis S.E., Richards S., Changpe M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y. H.C., Blazel R.G., Changpe M., Pfelifer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Ballew R.M., Basu A., Baxendale J., Barktaroglu L., Beasley E.M.,
Ballew R.C., Blasm D.P., Bhandari D., Bolshakov S.,
RA Ballew R.C., Busam D.A., Buller H., Cadleu E., Center A., Chandra I.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Borkova D., Botcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Buris K., Combones M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Helman T.J., Wei M.-H., Ibeywam C.,
RA Harris N.L., Harvey D., Helman T.J., Wei M.-H., Ibeywam C.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J.J., Li Z., Liang Y., Lin X.,
RA Linko P., Leil Y., Levitsky A.A., Li J.J., Li Z., Liang Y., Lin X.,
RA Liux K., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBL_TaxID=7227;
                                                           Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBL_TaxID-6239;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 372;
                                                                                                                                                                                                                                                                                                                                                                                                             Genome sequence of the nematode C.elegans: A platform for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                51.6%; Score 110; DB 5; Length 37 52.5%; Pred. No. 3.4e-07; Live 10; Mismatches 9; Indels
                                                                                                                                                                                                                                                               Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SMART; SM00116; CBS; 4.
SEQUENCE 372 AA; 41376 MW; 81A39670877167DF CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SNF4AGAMMA Protein.
SNF4A-GAMMA OR SNF4AGAMMA OR CG17299.
                                                                                                                                                                                                                                                                                                                                                     MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AL132904; CAC35836.1; -.
InterPro: IPR000644; CBS_domain.
Pfam; PF00571; CBS; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                        investigating biology.";
Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21; Conservative
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        x111B2A.8 protein.
x111B2A.8.
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Gaps ;

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Gaps
                                                                       Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
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Rhabditidae; Peloderinae; Caenorhabditis.
NCBL_TaxID=6239;
                                                                                                                                                                                                                                                      "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL: U97550; AAK18981.2; -.
InterPro: IPR000644; CBS_domain.
Pfam: PF00571; CBS; 4.
SWART; SM00116; CBS; 4.
BYPOCHELICAI protein, 4.
BYPOCHELICAI protein, 4.
SEQUENCE 423 AA; 47451 MW; 6997065D515E7B21 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                STRAIN-BRISTOL N2;
Miller N., Gattung S.;
"The sequence of C. elegans cosmid T20F7.";
Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ryan E., Wohldman P., Walker C., Fielder T.;
"The sequence of C. elegans cosmid Y41G9A.";
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 51.5 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 97; DB 5; Le
Pred. No. 2.6e-05;
9; Mismatches 8;
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SEQUENCE FROM N.A.
STRAIN-ERISTOL N2;
MEDLINE-99069613; PubMed-9851916;
                                                                                                                                                                                                           MEDLINE=99069613; PubMed=9851916;
  Hypothetical 47.5 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         45.5%; 52.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 52.89
                                             Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Waterston R.; "Direct Submission.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                             [3]
SEQUENCE FROM N.A.
STRAIN=BRISTOL N2;
                                                                                                                                                              SEQUENCE FROM N.A. STRAIN=BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. STRAIN=BRISTOL N2;
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                                                                                                                      NCBI_TaxID=6239;
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                                                      Drosophila melanogaster (Fruit fly).

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Eukaryota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.
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Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Bukaryota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophilia.
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                                                                                                                                                                                                                                               Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E., George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G., Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S., Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.B., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E., George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G., Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S., Patel S., Phouanenavong S., Man K., Yu C., Lewis S.E., Rubin G.M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           49.3%; Score 105; DB 5; Length 906;
40.0%; Pred. No. 4.2e-06;
Live 18; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 105; DB 5; Length 14
Pred. No. 6.6e-06;
8; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (DEC-2001) to the EWBL/GenBank/DDBJ databases. EMBL; AY070541; AAL48012.1; -. SEQUENCE 1400 AA; 152380 MW; 411B93CCGB9EC7AF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                      Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AY084138; AAL89876.1; -.
SEQUENCE 906 AA; 99970 MW; C867D9556F42D57F CRC64;
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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Last annotation update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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(TrEMBLrel. 19, Last sequ
(TrEMBLrel. 21, Last anno
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Best Local Similarity 40.0°
Matches 16; Conservative
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Les 16; Conserva
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Celniker S.;
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01-JUL-1997 (
01-DEC-2001 (
01-JUN-2002 (
                                          SNF4 AGAMMA.
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Q8SZS7;
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Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases. EMBL; AC115599; AAL92329.1; -.
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                                                                                                                                                                                                                                                                                                                                                  379 AA.
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01-DEC-2001 (TrEMBLrel. 19, Last sequ
01-JUN-2002 (TrEMBLrel. 21, Last anno
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01, Last sequ
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Science 282:2012-2018(1998).
EMBL; AL021488; CAC42378.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 48.6
nes 17; Conservative
                                                                                                                Best Local Similarity 48.6
Matches 18; Conservative
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01-JUN-2002 (TrEMBLrel.
Y45F10A.6b protein.
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01-JUN-2002
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                                             SEQUENCE
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Q41108;
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Q95NR8
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AAC Q44
AAC Q44
AAC Q44
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Gloeckner G., Eichinger L., Szafranski K., Pachebat J., Dear P.,
Lehmann R., Baumgart C., Parra G., April J.F., Guigo R., Kumpf K.,
Tunggal B., Cox E., Quall M.A., Platzer M., Rosenthal A., Noegel A.A.;
"Sequence and Analysis of Chromosome 2 of Dictyostelium.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bahr U., Darai G.;
"Analysis and Characterization of the Complete Genome of Tupaia (Tree
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                            Length 448;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8; Mismatches 13; Indels
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Darai G., Bahr U.;
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AP281817; AR877095.1; -.
SEQUENCE 1055 Aa, 117780 MW; CCA51E416FD38C39 CRC64;
                                                                                                                                                                                                                                                         11; Indels
"Direct Submission.";
Submitted (JUL-2011) to the EMBL/GenBank/DDBJ databases.
EMBL, AC006761; AAF60550.1; -.
Interpro; IPR000644; CBS_domain.
Pfam; PF00571; CBS; 4.
SMART; SM00116, CBS; 3.
Hypothetical protein.
SEQUENCE 448 AA; 51514 MW; B689218979299479 CRC64;
                                                                                                                                                                                                                                                                                                                             269 YILTHRRILHYIWKHCALLPKPECLSQRVVDLEIGSWKNL 308
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01-5UN-2002 (TrEMBLrel. 21, Last sequence update)
01-5UN-2002 (TrEMBLrel. 21, Last annotation update)
01-5UN-2002 (TrEMBLrel. 21, Last annotation update)
SNF4/AMP-activated protein kinase gamma subunit.
Dictyostelium discoideum (Slime mold).
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Betaherpesvirinae.
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01-DEC-2001 (TrEWBLrel. 19, Last sequence update)
01-JUN-2002 (TrEWBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                     1 HILTHKRLLKFLHIFGSLLPRPSFLYRTIQDLGIGTFRDL
                                                                                                                                                                                                         Query Match 39.4%; Score 84; DB 5; Best Local Similarity 40.0%; Pred. No. 0.0018; Matches 16; Conservative 13; Mismatches 11
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MEDLINE=21211637; PubMed=11312357;
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J. Virol. 75:4854-4870(2001).
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nes 15; Conservative
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Matches
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TISSUB-IMMATURE SEEDS;
Abe H., Kamiya Y., Sakurai A.;
Acha Clone Encoding Yeast SNF4-Like Protein (Accession No. U40713)
from Phaseolus Vulgaris L (PGR95-126).";
Plant Physiol. 110:336-336(1995).
EMBL; U40713; AAA91175.1; -.
InterPro: IPR000644; CBS.domain.
Fram; PR00571; CBS; 2.
SMART; SM00116; CBS; 1.
SRQUENCE 379 AA; 41311 MW; 689A86EFC4DE5D14 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Phaseolus vulgaris (Kidney bean) (French bean).
Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryotatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Phaseolus.
NCBI_TaxID=3885;
                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBL_TaxID-6239;
                                                                                                                       ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5;
                                                   30.8%; Score 65.5; DB 5; Length 577; 48.6%; Pred. No. 0.91; tive 2; Mismatches 16; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29.6%; Score 63; DB 10; Length 379; 48.6%; Pred. No. 1.3; Live 5; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Genome seguence of the nematode C.elegans: A platform for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
577 AA; 64209 MW; 3FBC56EA649B25A9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (TrEMBLrel. 01, Last sequence update) (TrEMBLrel. 21, Last annotation update)
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Last annotation update)
                                                                                                                                                                                                                        406 HILTHSRILAFMMKSFPQLPE-KLLSIPIGSLGIGTF 441
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EQUENCE FROM N.A.
SEQUENCE FROM N.A.
SEQUENCE TOR N16961 / SEROTYPE 01;
MEDLINE=20406833; PubMed=10952301;
Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-TRREIG.

MEDLINE-97386405; PubMed-9244254;

MEDLINE-97386405; PubMed-9244254;

Takata H., Takaha T., Okada S., Takagi M., Imanaka T.;

Takaha T., Okada S., Takagi M., Imanaka T.;

"Characterization of a gene cluster for glycogen biosynthesis and a heterotetrameric ADP-glucose pyrophosphorylase from Bacillus stearothermophilus.";

J. Bacteriol. 179:4689-4698(1997).

-!- FUNCTION: PHOSPHORYLASE IS AN IMPORTANT ALLOSTERIC ENIYME IN CARBOHYDAATE BETABOLISM: NAYMENT SOURCES DIFFERE THEIR REGULATORY MECANISMS AND IN THEIR NAYURAL SUBSTRAIES.

HOWEVER, ALL KNOWN PHOSPHORYLASES SHARE CATALYTIC AND STRUCTURAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
NCBL_TaxID=666;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ol-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Glycogen phosphorylase (EC 2.4.1.1) (Alpha-glucan phosphorylase)
(Starch phosphorylase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "DNA sequence of both chromosomes of the cholera pathogen Vibrio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 516;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             :|: | :|:|| | ||: :|: | 305 LLSDKFMLEFLHSHTSVVAQPPYNSRYFSGINPYALGFAMFRDI 348
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical protein, Complete proteome. SEQUENCE 516 AA; 60882 MW; 18F2C1365D46DFF7 CRC64;
                                                               | :| ||| | |: | |||| | 895 FSEVFPRLLPWPVTNIFIIRVFRLLDISDNGLLTFRDLA 933
                            11 FLHIFGSLLPRP---SFLYRT-----IQDLGIGTFRDLA 41
                                                                                                                                                                                                                                                                                                 01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein VC1874.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26.1%; Score 55.5; DE 31.8%; Pred. No. 20; Live 9; Mismatches
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                                                                                                                                                                                                                                                  PRT;
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TIGR; VC1874; -.
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                                                                                                                                                                                                                                              PRELIMINARY;
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Q9KQX3
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Milson R., Ainscough R., Anderson K., Baynes C., Berks M.,
Milson R., Ainscough R., Anderson K., Depey T., Cooper J., Coulson A.,
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.
Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
Watson A., Welnstock L., Wilkinson-Sproat J., Wohldman P.;
T. 2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
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                                                                                                                                                                                                                                                                                                                                                                                                    11; Indels
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1270 Aa; 144948 MW; ED95EBA90E4D8115 CRC64;
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SEQUENCE 1268 AA; 144714 MW; 6D9FAA919E19CB16 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          11 FLHIFGSLLPRP---SFLYRT-----IQDLGIGTFRDLA 41
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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                                                                                                                                                                                                                                                                                                              26.3%; Scc. No. 4., 43.6%; Pred. No. 4., ... 3; Mismatches ?
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EMBL; AL021483; CAA16368.1; -.
EMBL; AL021483; CAA16349.1; -.
EMBL; AL021488; CAA16349.1; -.
InterPro; IPR002048; EF-hand.
InterPro; IPR004183; GRAM_dom.
InterPro; IPR004183; GRAM_dom.
Pfam; PF02893; GRAM; 2.
                                                  EMBL; AL021488; CAC42374.1; JOINED.
InterPro; IPR002048; EF-hand.
InterPro; IPR004182; GRAM.dom.
InterPro; IPR00195; RabGAP_TBC.
Pfam; PF02893; GRAM; 2.
Pfam; PF00566; TBC; 1.
EMBL; AL021483; CAC42378.1; JOINED
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Matches 17; Conservative
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PROSITE; PS00018; EF_H
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Submitted (JAN-1998)
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 Sequence 7, Appliance 5, Appliance 21, Appliance 64, Appliance 21, Appliance 21, Appliance 21, Appliance 5, Appliance 10, 5463025
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                                                                                                               June 6, 2003, 10:59:34 ; Search time 2.44133 Seconds (without alignments) 494.132 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Description
                                                                                                                                                                                                    213
1 HILTHKRLLKFLHIFGSLLP......PSFLYRTIQDLGIGTFRDLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/FCTUS_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
              GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-905-223-497
US-08-310-611-8
US-09-134-001C-3105
US-08-924-183-9
US-08-889-2
US-08-889-2
US-08-980-060-5
US-08-980-060-5
US-09-307-185-5
PCT-0596-09193-2
US-09-576-160B-4
US-09-576-160B-4
US-09-188-930-337
US-09-188-930-337
US-09-188-930-337
US-09-188-930-337
US-09-188-930-337
US-09-576-160B-1
US-09-576-160B-1
US-09-576-160B-2
US-09-576-160B-3
US-09-576-160B-3
US-09-576-160B-3
US-09-576-160B-3
US-09-576-160B-3
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US-09-359-161-6
US-09-359-161-6
US-08-878-989-21
US-09-101-146-64
US-09-359-161-5
5463025-1
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                                                                                                                                                                                                                                                                                                     262574 seqs, 29422922 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUMMARIES
                                                                                                                                                                                  US-09-826-581-6_COPY_320_360
                                                                                                                                                                                                                                                                                                                                                                                                                       Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                 protein search, using sw model
                                                                                                                                                                                                                                                    BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                     Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Match Length
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466.5
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APPLICANT: Bradford, Kent J.
APPLICANT: Bradford, Kent J.
APPLICANT: Dahal, Peetambar
APPLICANT: Yang, Hong
APPLICANT: Cooley, Michael
APPLICANT: Cooley, Michael
APPLICANT: Gee, Oliver
APPLICANT: Gee, Oliver
APPLICANT: Gee, Oliver
APPLICANT: Gee, Oliver
APPLICANT: He Regents of the University of California
TITLE OF INVENTION: Regulation of Source-Sink Relationships and Responses
TITLE OF INVENTION: to Stress Conditions in Plants
TITLE OF INVENTION: 1999-0035900US
CURRENT APPLICATION NUMBER: US/09/359,161A
NUMBER OF SEO ID NOS: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ) OTHER INFORMATION: gamma subunit of AMP-activated protein kinase; OTHER INFORMATION: (AMPK-gamma)
US-09-359-161-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 330;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 HILTHKRLLKFLHIFGSLLPRPSFLYRTIQDLGIGTFRDLA 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Bandman, Olga
APPLICANT: Hillman, Jennifer L.
APPLICANT: Corley, Neil C.
APPLICANT: Corley, Neil C.
APPLICANT: Galegier, Karl G.
APPLICANT: Gal, Preeti
APPLICANT: Goli, Surya K.
APPLICANT: Goli, Surya K.
APPLICANT: Shah, Purvi
TITLE OF INVENTION: KINASES
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 112; DB 4;
Pred. No. 2.2e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM Compatible OPERATING SYSTEM: DOS SOTWARE: FastSED for Windows Version 2.0 CURRING APPLICATION DATA:
APPLICATION NUMBER: US/08/878,989
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14; Mismatches
                                                         Sequence 6, Application US/09359161A
Patent No. 6342656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 21, Application US/08878989; Patent No. 5885803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         52.6%;
46.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 46.3%
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Ver. 2.1 SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
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                                                                                                           GENERAL INFORMATION:
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                                           JS-09-359-161-6
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                                                                Length 328;
                                                             58.2%; Score 124; DB 2; Length 32
51.2%; Pred. No. 4.2e-10;
tive 13; Mismatches 7; Indels
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                                                                                                                                                  1 HILTHKRLLKFLHIFGSLLPRPSFLYRTIQDLGIGTFRDLA 41
                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Bandman, Olga
APPLICANT: Hillman, Jennifer L.
APPLICANT: COTIEV, Nell C.
APPLICANT: Cotiev, Nell C.
APPLICANT: Lal, Preeti
APPLICANT: Gall, Surya K.
APPLICANT: Gall, Surya K.
APPLICANT: Shah, Purvi
TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN
WITHER OF INVENTION: KIRASES
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: DOS
SOFTWARE: FastStEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/272,796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PF-0321 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/878,989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Billings, Lucy J J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-07
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFRAX: 415-845-4166
                                                                                                                                                                                                                                                                                                          Sequence 7, Application US/09272796
Patent No. 6207148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
~^MPITER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: ATTORNEY/AGENT INFORMATION:
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                                                                                                         21; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; IMMEDIATE SOURCE:
| LIBRARY: PENITUT01
| CLONE: 1452972
| US-09-272-796-7
                                                                                  Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Palo Alto
                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
; CLONE: 1452972
US-08-878-989-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
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                                                                                                                                                                                                                                                                                   US-09-272-796-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE:
                                                                Query Match
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                           1 HILTHKRLLKFLHIFGSLLPRPSFLYRTIQDLGIGTFRDLA 41
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                                                                                                                                                                                          GENERAL INCORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Hillman, Jennifer L.
APPLICANT: Corley, Neil C.
APPLICANT: Lal, Preeti
APPLICANT: Lal, Preeti
APPLICANT: Goli, Surya K.
APPLICANT: Shah, Purvi
TITLE OF INVENTION: DISBASE ASSOCIATED PROTEIN
TITLE OF INVENTION: LIANSES
NUMBER OF SEQUENCES: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   52.6%; Score 112; DB 4;
46.3%; Pred. No. 2.3e-08;
tive 14; Mismatches 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASISED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/272,796
FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/878,989
FILING DATE:
ATTORIEV AGENT INFORMATION:
NAME: Billings, Lucy J J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0321 US
TELECOMMULICATION INFORMATION:
TELECHONE: 415-855-0555
TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-359-161-5; Sequence 5, Application US/09359161A; Patent No. 6342656; CENERAL INFORMATION: APPLICANT: Bradford, Kent J.
                                                                                                                                                    ; Sequence 21, Application US/09272796
; Patent No. 6207148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: >*>>>
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 331 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 52.6*
Best Local Similarity 46.3*
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LIBRARY: GenBank
CLONE: 1335856
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Dartmouth College, St. Vincents Institute of APPLICANT: Medical Research, Kemp et al.
TITLE OF INVENTION: No. 6124125el AMP Activated Protein Kinase NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jane Massey Licata, Esq.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
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                                                                                                                                                                                                                                                                                                                                                                                            Query Match 52.6%; Score 112; DB 2; Length 33 Best Local Similarity 46.3%; Pred. No. 2.3e-08; Matches 19; Conservative 14; Mismatches 8; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 HILTHKRLLKFLHIFGSLLPRPSFLYRTIQDLGIGTFRDLA 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
COMPUTER: IBM PC
OPERATING SYSTEM: WINDOWS 95
SOFTWARE: WORDPERFECT 6.0 FOR WINDOWS
CURRENT APPLICATION DATA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 52.6%; Score 112; DB 3;
Best Local Similarity 46.3%; Pred. No. 2.3e-08;
Matches 19; Conservative 14; Mismatches 8;
NAME: Billings, Lucy J J
REGISTRATION NUMBER: 36,749
REPERENCE/DOCKET WNBER: PF-0321 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFRAX: 415-845-4166
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66 E. Main Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/09/101,146
FILING DATE: October 7, 1998
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 64, Application US/09101146
Patent No. 6124125
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Jane Massey Licata
REGISTRATION NUMBER: 32,257
REFERENCE/DOCKET NUMBER: DC-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (856) 810-1515
TELEFAX: (865) 810-1454
INFORMATION FOR SEQ ID NO: 64:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 331 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: PN7450
FILING DATE: 8 JAN 1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                      ; LIBRARY: GenBank
; CLONE: 1335856
US-08-878-989-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Amino Acid
                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                              TOPOLOGY: line IMMEDIATE SOURCE:
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US-09-101-146-64
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STATE:
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                                                                                                                          Length 464;
                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 54; DB 4; Length 92;
Pred. No. 1.2;
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                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Edwards, Jean-Baptiste D.
APPLICANT: Duelert, Aymeric
APPLICANT: Lacroix, Bunno
AITLE OF INVENTION: 5' ESTS FOR SECRETED PROTEINS
NUMBER OF SEQUENCES: 503
CORRESPONDENCE ADDRESS:
                                                                                                                        Score 54.5; DB 6;
Pred. No. 6;
2; Mismatches 15;
                                                                                                                                                                                                                                      4 THKRLLKFLHIFGSLLPRPSFLYRTIQDLGIGTFR 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Knobbe, Martens, Olson & Bear STRET: 501 West Broadway CITY: San Diego STATE: California COUWIRY: USA ZIP: 92101-3505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IDENTIFICATION METHOD: Von Heijne matrix
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTHER INFORMATION: SCORE 3.6 OTHER INFORMATION: SEQ ARSLLOFLELUGO/LK US-08-905-223-497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7; Mismatches
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15 RSLLQFLREVGQLKRVPRTGWYRNVQ 41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/905,223
                                                                                                                                                                                                                                                                                                                                                    Sequence 497, Application US/08905223
Patent No. 6222029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550
TELEFAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 497:
SEQUENCE CHARACTERISTICS:
LENGTH: 92 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: RLOPPY DISK
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Win95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Israelsen, Ned A.
REGISTRATION NUMBER: 29,655
  APPLICATION NUMBER: 419,913
FILING DATE: 05-SEP-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 25.4%;
Best Local Similarity 40.7%;
Matches 11; Conservative 7
                                                                                                                        Query Match 25.6%;
Best Local Similarity 48.6%;
Matches 17; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 536
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TISSUE TYPE: Brain
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ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                              LENGTH: 464
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                                             SEQ ID NO:1
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            APPLICANT: Yang, Hong
APPLICANT: Cooley, Michael
APPLICANT: Cooley, Michael
APPLICANT: Cooley, Michael
APPLICANT: Cooley, Michael
APPLICANT: Gee, Oliver
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Regulation of Source-Sink Relationships and Responses
TITLE OF INVENTION: Lo Stress Conditions in Plants
FILE REFERENCE: 023070-0959000S
CURRENT APPLICATION NUMBER: US/09/359,161A
KUNBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: PROTEIN HAVING HUMAN PLASMIN INHIBITING
                                                                                                                                                                                                                                                                                                                                                                                                                                    29.6%; Score 63; DB 4; Length 379; 48.6%; Pred. No. 0.29; arive 5; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;Patent No. 5463025
; APPLICANT: Sumi, Yoshihiko;Ichikawa, Yataro;Aoki, Nobuo
;Muramatsu, Masami
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; APPLICANT: Sumi, Yoshihiko;Ichikawa, Yataro;Aoki, Nobuo;Muramatsu, Masami
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 THKRLLKFLHIFGSLLPRPSFLYRTIQDLGIGTFR 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 ILTHKRLLKFLHIFGSLLPRPSFLYRTIQDLGIGT 36
                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Phaseolus vulgaris L. Pv42 US-09-359-161-5
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/185,162
FILING DATE: 24-JAN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60,691
FILING DATE: 13-MAY-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/185,162
FILING DATE: 24-JAN-1994
FRIOR APPLICATION DATA:
APPLICATION NUMBER: 60,691
FILING DATE: 13-MAY-1993
APPLICATION NUMBER: 419,913
FILING DATE: 05-SEP-1989
                                                                                                                                                                                                                                                                                                                               ORGANISM: Phaseolus vulgaris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 48.65
Matches 17; Conservative
APPLICANT: Dahal, Peetambar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                  SEQ ID NO 5
LENGTH: 379
                                                                                                                                                                                                                                                                                                             TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                      FEATURE:
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5463025-4
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                                                                                                                                                                                                                                                                      Length 483;
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APPLICANT: Eledge, Stephen J.
APPLICANT: Sanchez, Yolanda
TITLE OF INVENTION: MAMMALLAN CHECKPOINT GENES AND PROPEINS
FILE REFERENCE: 12054-1013
CURRENT APPLICATION NUMBER: US/09/488,364
CURRENT FILING DATE: 2000-01-12
NUMBER OF SEQ ID NOS: 15
SOFTWARRE: Patentin Ver. 2.0
SEQ ID NO 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 483;
                                                                                                                                                                                                                                                                                                                                    7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT STRET: 4 Embarcadero Center, Suite 3400 CITE: San Francisco STATE: California COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: INTERLEUKIN-1 RECEPTOR-ASSOCIATED TITLE OF INVENTION: PROTEIN KINASE AND BINDING ASSAY NUMBER OF SEQUENCES: 2 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
2IF: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPOTER: IBM PC compatible
SOFERATIOR SYSTEM: PC-TOOS/MS-TOOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                               Score 49; DB 4;
Pred. No. 38;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 49; DB 4;
Pred. No. 38;
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APPLICATION NUMBER: US/08/587,889
                                                                                                                                                                                                                                                                                                                                                                                                                                    : | | | | | : | | | | : | | | | 19 QPESLYRVVQTLGEGAFGEV 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                :| ||| :| || :| || 13 || :: || 14 || :: || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 ||
                                                                                                                                                                                                                                                                                                                                                                                                  21 RPSFLYRTIQDLGIGTFRDL 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-488-364-9; Sequence 9, Application US/09488364; Sequence 0, Application US/09488364; Patent No. 6307015; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21 RPSFLYRTIQDLGIGTFRDL 40
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Patent No. 5654397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Caenorhabditis elegans US-09-488-364-9
                                                                                                                                                              ) ORGANISM: Caenorhabditis elegans US-08-924-183-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: CAO, Zhaodan
APPLICANT: CROSTON, Glenn E.
APPLICANT: GOEDDEL, David V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23.0%;
                                                                                                                                                                                                                                                               Query Match 23.0%;
Best Local Similarity 45.0%;
Matches 9; Conservative
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Best Local Similarity 45.0%
...ac 9; Conservative
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
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CLASSIFICATION:
                                                                                                LENGTH: 483
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                                                                                                                                      TYPE: PRT
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APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
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                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: FREY, PETTY A.
APPLICANT: RIZICKA, FYZAR, J.
TITLE OF INVENTION: DNA MOLECULES ENCODING BACTERIAL LYSINE 2,3-AMINOMUTASE
FILE REPERENCE: 032026/0476
CURRENT APPLICATION NUMBER: 19599-06-11
CURRENT FILING DATE: 1999-06-11
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Pred. No. 10;
5; Mismatches 12; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Elledge, Stephen J.
APPLICANT: Sanchez, Yolanda
TITLE OF INVENTION: MANALIAN CHECKPOINT GENES AND PROTEINS
FILE REFERENCE: 120541-1003
CURRENT APPLICATION NUMBER: US/08/924,183A
CURRENT FILING DATE: 1997-09-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 ILTHKRLLKFLH------IFGSLLPRPSFLYRTIQDLGIGTF 37
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                                                                                                                                                                                                                                                                                                                                                                                       EARLIER APPLICATION NUMBER: US 09/198,942
EARLIER FILING DATE: 1998-11-24
NUMBER OF SEG ID NOS: 32
SOFTWARE: Patentin Ver. 2.0
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PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 3105
LENGTH: 808
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PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Porphyromonas gingivalis
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                                                       US-09-330-611-8
; Sequence 8, Application US/09330611
; Patent No. 6248874
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Best Local Similarity 40.5%;
Matches 15; Conservative 5
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Best Local Similarity 30.29
Matches 13; Conservative
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US-09-134-001C-3105
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US-08-924-183-9
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June 6, 2003, 11:02:59; Search time 3.37478 Seconds (without alignments) 1254.259 Million cell updates/sec
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1 HILTHKRLLKFLHIFGSLLP......PSFLYRTIQDLGIGTFRDLA
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/cgn2_6/ptodata/2/pubpaa/NET_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/NEO6_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Sequence 6, Appli	Sequence 461, App	Sequence 71, Appl	Sequence 47, Appl	200,	200,	200,	200,	200,	200,	200,		200,	200,	200,	200,	200,	200,	Sequence 200, App
	3 ID	10 US-09-826-581-6	10 US-09-925-297-461	9 US-10-108-605-71	9 US-09-510-332-47	US-10-028-072-200	9 US-10-121-049-200	US-10-123-904-200	9 US-10-140-470-200	9 US-10-175-746-200	9 US-10-176-918-200	9 US-10-176-921-200	9 US-10-137-865-200	9 US-10-140-474-200	9 US-10-142-431-200	3 US-10-143-114-200	US-10-140-002-200	3 US-10-142-419-200	US-10-123-262-200	9 US-10-142-423-200
	Query Match Length DB	489	344	1207	264	1023	1023	1023	1023	1023	1023	1023	1023	1023	1023	1023	1023	1023	1023	1023
æ	Query Match	100.0	52.6	49.3	25.4	24.9	24.9	24.9	24.9	24.9	24.9	24.9	24.9	24.9	24.9	24.9	24.9	24.9	24.9	24.9
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US-10-121-050-2 US-10-141-755-2 US-10-133-108-2 US-10-123-236-2 US-10-123-251-2 US-10-123-251-2 US-10-123-292-2 US-10-121-045-2 US-10-124-819-2 US-10-124-813-2 US-10-121-047-2 US-10-121-047-2 US-10-121-047-2 US-10-123-908-2	NMENT 7,581 65	3; ches QDLG QDLG QDLG ins
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700533333333333333333333333333333333333	on US/098: 310A1 1. Leif 1. Stefan VARIANTS C.500700 5500104 MBER: US (200104 00104 00104 00104 00104 00104 00104	1000 .vative .vative .KFLHIFC
44444444444444444444444444	ULT 1 09-826-581-6 atent No. US2020142310A1 APPLICANT: Andersson, Leif APPLICANT: Luthman, L. Holg APPLICANT: Luthman, L. Holg APPLICANT: AAPLICANON FILE REFERENCE: 11145-007001 CURRENT APPLICATION NUMBER: 2001-0 PRIOR APPLICATION NUMBER: US PRIOR FILING DATE: 2001-0 PRIOR PTLING DATE: 2001-0 PRIOR PTLING DATE: 2000-04-0 BOTHARE: FastSEQ for Window, EQ ID NO 6 IEBNGTH: 489 TYPE: PRI ORGANISM: Homo sapiens	Query Match Best Local Similarity 100.0%; Batches 41; Conservative 0; Matches 1; HILTHKRLIKFLHIFGSLLPR
	SULT 1 -09-826-581-6 Sequence 6, Applicat Sequence 7, Applicat GENERAL INFORMATION: APPLICANT: Anderso APPLICANT: Luthman APPLICANT: Luthman TITLE OF INVENTION: FILE REFERENCE: 111 CURRENT APPLICATION CURRENT APPLICATION FILE REFERENCE: 111 CURRENT FILING DATE PRIOR APPLICATION OF REAL FELING DATE PRIOR APPLICATION OF SOFTWARE: FSSESO 1 SOFTWARE: FSSESO 1 TYPE: PRI ORGANISM: HOMO SAP TYPE: PRI ORGANISM: HOMO SAP	1 1 320 320 320 10 10 10 10 10 10 10 10 10 10 10 10 10
011020202020202020202020202020202020202	RESULT 1 US-09826-58 Sequence 6 Ratent NO. GENERAL NO. GENERAL IN. APPLICANT APPLICANT APPLICANT TITLE OF FILE REFE CURRENT F PRIOR FILE NUMBER OF SOFTWARE: SEQ ID NO LENGTH: TYPE: PROGRIS CORRENT CORRENT F CURRENT F	Query Matches Matches Qy Db RESULT 2 US-09-925; Sequence ; Patent NA GENERAL ; APPLICAN ; TITLE OI ; TITLE

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73 HLYAFNKLIKFIHIFWALTNHLVTWLACCLSVFYFFKIAYFSHPCFIWLRWRISRTLLEL 132
                                                                                                                                                                                                                                                                                                                                                                         1 HILTHKRLIKFLHIFGSL-----RTIQDL 32
                                                                                                                                                                                                                                                                                                                              28; Gaps
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; Pred. No. 10;
11; Mismatches 11; Indels
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CURRENT FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 60/049911
PRIOR PILING DATE: 1997-06-18
PRIOR PLING DATE: 1997-06-18
PRIOR PLING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-17
PRIOR PLICATION NUMBER: 60/059115
PRIOR PLICATION NUMBER: 60/059115
                                                                                                                                                                                       COCATION: (20)
COTHER INFORMATION: Xaa = any amino acid
US-09-510-332-47
                                                                                                                 FEATURE:
OTHER INFORMATION: human T2R26 (hGR26)
NAME/KEY: MOD_RES
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Publication No. US20030004311Al
GENERAL INFORMATION:
APPLICANT: Baker.Kevin P.
APPLICANT: Beresini,Maureen
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PRIOR APPLICATION NUMBER: 60/059122
PRIOR FILING BATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059184
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059263
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PRIOR APPLICATION NUMBER: 60/059588
PRIOR FILING DATE: 1997-09-19
PRIOR APPLICATION NUMBER: 60/059836
PRIOR FILING DATE: 1997-09-24
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PRIOR APPLICATION NUMBER: 60/059352
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21.9%;
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Stewart, Timothy A.
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Goddard, Audrey
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Gurney, Austin L.
Sherwood, Steven
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    PatentIn Ver. 2.1
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Best Local Similarity 21.9%
Matches 14; Conservative
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Filvaroff, Ellen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wood, William
                                                                          TYPE: PRT
ORGANISM: Homo sapiens
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TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33 GIGT 36
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                                                  LENGTH: 264
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APPLICANT:
APPLICANT:
    SOFTWARE: 1
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APPLICANT:
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APPLICANT:
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APPLICANT: Broadus, Julie

APPLICANT: Stam, Lynn

APPLICANT: Randar, Lynn

APPLICANT: Kamdar, Kim

TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FROM DROSOPHILA MELANOGASTER THAT ENCODE

TITLE OF INVENTION: PROTEINS ESSENTIAL FOR LARVAL VIABILITY AND USES THEREOF

FILE REFERENCE: 31133B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 47, Application US/09510332

Publication No. US20030022278A1

GENERAL INFORMATION:
APPLICANT: 2 UREr. Charles S.
APPLICANT: Ryba, Nick
APPLICANT: Ryba, Nick
APPLICANT: The Regents of the University of California
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: TO US20030022278A1e1 Family of Taste Receptors
FILE REFERENCE: 02307E-09801008;
FILE REFERENCE: 02307E-09801008;
CURRENT APPLICATION NUMBER: US/09/510,332
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                                                                                                                                                                                                                                                          Length 344;
                                                                                                                                                                                                                                                                                                        Indels
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                                                                                                                                                                                                                                                          Query Match 52.6%; Score 112; DB 10; Best Local Similarity 46.3%; Pred. No. 1.2e-07; Matches 19; Conservative 14; Mismatches 8;
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CURRENT FILING DATE: 2002-03-27
PRIOR APPLICATION NUMBER: US 09/761,142
PRIOR FILING DATE: 2001-01-16
PRIOR PETLING DATE: 2000-01-14
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PRIOR APPLICATION NUMBER: US 09/393,634
PRIOR FILING DATE: 1999-09-10
NUMBER OF SEQ ID NOS: 172
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
SOFTWARE: PATENTIN VEY: 2.0
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; Patent No. US20020160934A1
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US-10-108-605-71
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SEQ ID NO 71
LENGTH: 1207
TYPE: PRT
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US-09-925-297-461
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                                                                                                                   SEQ ID NO 461
LENGTH: 344
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JUMBER: 60/0622: 1997-10-17 JUMBER: 60/0622: 1997-10-17 JUMBER: 60/0628 JUMBER: 60/0628 JUMBER: 60/0638 JUMBER	NUMBER 1997-	1997-11-24 NUMBER: 60/0667 1997-11-24 NUMBER: 60/0692 1997-12-11 NUMBER: 60/0693 1997-12-11 NUMBER: 60/0693 1997-12-12 1997-12-16 NUMBER: 60/0693 1998-01-23 1998-02-09 NUMBER: 60/0736 1998-02-09 NUMBER: 60/0740 1998-02-09 NUMBER: 60/0740 NUMBER: 60/0740 NUMBER: 60/0740 1998-03-12 NUMBER: 60/0740 1998-03-12 NUMBER: 60/0740 1998-03-12 NUMBER: 60/0793 1998-03-12 NUMBER: 60/0793 1998-03-12 NUMBER: 60/0793
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RAPLICATION NUMBER: 60/082999
RETLING DATE: 1998-04-24
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RETLING DATE: 1998-04-29
RETLING DATE: 1998-04-29
RETLING DATE: 1998-05-07
RETLING DATE: 1998-05-07 RAPLICATION NUMBER: 60/088730
RR PELLING DATE: 1998-06-10
RR PELLING DATE: 1998-06-10
RR PELLING DATE: 1998-06-10
RR APPLICATION NUMBER: 60/088910
RR APPLICATION NUMBER: 60/088810
RR FILING DATE: 1998-06-10
RR FILING DATE: 1998-06-10 DR APPLICATION NUMBER: 60/085704

DR FILING DATE: 1998-05-15

DR APPLICATION NUMBER: 60/086414

DR APPLICATION NUMBER: 60/086430

DR FILING DATE: 1998-05-22

DR FILING DATE: 1998-05-22

DR APPLICATION NUMBER: 60/087106

DR PILING DATE: 1998-05-28

R FILING DATE: 1998-06-07

DR APPLICATION NUMBER: 60/087106

DR APPLICATION NUMBER: 60/087106

DR APPLICATION NUMBER: 60/088026

DR FILING DATE: 1998-06-04 FILING DATE: 1998-02-27 APPLICATION NUMBER: 60/079728 FILING DATE: 1998-03-27 APPLICATION NUMBER: 60/080165 FILING DATE: 1998-03-31 FILING DATE: 1998-05-13
APPLICATION NUMBER: 60/085339
FILING DATE: 1998-05-13
APPLICATION NUMBER: 60/085579
FILING DATE: 1998-05-15 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090445 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090538 APPLICATION NUMBER: 60/081203 FILING DATE: 1998-04-09 APPLICATION NUMBER: 60/081229 FILING DATE: 1998-04-09 APPLICATION NUMBER: 60/081695 FILING DATE: 1998-04-14 APPLICATION NUMBER: 60/081817 FILING DATE: 1998-04-15 APPLICATION NUMBER: 60/081818 FILING DATE: 1998-04-15 APPLICATION NUMBER: 60/085149 FILING DATE: 1998-05-12 APPLICATION NUMBER: 60/085323 FILING DATE: 1998-05-13 APPLICATION NUMBER: 60/085338 FILING DATE: 1998-05-15 APPLICATION NUMBER: 60/085697 FILING DATE: 1998-05-15 APPLICATION NUMBER: 60/089599 FILING DATE: 1998-06-17 APPLICATION NUMBER: 60/089907 FILING DATE: 1998-06-18 60/089947 APPLICATION NUMBER: 60/090349 FILING DATE: 1998-06-23 APPLICATION NUMBER: 60/0 FILING DATE: 1998-06-17 APPLICATION NUMBER: 60/1 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/ FILING DATE: 1998-06-19

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CURRENT FILING DATE: 2002-04-16
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
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                                                                                                                    Stewart, Timothy A.
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Goddard, Audrey
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Watanabe, Colin K
Wood, William
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Wood,William
                                             Godowski, Paul J.
Gurney, Austin L.
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Filvaroff, Ellen
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Sherwood, Steven
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Best Local Similarity 34.13
Matches 14; Conservative
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                                                                                                  Smith, Victoria
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US-10-123-904-200
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Best Local Similarity
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LENGTH: 1023
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APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDE ENCODING THE SAME
FILE REFERENCE: P3330R.C17
CURRENT APPLICATION NUMBER: US/10/121,049
CURRENT FILING DATE: 2002-04-12
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Pred. No. 66;
9; Mismatches 10; Indels
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SEQ ID NO 200
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PRIOR APPLICATION NUMBER: 60/090863
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/091360
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091519
PRIOR APPLICATION NUMBER: 60/091982
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
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Publication No. US20030022239A1
GENERAL INFORMATION:
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Publication No. US20030022328A1
GENERAL INFORMATION:
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34.1%;
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DeForge, Laura
Desnoyers, Luc
Filvaroff, Ellen
Gao, Wei-Qiang
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Watanabe, Colin K
Wood, William
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Gurney, Austin L.
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Best Local Similarity 34.1:
Matches 14; Conservative
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; ORGANISM: Homo Sapien
US-10-121-049-200
                                                                                                                                                                  Query Match
Best Local Similarity
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US-10-121-049-200
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3330R1C2B CURRENT APPLICATION NUMBER: US/10/176,921
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CURRENT FILING DATE: 2002-06-20
PRIOT APPLICATION removed - See File Wrapper or Palm
SEQ ID NO 200
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Pred. No. 66;
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9; Mismatches
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; Publication No. US20030027276A1
; GENERAL INFORMATION:
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34.1%;
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Tumas, Daniel
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Wood,William
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APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
APPLICANT: Pilvaroff, Ellen
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Best Local Similarity 34.1.
...hes 14; Conservative
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Filvaroff, Ellen
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Filvaroff, Ellen
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                                                                                                                          ORGANISM: Homo Sapien US-10-176-918-200
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US-10-176-921-200
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US-10-137-865-200
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                                                                                       LENGTH: 1023
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APPLICANT: Vacanabe, Colin K
APPLICANT: Shang, Zenin
APPLICANT: School Section and Transmembrane Polybeptides and NUCLEIC
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C382
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 2 ILTHKRLLKFLHIFGSLLPRP----SFLYRTIQDLGIGTFR 38
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CURRENT APPLICATION NUMBER: US/10/175,746
CURRENT FILING DATE: 2002-06-19
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Pred. No. (
                                                                                                    Sequence 200, Application US/10175746
Publication No. US20030027270A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
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Stewart, Timothy A.
Tumas, Daniel
Watanabe, Colin K
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34.1%;
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Stewart, Timothy A.
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Best Local Similarity 34.1.,
-t-hes 14; Conservative
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Goddard, Audrey
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APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
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Godowski, Paul J.
Gurney, Austin L.
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Filvaroff, Ellen
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Filvaroff, Ellen
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Sherwood, Steven
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ORGANISM: Homo Sapien
US-10-175-746-200
                                                                    RESULT 9
US-10-175-746-200
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34.1%;
                                                                                                                                           Publication No. US20030036179AI; GENERAL INFORMATION: APPLICANT: Baker, Kevin P.
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Smith, Victoria
Stewart, Timothy A.
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Goddard, Audrey
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Filvaroff, Ellen
Gao, Wei-Qiang
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Wood, William
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APPLICANT: Beresini, Maureen
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Goddard, Audrey
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Filvaroff, Ellen
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ORGANISM: Homo Sapien
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Best Local Similarity
Matches 14; Conserv
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US-10-143-114-200
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APPLICANT: Watanabe, Colin K
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R21G62
                                                                                                                                                                                              APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C15A
CURRENT APPLICATION NUMBER: US/10/137,865
CURRENT FILING DATE: 2002-05-03
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                                Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
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Godowski, Paul J.
Gurney, Austin L.
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Wood, William
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APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
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Smith, Victoria
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Filvaroff, Ellen
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Smith, Victoria
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Gao, Wei-Qiang
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; ORGANISM: Homo Sapien
US-10-140-474-200
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US-10-137-865-200
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APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
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